

XX AC ADD12949;
 XX DT 01-JAN-2004 (first entry)
 XX DE HCV NS3 probe.
 XX KW double-stranded RNA; dsRNA; infection; NS3 helicase; virucide;
 XX KW antiinflammatory; hepatotropic; hepatitis C virus infection; ss; probe.
 XX OS Hepatitis C virus.
 XX FH Key Location/Qualifiers
 XX FT modified_base 1
 XX FT /*tag= a
 XX FT /mod_base= OTHER
 XX FT /note= "FAM labelled"
 XX FT modified_base 30
 XX FT /*tag= b
 XX FT /mod_base= OTHER
 XX FT /note= "TAMRA labelled"
 XX PN WO2003035876-A1.
 XX PD 01-MAY-2003.
 XX KW 25-OCT-2002; 2002WO-EP011973.
 XX PF 26-OCT-2001; 2001DE-01055280.
 XX PR 29-NOV-2001; 2001DE-01058411.
 XX PR 07-DEC-2001; 2001DE-01060151.
 XX PR 09-JAN-2002; 2002WO-EP000151.
 XX PR 09-JAN-2002; 2002WO-EP000152.
 XX PR 02-AUG-2002; 2002DE-01035621.
 XX PA (RIBO-) RIBOPHARMA AG.
 XX PI Krebs A, John M, Schuppan D, Limmer S, Kreutzner R;
 XX WPI; 2003-430419/40.
 XX PT New double-stranded RNA for treating viral infections, useful especially
 XX PT for hepatitis C infection, is complementary to a region of a positive-
 XX PT strand RNA viral genome.
 XX PS Disclosure; SEQ ID NO 5; 35pp; German.
 XX CC This invention describes a novel use of a double-stranded RNA for
 XX CC treating infections by a (+)-strand RNA virus, where one strand (S1) of
 XX CC dsRNA includes a segment that is at least partly complementary to the
 XX CC translatable region of the viral genome. dsRNA is directed against
 XX CC hepatitis C virus (HCV) and inhibits expression of a polyprotein encoded
 XX CC by the viral genome, preferably a protease or helicase and most
 XX CC particularly the NS3 helicase, with the complementary region, in the
 XX CC reading direction of viral RNA, being upstream of, or within, the
 XX CC helicase coding region. dsRNA has, at least one end, an overhang of 1-4,
 XX CC preferably 2-3 nucleotides particularly at the 3'-end of S1. The second
 XX CC strand (S2) of dsRNA contains a 2-nucleotide overhang at the 3'-end of S1
 XX CC but no overhang at the other end (blunt). A single overhang increases
 XX CC inhibitory activity without causing significant loss of in vivo
 XX CC stability. dsRNA is formulated with a conventional solvent (especially
 XX CC phosphate-buffered saline) or it is incorporated into a micellar
 XX CC structure, particularly a liposome, viral capsid, capsoid or a polymeric
 XX CC nano- or micro-capsule (or it is bound to such capsules). The products of
 XX CC the invention have virucide, antiinflammatory and hepatotropic activity.
 XX CC dsRNA is administered by inhalation, infusion or injection, or orally,
 XX CC especially by intravenous or intraperitoneal injection or infusion. dsRNA
 XX CC is specifically used for treatment of hepatitis C virus infections. dsRNA
 XX CC permanently destroys the integrity of the viral genome. HuH-7 cells were
 XX CC transfected with double-stranded RNA (dsRNA), directed against the NS3
 XX CC coding region of the hepatitis C virus (HCV) genome and a fragment of the
 XX CC HCV genome that replicated stably without formation of infectious
 XX CC particles. Transfection with dsRNA resulted in a 60-fold inhibition of

CC viral RNA production, relative to transfection with an irrelevant control
 CC dsRNA. This sequence represents a probe used to detect the HCV NS3 gene.
 XX Sequence 30 BP; 8 A; 8 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 61.0%; Score 12.8; DB 10; Length 30;
 Best Local Similarity 87.5%; Pred. No. 3.2e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CGTACGGTCTAATGAC 19
 |||||
 DB 15 CGGACGCTCTAATGAC 30
 RESULT 12
 ABI95516
 ID ABI95516 standard; DNA; 20 BP.
 XX AC ABI95516;
 XX DT 16-FEB-2002 (first entry)
 XX DE Capture oligonucleotide Zip ID#2603 oligo #9.
 XX KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KW oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 XX OS Synthetic.
 XX PN WO200179548-A2.
 XX PD 25-OCT-2001.
 XX PF 04-APR-2001; 2001WO-US010958.
 XX PR 14-APR-2000; 2000US-0197271P.
 XX PA (CORR) CORNELL RES FOUND INC.
 XX PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 XX WPI; 2002-034366/04.
 XX PT Designing capture oligonucleotide probes for use on a support to which
 XX PT complementary oligonucleotides hybridize with little mismatch.
 XX Example 5; Fig 29; 300pp; English.
 XX The present invention describes a method (M1) for designing capture
 XX oligonucleotide probes (I) for use on a support to which complementary
 XX oligonucleotide probes (II) will hybridize with little mismatch, where
 XX (I) have melting temperatures within a narrow range. The method is useful
 XX for detecting infectious diseases caused by bacterial infectious agents
 XX e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 XX infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 XX Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 XX Epstein-Barr virus and polio virus, and parasitic infectious agents
 XX selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 XX medinis. The method is also useful for detecting genetic diseases such
 XX as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 XX Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 XX involved in DNA amplification, replication, recombination or repair, the
 XX cancer is specifically associated with a gene selected from BRCA1 gene,
 XX p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 XX method is also used for environmental monitoring, forensics and the food
 XX and feed industry, detecting comprises scanning (using e.g. a scanning
 XX electron microscope and infrared microscope) the support at the
 XX particular sites and identifying if ligation of the oligonucleotide probe
 XX seers occurred and correlating (using a computer) identified ligation to a
 XX presence or absence of the target nucleotide sequences. ABI92074 to

CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention

SQ Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 20;
Best Local Similarity 78.9%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCGTACGGTCTAATGACCG 21
|||||
Db 2 GCGTCTGGTCTAGTGACCG 20

RESULT 13

ABI87602

ID ABI87602 standard; DNA; 24 BP.

XX AC ABI87602;

XX DT 15-FEB-2002 (first entry)

XX DE Capture oligonucleotide Zip ID#2603 oligo #1.

XX KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.

XX OS Synthetic.

XX PN WO200179548-A2.

XX XX 25-OCT-2001.

XX PF 04-APR-2001; 2001WO-US010958.

XX PR 14-APR-2000; 2000US-0197271P.

XX XX (CORR) CORNELL RES FOUND INC.

XX PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;

XX DR WPI; 2002-034366/04.

XX PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch.

XX PS Example 5; Fig 25; 300pp; English.

XX The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to

CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention

SQ Sequence 24 BP; 2 A; 5 C; 10 G; 7 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 24;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCGTACGGTCTAATGACCG 21
|||||
Db 2 GCGTCTGGTCTAGTGACCG 20

RESULT 14

ABI87603/c

ID ABI87603 standard; DNA; 24 BP.

XX AC ABI87603;

XX DT 15-FEB-2002 (first entry)

XX DE Capture oligonucleotide Zip ID#2603 oligo #2.

XX KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.

XX OS Synthetic.

XX PN WO200179548-A2.

XX XX 25-OCT-2001.

XX PF 04-APR-2001; 2001WO-US010958.

XX PR 14-APR-2000; 2000US-0197271P.

XX XX (CORR) CORNELL RES FOUND INC.

XX PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;

XX DR WPI; 2002-034366/04.

XX PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch.

XX PS Example 5; Fig 25; 300pp; English.

XX The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to

Query Match 60.0%; Score 12.6; DB 9; Length 25;
 Best Local Similarity 78.9%; Pred. No. 4.1e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCGTACGGTCTTAATGACG 21
 | | | | | | | | | | | | |
 Db 3 GTGTGCGGTCTTAATGACG 21

RESULT 17
 ACI56057/c
 ID ACI56057 standard; DNA; 25 BP.

XX AC ACI56057;

XX DT 13-OCT-2003 (first entry)

XX DE Human microarray DNA oligonucleotide SEQ ID NO 56048.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW Genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX DR WPI; 2003-567953/53.

XX PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.

XX PS Claim 1; SEQ ID NO 56048; 9pp; English.

XX CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 7 A; 5 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 9; Length 25;

Best Local Similarity 78.9%; Pred. No. 4.1e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGGTACGGTCTTAATGAC 19
 | | | | | | | | | | | | |
 Db 24 TCGAACACGGTCTTAATGAC 6

RESULT 18

ACK18839

ID ACK18839 standard; DNA; 25 BP.

XX AC ACK18839;

XX DT 14-OCT-2003 (first entry)

XX DE Human microarray DNA oligonucleotide SEQ ID NO 118820.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW Genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX DR WPI; 2003-567953/53.

XX PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.

XX PS Claim 1; SEQ ID NO 118820; 9pp; English.

XX CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 6 A; 5 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 9; Length 25;

Best Local Similarity 78.9%; Pred. No. 4.1e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTAATGACCG 21
 ||| ||||| ||||| ||
 Db 3 GTGTGCGGTCCAATGACAG 21

RESULT 19
 AAC97127
 ID AAC97127 standard; DNA; 26 BP.
 XX
 AC AAC97127;
 XX
 DT 26-FEB-2001 (first entry)
 DE
 XX
 DE
 XX
 XX Cytochrome b PCR primer: SEQ ID 102.
 XX
 KW Mutation detection; fungi; cytochrome b; strobilurin analogue resistance;
 KW single nucleotide polymorphism; PCR primer; fungal resistance; crop;
 KW fruit; vegetable; ss.
 XX
 OS Venturia inaequalis.
 XX
 PN WO200066773-A2.
 XX
 PD 09-NOV-2000.
 XX
 XX 26-APR-2000; 2000WO-GB001620.
 PF
 XX 30-APR-1999; 95GB-00010100.
 PR 13-MAR-2000; 2000GB-00006004.
 PR 31-MAR-2000; 2000GB-00007901.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 PI Windaes JD, Heaney SP, Renwick A, Whitcombe DM, Little S;
 PI Gibson NJ, Theaker J, Stanger CP;
 XX
 DR WPI; 2001-007234/01.
 XX
 XX Detecting a cytochrome b mutation which leads to resistance to
 PT strobilurin analogs or compounds in the same resistance group in fungal
 PT nucleic acid using a single nucleotide polymorphism detection technique.
 XX
 PS Disclosure; Page 35; 173pp; English.
 XX
 CC The present invention relates to a method for detecting mutations in
 CC fungal cytochrome b coding sequences which give rise to resistance to
 CC strobilurin analogues. The method uses a single nucleotide polymorphism
 CC (SNP) detection technique. The present sequence is a PCR primer used in
 CC the method of the present invention. The method is suitable for
 CC monitoring fungal resistance to a strobilurin analogue or a compound in
 CC the same cross resistance group in crops such as cereals, fruit and
 CC vegetables such as canola, sunflower, tobacco, sugarbeet, cotton, soya,
 CC maize, wheat, barley, rice, sorghum, tomatoes, mangoes, peaches, apples,
 CC pears, strawberries, bananas, melons, potatoes and carrot
 XX
 SQ Sequence 26 BP; 7 A; 4 C; 8 G; 7 T; 0 U; 0 Other;
 Query Match 60.0%; Score 12.6; DB 4; Length 26;
 Best Local Similarity 78.9%; Pred. No. 4.1e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GCGTACGGTCTAATGACC 20
 ||| ||||| ||||| ||
 Db 2 CGTGTATGTCATGACC 20

RESULT 20
 AAZ50914
 ID AAZ50914 standard; DNA; 31 BP.
 XX
 AC AAZ50914;
 XX

DT 31-MAY-2000 (first entry)
 XX
 DE PCR primer RO204 to amplify Ptac promoter.
 XX
 KW Plasmid pRAB-84-69; recombinant; beta-casein; PCR primer; Ptac promoter;
 KW casein kinase II alpha subunit; casein kinase II beta subunit;
 KW kanamycin resistance marker; iminopeptidase; genetic stability;
 KW pharmaceutical; nutritional composition; vaccine formulation; ss.
 XX
 OS Unidentified.
 XX
 PN WO200008174-A1.
 XX
 PD 17-FEB-2000.
 XX
 PF 06-AUG-1999; 99WO-US017873.
 XX
 PR 07-AUG-1998; 98US-00131028.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 XX Mukerji P, Lemmel SA, Leonard AE, Chaudhary S;
 PI
 XX WPI; 2000-205721/18.
 DR
 XX Recombinant construct useful for producing human milk protein, edible
 PT plant protein, antibody, antigen or hormone, comprises nucleotide
 PT sequences expressing beta-casein protein.
 XX
 PS Example 1; Page 11; 73pp; English.
 XX
 CC The patent discloses a method of producing human milk protein, edible
 CC plant protein, antibody or an antigen in a host cell. It involves
 CC transforming host cells with a vector comprising the gene of interest
 CC linked to a promoter and nucleotide sequences encoding subunits of a
 CC kinase, resistance marker and a peptidase. This method is useful for
 CC improving the genetic stability of a plasmid-containing cell during
 CC fermentation. Proteins produced may be used in pharmaceutical or
 CC nutritional compositions and in vaccine formulations. The present
 CC sequence is that of PCR primer RO204, used to amplify Ptac promoter with
 CC multiple cloning site and rrmB1B2 terminator from plasmid pKK223-3. The
 CC PCR product is used for construction of plasmid pRAB-84-69. pRAB-84-69
 CC construct comprises genes encoding human beta-casein, casein kinase II
 CC alpha and beta subunits, bacterial kanamycin resistance marker and
 CC iminopeptidase
 XX
 SQ Sequence 31 BP; 7 A; 6 C; 9 G; 9 T; 0 U; 0 Other;
 Query Match 60.0%; Score 12.6; DB 3; Length 31;
 Best Local Similarity 78.9%; Pred. No. 4.2e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTAATGACCG 21
 ||| ||||| ||||| ||
 Db 12 GAGTACTGTCTCATGACCG 30

RESULT 21
 AAT04264
 ID AAT04264 standard; DNA; 33 BP.
 XX
 AC AAT04264;
 XX
 DT 16-APR-1996 (first entry)
 XX
 DE Primer #259 for IA beta chain gene.
 XX
 KW Polymerase chain reaction; PCR; primer; amplify;
 KW major histocompatibility complex; MHC; T-cell receptor; TCR;
 KW autoimmune disease; immunodeficiency disease; immune response;
 KW immunoproliferation disease; graft-host rejection; therapy; ss.
 XX
 OS Synthetic.

KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
KW amberyze; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; anti-HCV;
KW viral replication; degenerative; disease state; HBV infection;
KW HCV infection; cirrhosis; liver failure; hepatocellular carcinoma;
KW hepatotropic; cytostatic; virucide; antiinflammatory; ss.
XX
OS Hepatitis C virus.
XX
XX WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
XX WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Claim 1; Page 322; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberyze, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents one of the anti-HCV nucleic
CC acid molecules disclosed in the present invention
XX
SQ Sequence 36 BP; 10 A; 6 C; 14 G; 0 T; 5 U; 1 Other;
Query Match 60.0%; Score 12.6; DB 8; Length 36;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TCGCGTACGGTCTAATGACC 20
||| | | | | | | | |
DB 34 TGCNNTCGGCCTAAGCGCC 15
RESULT 24
ACN19551

ACN19551 standard; RNA; 37 BP.
XX
AC ACN19551;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV Zinzyme SEQ ID NO 19567.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberyze; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV). useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 24; SEQ ID NO 19567; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberyze and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 37 BP; 11 A; 8 C; 13 G; 0 T; 5 U; 0 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 37;
Best Local Similarity 57.9%; Pred. No. 4.3e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 CGCGTACGGTCTAATGACC 20
||| | | | | | | | |
DB 18 CGAGUGAGGUCUAGUGACC 36
RESULT 25
ACN31602
ID ACN31602 standard; RNA; 37 BP.
XX
AC ACN31602;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV minus strand Zinzyme SEQ ID NO 31618.

```
XX NNW; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
DR WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 24; SEQ ID NO 31618; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 37 BP; 9 A; 9 C; 13 G; 0 T; 6 U; 0 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 37;
Best Local Similarity 57.9%; Pred. No. 4.3e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 CGCGTACGGTCTAATGACC 20
DB 18 CGAGUGAGGUCUAGUGACC 36
RESULT 26
ACN19001
ID ACN19001 standard; RNA; 37 BP.
XX
AC ACN19001;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV Zinzyme SEQ ID NO 19017.
XX
XX NNW; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
```

```
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
DR WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 24; SEQ ID NO 19017; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 37 BP; 10 A; 6 C; 15 G; 0 T; 6 U; 0 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 37;
Best Local Similarity 57.9%; Pred. No. 4.3e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 CGCGTACGGTCTAATGACC 20
DB 18 CGAGUGAGGUCUAGUGACC 36
RESULT 27
ACAO7993
ID ACA07993 standard; RNA; 37 BP.
XX
AC ACA07993;
XX
DT 03-JUN-2003 (first entry)
XX
DE Necrosis factor kappa B (NFkB) sub-unit modulating zinzyme #97.
XX
KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; lung cancer;
KW prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
KW stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
KW head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
KW multitdrug resistant cancer; REL-A-specific inhibitor; chemotherapy;
KW paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide;
KW doxorubin; fluorouracil carboplatin; edatrexate; gemcitabine;
KW radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
```

XX OS Synthetic.

XX PN US2002177568-A1.

XX XX 28-NOV-2002.

XX PD

XX XX 23-MAY-2001; 2001US-00864785.

XX PF 07-DEC-1992; 92US-00987132.

XX PR 18-MAY-1994; 94US-00245466.

XX PR 15-AUG-1994; 94US-00291932.

XX PR 23-DEC-1996; 96US-00777916.

XX XX

XX PA (STIN/) STINCHOMB D T.

XX PA (MCSW/) MCSWIGGEN J.

XX PA (DRAP/) DRAPER K G.

XX XX

XX STinchomb DT, Mcswiggen J, Draper KG;

XX WPI; 2003-340953/32.

XX XX

XX Novel enzymatic nucleic acid molecules which down regulates expression of

XX PT a sequence encoding a subunit of nuclear factor kappa B useful for

XX PT treating cancer, inflammatory disorders and autoimmune diseases.

XX XX

XX Claim 2; Page 39; 72pp; English.

XX XX

XX The invention describes an enzymatic nucleic acid molecule (I) which down

XX CC regulates expression of a sequence encoding a subunit of nuclear factor

XX CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme

XX CC configuration. The enzymatic nucleic acid molecule is adapted to treat

XX CC cancer and is useful for down-regulating REL-A activity in a cell, for

XX CC treating a patient having a condition associated with the level of REL-A.

XX CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in

XX CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and

XX CC antisense nucleic acid molecules are useful for treating breast, lung,

XX CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,

XX CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or

XX CC multidrug resistant cancer. The method involves use of other drug

XX CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or

XX CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,

XX CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,

XX CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic

XX CC acid molecules are also useful for treating inflammatory disease such as

XX CC rheumatoid arthritis, testenosis, asthma, Crohn's disease, diabetes,

XX CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft

XX CC rejection, gene therapy applications, ischaemia/reperfusion injury

XX CC (central nervous system (CNS) and myocardial), glomerulonephritis,

XX CC sepsis, allergic airway inflammation, inflammatory bowel disease or

XX CC infection. This sequence represents an enzymatic nucleic acid used to

XX CC modulate the function of a necrosis factor kappa B sub-unit

XX SQ Sequence 37 BP; 11 A; 9 C; 13 G; 0 T; 4 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 8; Length 37;

Best Local Similarity 57.9%; Pred. No. 4.3e+03;

Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTATGACC 20

DB 18 CGAGUGAGGUCUAAUGGCC 36

RESULT 28

ABK04673/c

ID ABK04673 standard; RNA; 38 BP.

XX AC

XX ABK04673;

XX DT 12-MAR-2002 (first entry)

XX DE Human NOGO Inozyme substrate sequence #150.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW parkinson's disease; ataxia; Huntington's disease; substrate sequence;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX OS Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US004273.

XX PR 11-FEB-2000; 2000US-0181797P.

XX PR 28-FEB-2000; 2000US-0185516P.

XX PR 06-MAR-2000; 2000US-0187128P.

XX XX

XX (RIBO-) RIBOZYME PHARM INC.

XX PA (BLAT/) BLATT L.

XX PA (MCSW/) MCSWIGGEN J.

XX PA (CHOW/) CHOWKIRA B M.

XX PI

XX Blatt L, Mcswiggen J, Chowkira BM;

XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

XX constructs, which down regulate expression of a CD20 gene or neurite

XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

XX central nervous system injury.

XX Claim 89; Page 80; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates

XX expression of a CD20 gene and a nucleic acid molecule which down

XX regulates expression of a neurite growth inhibitor gene (NOGO). The

XX nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

XX DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule

XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or

XX an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

XX with a VGY motif). The CD20-targeting nucleic acid is used to cleave RNA

XX of CD20 in the presence of a divalent cation that is preferably Mg²⁺.

XX Furthermore, it may be contacted with a cell to reduce CD20 activity of

XX the cell and treat a patient having a condition associated with the level

XX of CD20. The treatment may further comprise the use of one or more

XX therapies. In particular, the CD20 targeting nucleic acid may be used to

XX treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

XX Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

XX leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

XX lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

XX immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

XX targeting nucleic acid is used to cleave RNA of the NOGO gene in the

XX presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

XX nucleic acid may be contacted with a cell to reduce NOGO activity of the

XX cell and treat a patient having a condition associated with the level of

XX NOGO. The treatment may further comprise the use of one or more

XX therapies. In particular, the NOGO-targeting nucleic acid may be used to

XX treat central nervous system (CNS) injury and cerebrovascular accident

XX (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

XX chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

XX Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

XX disease, muscular dystrophy, and/or other neurodegenerative disease

XX states which respond to the modulation of NOGO expression. The present

CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human NOGO sequence
 XX
 SQ Sequence 38 BP; 9 A; 8 C; 14 G; 0 T; 6 U; 1 Other;
 Query Match 60.0%; Score 12.6; DB 4; Length 38;
 Best Local Similarity 75.0%; Pred. No. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TCGCGTACGGTCTAATGACC 20
 ||||| ||||| ||||| ||||| |||||
 Db 35 TCGCNTTCGGCCTAACGGCC 16
 RESULT 29
 ABK04649/C
 ID ABK04649 standard; RNA; 38 BP.
 XX
 AC ABK04649;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Inozyme substrate sequence #126.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 XX
 XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;
 XX
 XX WPI; 2001-607195/69.
 XX
 DR Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX Claim 89; Page 80; 200pp; English.
 PS
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targetting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human NOGO sequence
 XX
 SQ Sequence 38 BP; 6 A; 12 C; 14 G; 0 T; 5 U; 1 Other;
 Query Match 60.0%; Score 12.6; DB 4; Length 38;
 Best Local Similarity 75.0%; Pred. No. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TCGCGTACGGTCTAATGACC 20
 ||||| ||||| ||||| ||||| |||||
 Db 35 TCGCNTTCGGCCTAACGGCC 16
 RESULT 30
 ABQ72447
 ID ABQ72447 standard; DNA; 38 BP.
 XX
 AC ABQ72447;
 XX
 DT 30-AUG-2002 (first entry)
 XX
 DE PCR primer MKV24 for ScFv and Fab library generation.
 XX
 XX PCR; primer; replicable genetic package; phage display; scFv; Fab;
 KW heavy chain variable region; light chain variable region; HP6002; HP6025;
 KW HP6054; ss.
 XX
 OS Synthetic.
 XX
 PN WO200194950-A2.
 XX
 PD 13-DEC-2001.
 XX
 XX 05-JUN-2001; 2001WO-US018421.
 XX
 XX 05-JUN-2000; 2000US-0209503P.
 PR 04-JUN-2001; 2001US-00874547.
 XX
 XX (ZYOM-) ZYOMYX INC.
 PA
 XX Nock S, Kassner PD;
 PI
 XX WPI; 2002-519063/55.
 DR
 XX Screening phase displayed peptides, for obtaining a replicable genetic
 PT package (RGP) that displays a fusion protein that binds to a target
 PT molecule, comprises contacting the molecule with an uncleared cell
 PT culture comprising the RGPs.
 PT
 XX

PS Example 1; Page 20; 39pp; English.

XX The present invention relates to a method for screening replicable

CC genetic packages (RGP) to obtain RGP that display on their surface a

CC fusion protein that specifically binds to a target molecule. The method

CC comprises contacting a target molecule with an uncloned cell culture

CC having: (i) RGP, each displaying a fusion protein having a surface-

CC displayed RGP polypeptide and a potential binding polypeptide; and (ii)

CC cells in which RGP were amplified. Phage displaying antibody fragments

CC scfvs or Fabs were generated by PCR amplification of cDNA corresponding

CC to the heavy and light chain variable regions from the HP6002, HP6025,

CC and HP6054 hybridomas. The regions were amplified using the PCR primers

CC ABQ72365-ABQ72448

XX

SQ Sequence 38 BP; 8 A; 13 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 78.9%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 CGCGTACGGTCTAATGACC 20

||||| ||| ||| ||| |||

Db 12 CGCGACATTGTAATGACC 30

RESULT 31

ABK20307/c

ID ABK20307 standard; RNA; 38 BP.

XX

AC ABK20307;

DT

DT 09-APR-2002 (first entry)

XX

DE Human ERG inozyme, Seq ID No 2954.

XX

KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;

KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;

KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;

KW tumour angiogenesis; diabetic retinopathy; macular degeneration;

KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;

KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;

KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;

KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;

XX

OS Homo sapiens.

XX

PN WO200188124-A2.

XX

XX 22-NOV-2001.

XX

PF 16-MAY-2001; 2001WO-US015866.

XX

PR 16-MAY-2000; 2000US-00572021.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (GLAX) GLAXO GROUP LTD.

XX

PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;

XX

DR WPI; 2002-082995/11.

XX

PT Novel polynucleotide which down regulates expression of Ets-related gene,

PT useful for treating cancer, diabetic retinopathy, macular degeneration,

PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

XX

PS Claim 5; Page 74; 149pp; English.

XX

CC The invention relates to a nucleic acid molecule (I) which down regulates

CC expression of an Ets-related gene (ERG). (I) is useful for treating

CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,

CC tumour angiogenesis, diabetic retinopathy, macular degeneration,

CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca

CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge

CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu

CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for

CC treating a patient having a condition associated with the level of ERG,

CC by contacting cells of the patient with (I) under conditions suitable for

CC the treatment. The method comprises the use of one or more therapies

CC under conditions suitable for the treatment. Leukaemia or tumour

CC angiogenesis is treated by administering (I) to the patient in

CC conjunction with one or more of other therapies such as radiation or

CC chemotherapy treatment. (I) is useful for reducing ERG activity in a

CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of

CC ERG gene, by contacting (I) with RNA, in the presence of a divalent

CC cation such as Mg2+. (I) is useful for diagnosis of conditions and

CC diseases related to the expression of ERG, and as diagnostic tool to

CC examine genetic drift and mutations within diseased cells or to detect

CC the presence of ERG RNA in a cell. (I) is useful for specifically

CC targeting genes that share homology with ERG gene or ERG fusion genes.

CC ABK17354-ABK22719 represent nucleic acids, including antisense and

CC enzymatic nucleic acid molecules which regulate expression of ERG, and

CC related PCR primers of the invention

XX

SQ Sequence 38 BP; 7 A; 10 C; 14 G; 0 T; 6 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 75.0%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 TCGCGTACGGTCTAATGACC 20

||||| ||| ||| ||| |||

Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 32

ABK20420/c

ID ABK20420 standard; RNA; 38 BP.

XX

AC ABK20420;

XX

DT 09-APR-2002 (first entry)

XX

DE Human ERG inozyme, Seq ID No 3067.

XX

KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;

KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;

KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;

KW tumour angiogenesis; diabetic retinopathy; macular degeneration;

KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;

KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;

KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;

KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;

XX

OS Homo sapiens.

XX

PN WO200188124-A2.

XX

XX 22-NOV-2001.

XX

PF 16-MAY-2001; 2001WO-US015866.

XX

PR 16-MAY-2000; 2000US-00572021.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (GLAX) GLAXO GROUP LTD.

XX

PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;

XX

DR WPI; 2002-082995/11.

XX

PT Novel polynucleotide which down regulates expression of Ets-related gene,

PT useful for treating cancer, diabetic retinopathy, macular degeneration,

PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

XX

PS Claim 5; Page 76; 149pp; English.

XX The invention relates to a nucleic acid molecule (I) which down regulates

CC expression of an Ets-related gene (ERG). (I) is useful for treating

CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,

CC tumour angiogenesis, diabetic retinopathy, macular degeneration,

CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca

CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge

CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu

CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for

CC treating a patient having a condition associated with the level of ERG,

CC by contacting cells of the patient with (I) under conditions suitable for

CC the treatment. The method comprises the use of one or more therapies

CC under conditions suitable for the treatment. Leukaemia or tumour

CC angiogenesis is treated by administering (I) to the patient in

CC conjunction with one or more of other therapies such as radiation or

CC chemotherapy treatment. (I) is useful for reducing ERG activity in a

CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of

CC ERG gene, by contacting (I) with RNA, in the presence of a divalent

CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and

CC diseases related to the expression of ERG, and as diagnostic tool to

CC examine genetic drift and mutations within diseased cells or to detect

CC the presence of ERG RNA in a cell. (I) is useful for specifically

CC targeting genes that share homology with ERG gene or ERG fusion genes.

CC ABK17354-ABK22719 represent nucleic acids, including antisense and

CC enzymatic nucleic acid molecules which regulate expression of ERG, and

CC related PCR primers of the invention

XX Sequence 38 BP; 8 A; 6 C; 15 G; 0 T; 8 U; 1 Other;

SQ

Query Match 60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 75.0%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20

||||| ||||| ||||| |||||

Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 33

ABK58655/c

ID ABK58655 standard; RNA; 38 BP.

XX

AC ABK58655;

XX

DT 02-JUL-2002 (first entry)

XX

DE Human CLCA1 gene enzymatic nucleic acid #3026.

XX

Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;

KW antinflammatory; chronic obstructive pulmonary disease; COPD; asthma;

KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;

KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;

KW acetylcysteine.

XX

OS Homo sapiens.

XX

PN WO200211674-A2.

XX

PD 14-FEB-2002.

XX

PF 09-AUG-2001; 2001WO-US024970.

XX

PR 09-AUG-2000; 2000US-0224383P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTEX USA LLC.

PA (THOM/) THOMPSON J.

XX

PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

PI Grupe A;

XX

DR WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride

PT channel calcium activated gene, useful for treating Chronic obstructive

PT pulmonary disease (COPD), chronic bronchitis and asthma.

XX

PS Claim 5; Page 71; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down

CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes

CC by cleaving RNA derived from the genes. The nucleic acid sequences are

CC useful as pharmaceutical agents for treating conditions such as chronic

CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic

CC fibrosis, obstructive bowel syndrome and any other diseases or conditions

CC that are related to or will respond to the levels of CLCA1 in a cell or

CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,

CC hence, are useful for treatment of a patient having a condition

CC associated with the level of CLCA1, where the invention further comprises

CC the use of one or more therapies under conditions suitable for the

CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,

CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The

CC nucleic acids of the invention are also used as diagnostic tools to

CC examine genetic drift and mutations within diseased cells or to detect

CC the presence of CLCA1 RNA in a cell. This sequence represents an

CC enzymatic nucleic acid molecule of the invention

XX

SQ Sequence 38 BP; 8 A; 7 C; 12 G; 0 T; 10 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 75.0%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20

||||| ||||| ||||| |||||

Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 34

ABK58826/c

ID ABK58826 standard; RNA; 38 BP.

XX

AC ABK58826;

XX

DT 02-JUL-2002 (first entry)

XX

DE Human CLCA1 gene enzymatic nucleic acid #3197.

XX

Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;

KW antinflammatory; chronic obstructive pulmonary disease; COPD; asthma;

KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;

KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;

KW acetylcysteine.

XX

OS Homo sapiens.

XX

PN WO200211674-A2.

XX

PD 14-FEB-2002.

XX

PF 09-AUG-2001; 2001WO-US024970.

XX

PR 09-AUG-2000; 2000US-0224383P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTEX USA LLC.

PA (THOM/) THOMPSON J.

XX

PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

PI Grupe A;

XX

DR WPI; 2002-217145/27.

XX

PT Enzymatic polynucleotide that down regulates expression of chloride

PT channel calcium activated gene, useful for treating Chronic obstructive

PT pulmonary disease (COPD), chronic bronchitis and asthma.

PS Claim 5; Page 76; 152pp; English.

CC The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention

XX Sequence 38 BP; 9 A; 9 C; 12 G; 0 T; 7 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 75.0%; Pred. NO. 4.3e+03;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20

Db 35 TCGCNTTCGGCCTAACGCC 16

RESULT 35

ACN17900/c

ID ACN17900 standard; RNA; 38 BP.

AC ACN17900;

DT 22-APR-2004 (first entry)

DE WNV Inozyme SEQ ID NO 17916.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme; Amberzyme; Zinzyne; ss.

OS West Nile Virus.

FN WO200268637-A2.

XX 06-SEP-2002.

PF 19-OCT-2001; 2001WO-US048350.

PR 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

DR WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 24; SEQ ID NO 17916; 495pp; English.

XX

CC The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX Sequence 38 BP; 7 A; 9 C; 12 G; 0 T; 9 U; 1 Other;

Query Match

60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 75.0%; Pred. NO. 4.3e+03;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20

Db 35 TCGCNTTCGGCCTAACGCC 16

RESULT 36

ACN17240/c

ID ACN17240 standard; RNA; 38 BP.

AC ACN17240;

DT 22-APR-2004 (first entry)

DE WNV Inozyme SEQ ID NO 17243.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme; Amberzyme; Zinzyne; ss.

OS West Nile Virus.

FN WO200268637-A2.

XX 06-SEP-2002.

PF 19-OCT-2001; 2001WO-US048350.

PR 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

DR WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 24; SEQ ID NO 17243; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The

CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX
SQ Sequence 38 BP; 6 A; 6 C; 15 G; 0 T; 10 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 37

ACN16711/c
ID ACN16711 standard; RNA; 38 BP.

XX ACN16711;

DT 22-APR-2004 (first entry)

XX WNV Inozyme SEQ ID NO 16714.

DE WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

OS WO200268637-A2.

XX 06-SEP-2002.

PF 19-OCT-2001; 2001WO-US048350.

PR 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

PI WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 24; SEQ ID NO 16714; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX
SQ Sequence 38 BP; 9 A; 11 C; 11 G; 0 T; 6 U; 1 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 38

ACN30373/c

ID ACN30373 standard; RNA; 38 BP.

XX ACN30373;

DT 22-APR-2004 (first entry)

XX WNV minus strand Inozyme SEQ ID NO 30389.

DE WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

OS WO200268637-A2.

XX 06-SEP-2002.

PF 19-OCT-2001; 2001WO-US048350.

PR 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

PI WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 24; SEQ ID NO 30389; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX Sequence 38 BP; 8 A; 9 C; 13 G; 0 T; 7 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACC 20
 Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 39

ACN29690/C
 ID ACN29690 standard; RNA; 38 BP.

XX AC ACN29690;
 XX 22-APR-2004 (first entry)
 XX WNV minus strand Inozyme SEQ ID NO 29706.
 DE WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.

XX OS West Nile Virus.

XX PN WO200268637-A2.

XX PD 06-SEP-2002.

XX PF 19-OCT-2001; 2001WO-US048350.

XX PR 20-OCT-2000; 2000US-0242411P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (BLAT/) BLATT L.

XX PA (MCSW/) MCSWIGGEN J A.

XX PI Blatt L, Mcswiggen JA;

XX DR WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 24; SEQ ID NO 29706; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX SQ Sequence 38 BP; 7 A; 11 C; 13 G; 0 T; 6 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;
 Best Local Similarity 75.0%; Pred. No. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACC 20
 Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 40

ACN27931/C

ID ACN27931 standard; RNA; 38 BP.

XX ACN27931;

XX 22-APR-2004 (first entry)

XX WNV minus strand Inozyme SEQ ID NO 27947.

DE WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.

XX OS West Nile Virus.

XX PN WO200268637-A2.

XX PD 06-SEP-2002.

XX PF 19-OCT-2001; 2001WO-US048350.

XX PR 20-OCT-2000; 2000US-0242411P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (BLAT/) BLATT L.

XX PA (MCSW/) MCSWIGGEN J A.

XX PI Blatt L, Mcswiggen JA;

XX DR WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 24; SEQ ID NO 27947; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX SQ Sequence 38 BP; 11 A; 8 C; 12 G; 0 T; 6 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;
 Best Local Similarity 75.0%; Pred. No. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACC 20
 Db 35 TCGCNTTCGGCCTAACGGCC 16

Search completed: November 23, 2004, 17:27:31
 Job time : 131.708 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 24.3034 Seconds
(without alignments)
614.177 Million cell updates/sec

Title: US-10-087-631B-2

Perfect score: 21

Sequence: 1 tcgcgtacggctaatgacgc 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents_NA.*

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.2	62.9	35	US-09-056-052-12	Sequence 12, Appl
2	13.2	62.9	39	US-09-056-052-13	Sequence 13, Appl
3	12.6	60.0	31	US-09-131-028A-17	Sequence 17, Appl
4	12.6	60.0	33	US-08-207-481-29	Sequence 29, Appl
5	12.6	60.0	33	PCT-US95-02689-31	Sequence 31, Appl
C 6	12.6	60.0	38	US-09-371-772B-11935	Sequence 11935, A
C 7	12.6	60.0	38	US-09-371-772B-13181	Sequence 13181, A
C 8	12.6	60.0	38	US-09-371-772B-13811	Sequence 13811, A
9	12.6	60.0	38	US-09-874-547-83	Sequence 83, Appl
10	12.4	59.0	38	US-08-373-124A-1680	Sequence 1680, Ap
11	12.4	59.0	38	US-08-435-628-1680	Sequence 1680, Ap
12	12.2	58.1	20	US-09-198-452A-4954	Sequence 4954, Ap
13	12.2	58.1	21	5451502-8	Patent No. 5451502
C 14	12.2	58.1	41	US-09-313-221A-19	Sequence 19, Appl
C 15	12	57.1	25	US-08-860-882A-75	Sequence 75, Appl
C 16	12	57.1	25	US-09-011-769A-61	Sequence 61, Appl
C 17	12	57.1	29	US-09-814-351-25	Sequence 25, Appl
C 18	12	57.1	32	US-09-709-103-34	Sequence 34, Appl
C 19	12	57.1	32	US-09-439-410A-34	Sequence 34, Appl
C 20	12	57.1	38	US-09-371-772B-7357	Sequence 7357, Ap
C 21	12	57.1	38	US-09-371-772B-7797	Sequence 7797, Ap
C 22	12	57.1	38	US-09-371-772B-8104	Sequence 8104, Ap
C 23	12	57.1	38	US-09-371-772B-8341	Sequence 8341, Ap
C 24	12	57.1	38	US-09-371-772B-9392	Sequence 9392, Ap
C 25	12	57.1	38	US-09-371-772B-9781	Sequence 9781, Ap
C 26	12	57.1	38	US-09-371-772B-9974	Sequence 9974, Ap
C 27	12	57.1	38	US-09-371-772B-10321	Sequence 10321, A

C 28	12	57.1	38	4	US-09-371-772B-10352	Sequence 10352, A
C 29	12	57.1	38	4	US-09-371-772B-10512	Sequence 10512, A
C 30	11.6	55.2	20	3	US-09-172-045-20	Sequence 20, Appl
C 31	11.6	55.2	20	4	US-09-342-325C-20	Sequence 20, Appl
C 32	11.6	55.2	35	3	US-09-056-052-10	Sequence 10, Appl
C 33	11.6	55.2	37	4	US-10-009-332-10	Sequence 10, Appl
C 34	11.6	55.2	38	4	US-09-371-772B-11413	Sequence 11413, A
C 35	11.6	55.2	38	4	US-09-371-772B-12074	Sequence 12074, A
C 36	11.6	55.2	38	4	US-09-371-772B-12155	Sequence 12155, A
C 37	11.6	55.2	38	4	US-09-371-772B-12380	Sequence 12380, A
C 38	11.6	55.2	38	4	US-09-371-772B-12396	Sequence 12396, A
C 39	11.6	55.2	38	4	US-09-371-772B-13189	Sequence 13189, A
C 40	11.6	55.2	38	4	US-09-371-772B-13450	Sequence 13450, A
C 41	11.6	55.2	39	3	US-09-056-052-11	Sequence 11, Appl
C 42	11.6	55.2	39	3	US-09-198-955A-26	Sequence 26, Appl
C 43	11.6	55.2	39	3	US-09-694-531-26	Sequence 26, Appl
C 44	11.6	55.2	39	4	US-10-072-152-26	Sequence 26, Appl
C 45	11.4	54.3	27	4	US-09-877-243A-11	Sequence 11, Appl
C 46	11.4	54.3	27	4	US-09-877-243A-12	Sequence 12, Appl
C 47	11.4	54.3	28	3	US-09-518-386B-31	Sequence 31, Appl
C 48	11.4	54.3	37	2	US-08-527-060-30	Sequence 30, Appl
C 49	11.4	54.3	43	1	US-08-616-133-5	Sequence 5, Appl
C 50	11.4	54.3	43	1	US-08-802-985-5	Sequence 5, Appl
C 51	11.4	54.3	44	1	US-08-452-083-17	Sequence 17, Appl
C 52	11.4	54.3	44	1	US-08-452-083-18	Sequence 18, Appl
C 53	11.2	53.3	28	2	US-08-781-620B-14	Sequence 14, Appl
C 54	11.2	53.3	31	3	US-08-860-904-23	Sequence 23, Appl
C 55	11.2	53.3	31	3	US-08-679-645-388	Sequence 388, Ap
C 56	11.2	53.3	34	3	US-09-205-114-3	Sequence 3, Appl
C 57	11.2	53.3	34	4	US-10-038-520-3	Sequence 3, Appl
C 58	11.2	53.3	38	4	US-08-874-547-65	Sequence 55, Appl
C 59	11.2	53.3	42	2	US-08-343-443B-55	Sequence 55, Appl
C 60	11.2	53.3	48	6	5240845-9	Patent No. 5240845
C 61	11.2	53.3	48	6	5240845-10	Patent No. 5240845
C 62	11	52.4	17	3	US-08-584-040-8046	Sequence 8046, Ap
C 63	11	52.4	17	3	US-08-584-040-8047	Sequence 8047, Ap
C 64	11	52.4	17	4	US-09-371-772B-3829	Sequence 3829, Ap
C 65	11	52.4	17	4	US-09-371-772B-3830	Sequence 3830, Ap
C 66	11	52.4	20	4	US-09-422-978-6875	Sequence 6875, Ap
C 67	11	52.4	20	4	US-09-198-452A-5503	Sequence 5503, Ap
C 68	11	52.4	22	4	US-10-270-313-4	Sequence 4, Appl
C 69	11	52.4	24	2	US-08-324-003A-6	Sequence 6, Appl
C 70	11	52.4	24	2	US-08-324-003A-7	Sequence 7, Appl
C 71	11	52.4	24	3	US-08-937-993-44	Sequence 44, Appl
C 72	11	52.4	24	4	US-09-755-836-6	Sequence 6, Appl
C 73	11	52.4	24	4	US-09-755-836-7	Sequence 7, Appl
C 74	11	52.4	32	4	US-09-527-073-15	Sequence 15, Appl
C 75	11	52.4	36	2	US-08-709-874A-29	Sequence 29, Appl
C 76	11	52.4	36	2	US-08-897-340-8	Sequence 8, Appl
C 77	11	52.4	36	3	US-09-252-329-8	Sequence 29, Appl
C 78	11	52.4	36	3	US-09-104-382-29	Sequence 29, Appl
C 79	11	52.4	36	4	US-09-833-555-29	Sequence 29, Appl
C 80	11	52.4	37	4	US-09-629-732-12	Sequence 12, Appl
C 81	11	52.4	38	4	US-09-371-772B-7156	Sequence 7156, Ap
C 82	11	52.4	38	4	US-09-371-772B-7161	Sequence 7161, Ap
C 83	11	52.4	38	4	US-09-371-772B-7794	Sequence 7794, Ap
C 84	11	52.4	38	4	US-09-371-772B-9089	Sequence 9089, Ap
C 85	11	52.4	38	4	US-09-371-772B-9378	Sequence 9378, Ap
C 86	11	52.4	38	4	US-09-371-772B-9462	Sequence 9462, Ap
C 87	11	52.4	38	4	US-09-371-772B-9690	Sequence 9690, Ap
C 88	11	52.4	38	4	US-09-371-772B-9720	Sequence 9720, Ap
C 89	11	52.4	38	4	US-09-371-772B-9731	Sequence 9731, Ap
C 90	11	52.4	38	4	US-09-371-772B-9766	Sequence 9766, Ap
C 91	11	52.4	38	4	US-09-371-772B-9773	Sequence 9773, Ap
C 92	11	52.4	38	4	US-09-371-772B-10480	Sequence 10480, A
C 93	11	52.4	38	4	US-09-371-772B-10654	Sequence 10654, A
C 94	11	52.4	38	4	US-09-371-772B-10718	Sequence 10718, A
C 95	11	52.4	38	4	US-09-371-772B-10776	Sequence 10776, A
C 96	11	52.4	38	4	US-09-371-772B-10822	Sequence 10822, A
C 97	11	52.4	38	4	US-09-371-772B-10962	Sequence 10962, A
C 98	11	52.4	38	4	US-09-371-772B-11224	Sequence 11224, A
C 99	11	52.4	38	4	US-09-371-772B-11244	Sequence 11244, A
C 100	11	52.4	38	4	US-09-371-772B-11261	Sequence 11261, A

C 101	11	52.4	38	4	US-09-371-772B-11301	Sequence 11301, A	174	11	52.4	38	4	US-09-874-547-79	Sequence 79, Appl
C 102	11	52.4	38	4	US-09-371-772B-11309	Sequence 11309, A	175	11	52.4	38	4	US-09-874-547-84	Sequence 84, Appl
C 103	11	52.4	38	4	US-09-371-772B-11358	Sequence 11358, A	176	11	52.4	38	4	US-09-133-914-5	Sequence 5, Appli
C 104	11	52.4	38	4	US-09-371-772B-11365	Sequence 11365, A	C 177	11	52.4	40	3	US-09-469-197-5	Sequence 5, Appli
C 105	11	52.4	38	4	US-09-371-772B-11401	Sequence 11401, A	C 178	11	52.4	40	4	US-09-949-109-5	Sequence 238, App
C 106	11	52.4	38	4	US-09-371-772B-11624	Sequence 11624, A	C 179	11	52.4	42	1	US-08-433-126A-238	Sequence 238, App
C 107	11	52.4	38	4	US-09-371-772B-11674	Sequence 11674, A	C 180	11	52.4	42	1	US-08-433-124A-238	Sequence 17, Appl
C 108	11	52.4	38	4	US-09-371-772B-11776	Sequence 11776, A	C 181	11	52.4	42	2	US-08-846-338-17	Sequence 238, App
C 109	11	52.4	38	4	US-09-371-772B-11790	Sequence 11790, A	C 182	11	52.4	42	3	US-08-976-413A-238	Sequence 238, App
C 110	11	52.4	38	4	US-09-371-772B-11810	Sequence 11810, A	C 183	11	52.4	42	5	PCT-US96-06059-238	Sequence 11, Appl
C 111	11	52.4	38	4	US-09-371-772B-11831	Sequence 11831, A	C 184	10.8	51.4	19	3	US-08-072-064-11	Sequence 37, Appl
C 112	11	52.4	38	4	US-09-371-772B-11859	Sequence 11859, A	C 185	10.8	51.4	20	2	US-08-557-128-37	Sequence 5, Appli
C 113	11	52.4	38	4	US-09-371-772B-11880	Sequence 11880, A	C 186	10.8	51.4	20	4	US-09-930-589-5	Sequence 1315, Ap
C 114	11	52.4	38	4	US-09-371-772B-11897	Sequence 11897, A	C 187	10.8	51.4	27	3	US-08-584-040-1315	Sequence 6604, Ap
C 115	11	52.4	38	4	US-09-371-772B-11904	Sequence 11904, A	C 188	10.8	51.4	27	3	US-08-584-040-6604	Sequence 6805, Ap
C 116	11	52.4	38	4	US-09-371-772B-11924	Sequence 11924, A	C 189	10.8	51.4	27	3	US-08-584-040-6805	Sequence 26, Appl
C 117	11	52.4	38	4	US-09-371-772B-11927	Sequence 11927, A	C 190	10.8	51.4	31	3	US-09-195-666A-26	Sequence 26, Appl
C 118	11	52.4	38	4	US-09-371-772B-12021	Sequence 12021, A	C 191	10.8	51.4	31	3	US-09-635-705-26	Sequence 26, Appl
C 119	11	52.4	38	4	US-09-371-772B-12024	Sequence 12024, A	C 192	10.8	51.4	31	4	US-09-634-858A-26	Sequence 26, Appl
C 120	11	52.4	38	4	US-09-371-772B-12030	Sequence 12030, A	C 193	10.8	51.4	31	4	US-08-869-927C-26	Sequence 23, Appl
C 121	11	52.4	38	4	US-09-371-772B-12063	Sequence 12063, A	C 194	10.8	51.4	34	2	US-08-319-866-23	Sequence 23, Appl
C 122	11	52.4	38	4	US-09-371-772B-12108	Sequence 12108, A	C 195	10.8	51.4	34	4	US-08-809-917-23	Sequence 407, App
C 123	11	52.4	38	4	US-09-371-772B-12168	Sequence 12168, A	C 196	10.8	51.4	36	1	US-08-363-240A-407	Sequence 812, App
C 124	11	52.4	38	4	US-09-371-772B-12194	Sequence 12194, A	C 197	10.8	51.4	36	2	US-08-292-620A-812	Sequence 812, App
C 125	11	52.4	38	4	US-09-371-772B-12218	Sequence 12218, A	C 198	10.8	51.4	36	3	US-08-373-124A-635	Sequence 635, App
C 126	11	52.4	38	4	US-09-371-772B-12281	Sequence 12281, A	C 199	10.8	51.4	38	1	US-08-435-628-635	Sequence 8412, Ap
C 127	11	52.4	38	4	US-09-371-772B-12284	Sequence 12284, A	C 200	10.8	51.4	38	1	US-09-371-772B-8412	Sequence 10476, A
C 128	11	52.4	38	4	US-09-371-772B-12288	Sequence 12288, A	C 201	10.8	51.4	38	4	US-09-371-772B-10476	Sequence 10663, A
C 129	11	52.4	38	4	US-09-371-772B-12310	Sequence 12310, A	C 202	10.8	51.4	38	4	US-09-371-772B-10663	Sequence 18, Appl
C 130	11	52.4	38	4	US-09-371-772B-12328	Sequence 12328, A	C 203	10.8	51.4	39	2	US-08-838-189D-18	Sequence 18, Appl
C 131	11	52.4	38	4	US-09-371-772B-12360	Sequence 12360, A	C 204	10.8	51.4	39	2	US-08-852-344D-18	Sequence 18, Appl
C 132	11	52.4	38	4	US-09-371-772B-12375	Sequence 12375, A	C 205	10.8	51.4	39	3	US-08-344-639E-18	Sequence 18, Appl
C 133	11	52.4	38	4	US-09-371-772B-12455	Sequence 12455, A	C 206	10.8	51.4	39	3	US-08-467-969A-18	Sequence 18, Appl
C 134	11	52.4	38	4	US-09-371-772B-12461	Sequence 12461, A	C 207	10.8	51.4	39	3	US-08-467-969A-18	Sequence 18, Appl
C 135	11	52.4	38	4	US-09-371-772B-12503	Sequence 12503, A	C 208	10.8	51.4	39	3	US-08-467-969A-18	Sequence 18, Appl
C 136	11	52.4	38	4	US-09-371-772B-12557	Sequence 12557, A	C 209	10.8	51.4	39	3	US-08-001-554A-18	Sequence 18, Appl
C 137	11	52.4	38	4	US-09-371-772B-12598	Sequence 12598, A	C 210	10.8	51.4	39	3	US-08-483-415-22	Sequence 22, Appl
C 138	11	52.4	38	4	US-09-371-772B-12588	Sequence 12588, A	C 211	10.8	51.4	45	1	US-08-483-415-22	Sequence 22, Appl
C 139	11	52.4	38	4	US-09-371-772B-12636	Sequence 12636, A	C 212	10.8	51.4	45	6	5487983-19	Patent No. 5487983
C 140	11	52.4	38	4	US-09-371-772B-12669	Sequence 12669, A	C 213	10.6	50.5	18	3	US-09-156-807-25	Sequence 25, Appl
C 141	11	52.4	38	4	US-09-371-772B-12681	Sequence 12681, A	C 214	10.6	50.5	18	4	US-09-387-341-127	Sequence 127, App
C 142	11	52.4	38	4	US-09-371-772B-12685	Sequence 12685, A	C 215	10.6	50.5	18	4	US-09-422-978-5416	Sequence 5416, Ap
C 143	11	52.4	38	4	US-09-371-772B-12700	Sequence 12700, A	C 216	10.6	50.5	21	3	US-09-344-520-3	Sequence 3, Appli
C 144	11	52.4	38	4	US-09-371-772B-12700	Sequence 12700, A	C 217	10.6	50.5	23	3	US-09-275-680-13	Sequence 13, Appl
C 145	11	52.4	38	4	US-09-371-772B-13192	Sequence 13192, A	C 218	10.6	50.5	24	3	US-09-275-680-13	Sequence 3, Appli
C 146	11	52.4	38	4	US-09-371-772B-13218	Sequence 13218, A	C 219	10.6	50.5	30	4	US-09-624-655A-3	Sequence 8, Appli
C 147	11	52.4	38	4	US-09-371-772B-13226	Sequence 13226, A	C 220	10.6	50.5	30	4	US-09-293-427-8	Sequence 2, Appli
C 148	11	52.4	38	4	US-09-371-772B-13246	Sequence 13246, A	C 221	10.6	50.5	34	4	US-09-859-724-2	Sequence 6, Appli
C 149	11	52.4	38	4	US-09-371-772B-13253	Sequence 13253, A	C 222	10.6	50.5	34	4	US-09-387-375-6	Sequence 6, Appli
C 150	11	52.4	38	4	US-09-371-772B-13421	Sequence 13421, A	C 223	10.6	50.5	36	1	US-10-041-400A-6	Sequence 11, Appl
C 151	11	52.4	38	4	US-09-371-772B-13441	Sequence 13441, A	C 224	10.6	50.5	36	1	US-08-074-121-11	Sequence 11, Appl
C 152	11	52.4	38	4	US-09-371-772B-13487	Sequence 13487, A	C 225	10.6	50.5	37	1	PCT-US94-06447-11	Sequence 517, App
C 153	11	52.4	38	4	US-09-371-772B-13518	Sequence 13518, A	C 226	10.6	50.5	37	3	US-08-411-796-517	Sequence 517, App
C 154	11	52.4	38	4	US-09-371-772B-13529	Sequence 13529, A	C 227	10.6	50.5	37	3	US-08-559-390-517	Sequence 517, App
C 155	11	52.4	38	4	US-09-371-772B-13591	Sequence 13591, A	C 228	10.6	50.5	37	5	PCT-US93-11198-517	Sequence 517, App
C 156	11	52.4	38	4	US-09-371-772B-13633	Sequence 13633, A	C 229	10.6	50.5	38	4	US-09-371-772B-11237	Sequence 11237, A
C 157	11	52.4	38	4	US-09-371-772B-13652	Sequence 13652, A	C 230	10.6	50.5	38	4	US-09-371-772B-11239	Sequence 11239, A
C 158	11	52.4	38	4	US-09-371-772B-13669	Sequence 13669, A	C 231	10.6	50.5	38	4	US-09-371-772B-11295	Sequence 11295, A
C 159	11	52.4	38	4	US-09-371-772B-13681	Sequence 13681, A	C 232	10.6	50.5	38	4	US-09-371-772B-11305	Sequence 11305, A
C 160	11	52.4	38	4	US-09-371-772B-13710	Sequence 13710, A	C 233	10.6	50.5	38	4	US-09-371-772B-11315	Sequence 11315, A
C 161	11	52.4	38	4	US-09-371-772B-13740	Sequence 13740, A	C 234	10.6	50.5	38	4	US-09-371-772B-11418	Sequence 11418, A
C 162	11	52.4	38	4	US-09-371-772B-13758	Sequence 13758, A	C 235	10.6	50.5	38	4	US-09-371-772B-11448	Sequence 11448, A
C 163	11	52.4	38	4	US-09-371-772B-13760	Sequence 13760, A	C 236	10.6	50.5	38	4	US-09-371-772B-11514	Sequence 11514, A
C 164	11	52.4	38	4	US-09-371-772B-13805	Sequence 13805, A	C 237	10.6	50.5	38	4	US-09-371-772B-11600	Sequence 11600, A
C 165	11	52.4	38	4	US-09-371-772B-13816	Sequence 13816, A	C 238	10.6	50.5	38	4	US-09-371-772B-11647	Sequence 11647, A
C 166	11	52.4	38	4	US-09-371-772B-13833	Sequence 13833, A	C 239	10.6	50.5	38	4	US-09-371-772B-11650	Sequence 11650, A
C 167	11	52.4	38	4	US-09-371-772B-13887	Sequence 13887, A	C 240	10.6	50.5	38	4	US-09-371-772B-11689	Sequence 11689, A
C 168	11	52.4	38	4	US-09-371-772B-13922	Sequence 13922, A	C 241	10.6	50.5	38	4	US-09-371-772B-11700	Sequence 11700, A
C 169	11	52.4	38	4	US-09-371-772B-13931	Sequence 13931, A	C 242	10.6	50.5	38	4	US-09-371-772B-11713	Sequence 11713, A
C 170	11	52.4	38	4	US-09-371-772B-13974	Sequence 13974, A	C 243	10.6	50.5	38	4	US-09-371-772B-11733	Sequence 11733, A
C 171	11	52.4	38	4	US-09-371-772B-13985	Sequence 13985, A	C 244	10.6	50.5	38	4	US-09-371-772B-11796	Sequence 11796, A
C 172	11	52.4	38	4	US-09-371-772B-14014	Sequence 14014, A	C 245	10.6	50.5	38	4	US-09-371-772B-11798	Sequence 11798, A
C 173	11	52.4	38	4	US-09-874-547-75	Sequence 75, Appl	C 246	10.6	50.5	38	4	US-09-371-772B-11818	Sequence 11818, A

c 247	10.6	50.5	38	4	US-09-371-772B-11824	Sequence 11824, A	c 320	10.6	50.5	45	3	US-08-939-323-13	Sequence 13, Appl
c 248	10.6	50.5	38	4	US-09-371-772B-11847	Sequence 11847, A	c 321	10.6	50.5	47	4	US-09-422-978-495	Sequence 495, App
c 249	10.6	50.5	38	4	US-09-371-772B-11849	Sequence 11849, A	c 322	10.6	50.5	47	4	US-09-422-978-2156	Sequence 2156, App
c 250	10.6	50.5	38	4	US-09-371-772B-11851	Sequence 11851, A	c 323	10.4	49.5	18	3	US-08-642-807A-11	Sequence 11, Appl
c 251	10.6	50.5	38	4	US-09-371-772B-11871	Sequence 11871, A	c 324	10.4	49.5	20	3	US-09-527-030G-150	Sequence 150, App
c 252	10.6	50.5	38	4	US-09-371-772B-11957	Sequence 11957, A	c 325	10.4	49.5	21	4	US-09-501-612A-27	Sequence 27, Appl
c 253	10.6	50.5	38	4	US-09-371-772B-11973	Sequence 11973, A	c 326	10.4	49.5	22	4	US-09-527-030G-151	Sequence 151, App
c 254	10.6	50.5	38	4	US-09-371-772B-11983	Sequence 11983, A	c 327	10.4	49.5	22	4	US-08-470-179-197	Sequence 197, App
c 255	10.6	50.5	38	4	US-09-371-772B-12000	Sequence 12000, A	c 328	10.4	49.5	24	3	US-07-876-288-12	Sequence 12, Appl
c 256	10.6	50.5	38	4	US-09-371-772B-12007	Sequence 12007, A	c 329	10.4	49.5	24	3	US-09-538-709-348	Sequence 348, App
c 257	10.6	50.5	38	4	US-09-371-772B-12038	Sequence 12038, A	c 330	10.4	49.5	25	4	US-09-513-764-6	Sequence 6, Appl
c 258	10.6	50.5	38	4	US-09-371-772B-12049	Sequence 12049, A	c 331	10.4	49.5	27	1	US-08-518-841B-20	Sequence 20, Appl
c 259	10.6	50.5	38	4	US-09-371-772B-12053	Sequence 12053, A	c 332	10.4	49.5	29	3	US-09-414-439-20	Sequence 20, Appl
c 260	10.6	50.5	38	4	US-09-371-772B-12096	Sequence 12096, A	c 333	10.4	49.5	32	4	US-09-373-720-3	Sequence 3, Appl
c 261	10.6	50.5	38	4	US-09-371-772B-12117	Sequence 12117, A	c 334	10.4	49.5	33	3	US-09-303-064-42	Sequence 42, Appl
c 262	10.6	50.5	38	4	US-09-371-772B-12178	Sequence 12178, A	c 335	10.4	49.5	33	3	US-09-086-503-42	Sequence 42, Appl
c 263	10.6	50.5	38	4	US-09-371-772B-12184	Sequence 12184, A	c 336	10.4	49.5	33	3	US-09-081-593-76	Sequence 76, Appl
c 264	10.6	50.5	38	4	US-09-371-772B-12184	Sequence 12184, A	c 337	10.4	49.5	34	1	US-08-044-621D-16	Sequence 16, Appl
c 265	10.6	50.5	38	4	US-09-371-772B-12192	Sequence 12192, A	c 338	10.4	49.5	34	1	US-08-044-621D-22	Sequence 22, Appl
c 266	10.6	50.5	38	4	US-09-371-772B-12210	Sequence 12210, A	c 339	10.4	49.5	34	1	US-08-803-973-8	Sequence 8, Appl
c 267	10.6	50.5	38	4	US-09-371-772B-12224	Sequence 12224, A	c 340	10.4	49.5	34	1	US-08-803-972-8	Sequence 8, Appl
c 268	10.6	50.5	38	4	US-09-371-772B-12238	Sequence 12238, A	c 341	10.4	49.5	35	4	US-09-165-868-9	Sequence 9, Appl
c 269	10.6	50.5	38	4	US-09-371-772B-12241	Sequence 12241, A	c 342	10.4	49.5	35	4	US-09-165-868-9	Sequence 9, Appl
c 270	10.6	50.5	38	4	US-09-371-772B-12270	Sequence 12270, A	c 343	10.4	49.5	36	2	US-08-292-620A-805	Sequence 805, App
c 271	10.6	50.5	38	4	US-09-371-772B-12286	Sequence 12286, A	c 344	10.4	49.5	36	2	US-08-292-620A-815	Sequence 815, App
c 272	10.6	50.5	38	4	US-09-371-772B-12364	Sequence 12364, A	c 345	10.4	49.5	36	2	US-08-292-620A-1187	Sequence 1187, App
c 273	10.6	50.5	38	4	US-09-371-772B-12368	Sequence 12368, A	c 346	10.4	49.5	36	2	US-08-292-620A-1186	Sequence 1186, App
c 274	10.6	50.5	38	4	US-09-371-772B-12387	Sequence 12387, A	c 347	10.4	49.5	36	2	US-08-292-620A-1185	Sequence 1185, App
c 275	10.6	50.5	38	4	US-09-371-772B-12404	Sequence 12404, A	c 348	10.4	49.5	36	2	US-08-292-620A-1225	Sequence 1225, App
c 276	10.6	50.5	38	4	US-09-371-772B-12424	Sequence 12424, A	c 349	10.4	49.5	36	2	US-08-292-620A-1289	Sequence 1289, App
c 277	10.6	50.5	38	4	US-09-371-772B-12428	Sequence 12428, A	c 350	10.4	49.5	36	2	US-08-292-620A-1346	Sequence 1346, App
c 278	10.6	50.5	38	4	US-09-371-772B-12444	Sequence 12444, A	c 351	10.4	49.5	36	3	US-09-071-845-806	Sequence 806, App
c 279	10.6	50.5	38	4	US-09-371-772B-12471	Sequence 12471, A	c 352	10.4	49.5	36	3	US-09-071-845-815	Sequence 815, App
c 280	10.6	50.5	38	4	US-09-371-772B-12584	Sequence 12584, A	c 353	10.4	49.5	36	3	US-09-071-845-1147	Sequence 1147, App
c 281	10.6	50.5	38	4	US-09-371-772B-12690	Sequence 12690, A	c 354	10.4	49.5	36	3	US-09-071-845-1186	Sequence 1186, App
c 282	10.6	50.5	38	4	US-09-371-772B-12693	Sequence 12693, A	c 355	10.4	49.5	36	3	US-09-071-845-1195	Sequence 1195, App
c 283	10.6	50.5	38	4	US-09-371-772B-12697	Sequence 12697, A	c 356	10.4	49.5	36	3	US-09-071-845-1225	Sequence 1225, App
c 284	10.6	50.5	38	4	US-09-371-772B-13238	Sequence 13238, A	c 357	10.4	49.5	36	3	US-09-071-845-1289	Sequence 1289, App
c 285	10.6	50.5	38	4	US-09-371-772B-13364	Sequence 13364, A	c 358	10.4	49.5	36	3	US-09-071-845-1346	Sequence 1346, App
c 286	10.6	50.5	38	4	US-09-371-772B-13405	Sequence 13405, A	c 359	10.4	49.5	36	3	US-08-948-381-19	Sequence 19, Appl
c 287	10.6	50.5	38	4	US-09-371-772B-13435	Sequence 13435, A	c 360	10.4	49.5	38	4	US-09-371-772B-7201	Sequence 7201, App
c 288	10.6	50.5	38	4	US-09-371-772B-13452	Sequence 13452, A	c 361	10.4	49.5	38	4	US-09-371-772B-7293	Sequence 7293, App
c 289	10.6	50.5	38	4	US-09-371-772B-13455	Sequence 13455, A	c 362	10.4	49.5	38	4	US-09-371-772B-7344	Sequence 7344, App
c 290	10.6	50.5	38	4	US-09-371-772B-13501	Sequence 13501, A	c 363	10.4	49.5	38	4	US-09-371-772B-7348	Sequence 7348, App
c 291	10.6	50.5	38	4	US-09-371-772B-13522	Sequence 13522, A	c 364	10.4	49.5	38	4	US-09-371-772B-7361	Sequence 7361, App
c 292	10.6	50.5	38	4	US-09-371-772B-13525	Sequence 13525, A	c 365	10.4	49.5	38	4	US-09-371-772B-7364	Sequence 7364, App
c 293	10.6	50.5	38	4	US-09-371-772B-13539	Sequence 13539, A	c 366	10.4	49.5	38	4	US-09-371-772B-7390	Sequence 7390, App
c 294	10.6	50.5	38	4	US-09-371-772B-13558	Sequence 13558, A	c 367	10.4	49.5	38	4	US-09-371-772B-7394	Sequence 7394, App
c 295	10.6	50.5	38	4	US-09-371-772B-13611	Sequence 13611, A	c 368	10.4	49.5	38	4	US-09-371-772B-7401	Sequence 7401, App
c 296	10.6	50.5	38	4	US-09-371-772B-13617	Sequence 13617, A	c 369	10.4	49.5	38	4	US-09-371-772B-7424	Sequence 7424, App
c 297	10.6	50.5	38	4	US-09-371-772B-13626	Sequence 13626, A	c 370	10.4	49.5	38	4	US-09-371-772B-7428	Sequence 7428, App
c 298	10.6	50.5	38	4	US-09-371-772B-13645	Sequence 13645, A	c 371	10.4	49.5	38	4	US-09-371-772B-7441	Sequence 7441, App
c 299	10.6	50.5	38	4	US-09-371-772B-13662	Sequence 13662, A	c 372	10.4	49.5	38	4	US-09-371-772B-7482	Sequence 7482, App
c 300	10.6	50.5	38	4	US-09-371-772B-13664	Sequence 13664, A	c 373	10.4	49.5	38	4	US-09-371-772B-7485	Sequence 7485, App
c 301	10.6	50.5	38	4	US-09-371-772B-13675	Sequence 13675, A	c 374	10.4	49.5	38	4	US-09-371-772B-7521	Sequence 7521, App
c 302	10.6	50.5	38	4	US-09-371-772B-13679	Sequence 13679, A	c 375	10.4	49.5	38	4	US-09-371-772B-7552	Sequence 7552, App
c 303	10.6	50.5	38	4	US-09-371-772B-13684	Sequence 13684, A	c 376	10.4	49.5	38	4	US-09-371-772B-7556	Sequence 7556, App
c 304	10.6	50.5	38	4	US-09-371-772B-13718	Sequence 13718, A	c 377	10.4	49.5	38	4	US-09-371-772B-7558	Sequence 7558, App
c 305	10.6	50.5	38	4	US-09-371-772B-13722	Sequence 13722, A	c 378	10.4	49.5	38	4	US-09-371-772B-7583	Sequence 7583, App
c 306	10.6	50.5	38	4	US-09-371-772B-13724	Sequence 13724, A	c 379	10.4	49.5	38	4	US-09-371-772B-7590	Sequence 7590, App
c 307	10.6	50.5	38	4	US-09-371-772B-13764	Sequence 13764, A	c 380	10.4	49.5	38	4	US-09-371-772B-7619	Sequence 7619, App
c 308	10.6	50.5	38	4	US-09-371-772B-13838	Sequence 13838, A	c 381	10.4	49.5	38	4	US-09-371-772B-7652	Sequence 7652, App
c 309	10.6	50.5	38	4	US-09-371-772B-13853	Sequence 13853, A	c 382	10.4	49.5	38	4	US-09-371-772B-7696	Sequence 7696, App
c 310	10.6	50.5	38	4	US-09-371-772B-13882	Sequence 13882, A	c 383	10.4	49.5	38	4	US-09-371-772B-7738	Sequence 7738, App
c 311	10.6	50.5	38	4	US-09-371-772B-13907	Sequence 13907, A	c 384	10.4	49.5	38	4	US-09-371-772B-7838	Sequence 7838, App
c 312	10.6	50.5	38	4	US-09-371-772B-13934	Sequence 13934, A	c 385	10.4	49.5	38	4	US-09-371-772B-7922	Sequence 7922, App
c 313	10.6	50.5	38	4	US-09-371-772B-13970	Sequence 13970, A	c 386	10.4	49.5	38	4	US-09-371-772B-7973	Sequence 7973, App
c 314	10.6	50.5	38	4	US-09-371-772B-13976	Sequence 13976, A	c 387	10.4	49.5	38	4	US-09-371-772B-8031	Sequence 8031, App
c 315	10.6	50.5	38	4	US-09-371-772B-14021	Sequence 14021, A	c 388	10.4	49.5	38	4	US-09-371-772B-8084	Sequence 8084, App
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c 317	10.6	50.5	39	4	US-09-060-299-189	Sequence 189, App	c 390	10.4	49.5	38	4	US-09-371-772B-8166	Sequence 8166, App
c 318	10.6	50.5	39	4	US-09-402-923A-189	Sequence 189, App	c 391	10.4	49.5	38	4	US-09-371-772B-8168	Sequence 8168, App
c 319	10.6	50.5	45	1	US-08-681-935-13	Sequence 13, Appl	c 392	10.4	49.5	38	4	US-09-371-772B-8173	Sequence 8173, App

C 393	10.4	49.5	38	4	US-09-371-772B-8209	Ap	Sequence 8209, Ap	Sequence 8209, Ap	49.5	38	4	US-09-371-772B-10589	A	Sequence 10589, A
C 394	10.4	49.5	38	4	US-09-371-772B-8467	Ap	Sequence 8467, Ap	Sequence 8467, Ap	49.5	38	4	US-09-371-772B-10631	A	Sequence 10631, A
C 395	10.4	49.5	38	4	US-09-371-772B-8488	Ap	Sequence 8488, Ap	Sequence 8488, Ap	49.5	38	4	US-09-371-772B-10764	A	Sequence 10764, A
C 396	10.4	49.5	38	4	US-09-371-772B-8520	Ap	Sequence 8520, Ap	Sequence 8520, Ap	49.5	38	4	US-09-371-772B-10768	A	Sequence 10768, A
C 397	10.4	49.5	38	4	US-09-371-772B-8649	Ap	Sequence 8649, Ap	Sequence 8649, Ap	49.5	38	4	US-09-371-772B-10769	A	Sequence 10769, A
C 398	10.4	49.5	38	4	US-09-371-772B-8658	Ap	Sequence 8658, Ap	Sequence 8658, Ap	49.5	38	4	US-09-371-772B-10782	A	Sequence 10782, A
C 399	10.4	49.5	38	4	US-09-371-772B-8676	Ap	Sequence 8676, Ap	Sequence 8676, Ap	49.5	38	4	US-09-371-772B-10823	A	Sequence 10823, A
C 400	10.4	49.5	38	4	US-09-371-772B-8694	Ap	Sequence 8694, Ap	Sequence 8694, Ap	49.5	38	4	US-09-371-772B-10823	A	Sequence 10823, A
C 401	10.4	49.5	38	4	US-09-371-772B-8710	Ap	Sequence 8710, Ap	Sequence 8710, Ap	49.5	38	4	US-09-371-772B-10902	A	Sequence 10902, A
C 402	10.4	49.5	38	4	US-09-371-772B-8729	Ap	Sequence 8729, Ap	Sequence 8729, Ap	49.5	38	4	US-09-371-772B-10905	A	Sequence 10905, A
C 403	10.4	49.5	38	4	US-09-371-772B-8821	Ap	Sequence 8821, Ap	Sequence 8821, Ap	49.5	38	4	US-09-371-772B-10935	A	Sequence 10935, A
C 404	10.4	49.5	38	4	US-09-371-772B-8856	Ap	Sequence 8856, Ap	Sequence 8856, Ap	49.5	38	4	US-09-371-772B-10969	A	Sequence 10969, A
C 405	10.4	49.5	38	4	US-09-371-772B-8863	Ap	Sequence 8863, Ap	Sequence 8863, Ap	49.5	38	4	US-09-371-772B-10970	A	Sequence 10970, A
C 406	10.4	49.5	38	4	US-09-371-772B-8866	Ap	Sequence 8866, Ap	Sequence 8866, Ap	49.5	38	4	US-09-371-772B-10972	A	Sequence 10972, A
C 407	10.4	49.5	38	4	US-09-371-772B-8897	Ap	Sequence 8897, Ap	Sequence 8897, Ap	49.5	38	4	US-09-371-772B-11005	A	Sequence 11005, A
C 408	10.4	49.5	38	4	US-09-371-772B-8945	Ap	Sequence 8945, Ap	Sequence 8945, Ap	49.5	38	4	US-09-371-772B-11059	A	Sequence 11059, A
C 409	10.4	49.5	38	4	US-09-371-772B-8958	Ap	Sequence 8958, Ap	Sequence 8958, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 410	10.4	49.5	38	4	US-09-371-772B-8986	Ap	Sequence 8986, Ap	Sequence 8986, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 411	10.4	49.5	38	4	US-09-371-772B-9013	Ap	Sequence 9013, Ap	Sequence 9013, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 412	10.4	49.5	38	4	US-09-371-772B-9097	Ap	Sequence 9097, Ap	Sequence 9097, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 413	10.4	49.5	38	4	US-09-371-772B-9113	Ap	Sequence 9113, Ap	Sequence 9113, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 414	10.4	49.5	38	4	US-09-371-772B-9131	Ap	Sequence 9131, Ap	Sequence 9131, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 415	10.4	49.5	38	4	US-09-371-772B-9143	Ap	Sequence 9143, Ap	Sequence 9143, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 416	10.4	49.5	38	4	US-09-371-772B-9194	Ap	Sequence 9194, Ap	Sequence 9194, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 417	10.4	49.5	38	4	US-09-371-772B-9211	Ap	Sequence 9211, Ap	Sequence 9211, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 418	10.4	49.5	38	4	US-09-371-772B-9260	Ap	Sequence 9260, Ap	Sequence 9260, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 419	10.4	49.5	38	4	US-09-371-772B-9368	Ap	Sequence 9368, Ap	Sequence 9368, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 420	10.4	49.5	38	4	US-09-371-772B-9454	Ap	Sequence 9454, Ap	Sequence 9454, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 421	10.4	49.5	38	4	US-09-371-772B-9460	Ap	Sequence 9460, Ap	Sequence 9460, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 422	10.4	49.5	38	4	US-09-371-772B-9542	Ap	Sequence 9542, Ap	Sequence 9542, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 423	10.4	49.5	38	4	US-09-371-772B-9545	Ap	Sequence 9545, Ap	Sequence 9545, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 424	10.4	49.5	38	4	US-09-371-772B-9631	Ap	Sequence 9631, Ap	Sequence 9631, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 425	10.4	49.5	38	4	US-09-371-772B-9633	Ap	Sequence 9633, Ap	Sequence 9633, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 426	10.4	49.5	38	4	US-09-371-772B-9658	Ap	Sequence 9658, Ap	Sequence 9658, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 427	10.4	49.5	38	4	US-09-371-772B-9658	Ap	Sequence 9658, Ap	Sequence 9658, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 428	10.4	49.5	38	4	US-09-371-772B-9764	Ap	Sequence 9764, Ap	Sequence 9764, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 429	10.4	49.5	38	4	US-09-371-772B-9806	Ap	Sequence 9806, Ap	Sequence 9806, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 430	10.4	49.5	38	4	US-09-371-772B-9821	Ap	Sequence 9821, Ap	Sequence 9821, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 431	10.4	49.5	38	4	US-09-371-772B-9838	Ap	Sequence 9838, Ap	Sequence 9838, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 432	10.4	49.5	38	4	US-09-371-772B-9877	Ap	Sequence 9877, Ap	Sequence 9877, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 433	10.4	49.5	38	4	US-09-371-772B-9881	Ap	Sequence 9881, Ap	Sequence 9881, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 434	10.4	49.5	38	4	US-09-371-772B-9934	Ap	Sequence 9934, Ap	Sequence 9934, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 435	10.4	49.5	38	4	US-09-371-772B-9949	Ap	Sequence 9949, Ap	Sequence 9949, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 436	10.4	49.5	38	4	US-09-371-772B-9977	Ap	Sequence 9977, Ap	Sequence 9977, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 437	10.4	49.5	38	4	US-09-371-772B-10011	Ap	Sequence 10011, Ap	Sequence 10011, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 438	10.4	49.5	38	4	US-09-371-772B-10017	Ap	Sequence 10017, Ap	Sequence 10017, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 439	10.4	49.5	38	4	US-09-371-772B-10053	Ap	Sequence 10053, Ap	Sequence 10053, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 440	10.4	49.5	38	4	US-09-371-772B-10064	Ap	Sequence 10064, Ap	Sequence 10064, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 441	10.4	49.5	38	4	US-09-371-772B-10068	Ap	Sequence 10068, Ap	Sequence 10068, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 442	10.4	49.5	38	4	US-09-371-772B-10172	Ap	Sequence 10172, Ap	Sequence 10172, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 443	10.4	49.5	38	4	US-09-371-772B-10182	Ap	Sequence 10182, Ap	Sequence 10182, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 444	10.4	49.5	38	4	US-09-371-772B-10189	Ap	Sequence 10189, Ap	Sequence 10189, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 445	10.4	49.5	38	4	US-09-371-772B-10197	Ap	Sequence 10197, Ap	Sequence 10197, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 446	10.4	49.5	38	4	US-09-371-772B-10209	Ap	Sequence 10209, Ap	Sequence 10209, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 447	10.4	49.5	38	4	US-09-371-772B-10296	Ap	Sequence 10296, Ap	Sequence 10296, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 448	10.4	49.5	38	4	US-09-371-772B-10317	Ap	Sequence 10317, Ap	Sequence 10317, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 449	10.4	49.5	38	4	US-09-371-772B-10325	Ap	Sequence 10325, Ap	Sequence 10325, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 450	10.4	49.5	38	4	US-09-371-772B-10356	Ap	Sequence 10356, Ap	Sequence 10356, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 451	10.4	49.5	38	4	US-09-371-772B-10363	Ap	Sequence 10363, Ap	Sequence 10363, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 452	10.4	49.5	38	4	US-09-371-772B-10363	Ap	Sequence 10363, Ap	Sequence 10363, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 453	10.4	49.5	38	4	US-09-371-772B-10365	Ap	Sequence 10365, Ap	Sequence 10365, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 454	10.4	49.5	38	4	US-09-371-772B-10368	Ap	Sequence 10368, Ap	Sequence 10368, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 455	10.4	49.5	38	4	US-09-371-772B-10382	Ap	Sequence 10382, Ap	Sequence 10382, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 456	10.4	49.5	38	4	US-09-371-772B-10403	Ap	Sequence 10403, Ap	Sequence 10403, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 457	10.4	49.5	38	4	US-09-371-772B-10431	Ap	Sequence 10431, Ap	Sequence 10431, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 458	10.4	49.5	38	4	US-09-371-772B-10437	Ap	Sequence 10437, Ap	Sequence 10437, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 459	10.4	49.5	38	4	US-09-371-772B-10449	Ap	Sequence 10449, Ap	Sequence 10449, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 460	10.4	49.5	38	4	US-09-371-772B-10459	Ap	Sequence 10459, Ap	Sequence 10459, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 461	10.4	49.5	38	4	US-09-371-772B-10467	Ap	Sequence 10467, Ap	Sequence 10467, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 462	10.4	49.5	38	4	US-09-371-772B-10485	Ap	Sequence 10485, Ap	Sequence 10485, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 463	10.4	49.5	38	4	US-09-371-772B-10485	Ap	Sequence 10485, Ap	Sequence 10485, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 464	10.4	49.5	38	4	US-09-371-772B-10491	Ap	Sequence 10491, Ap	Sequence 10491, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A
C 465	10.4	49.5	38	4	US-09-371-772B-10518	Ap	Sequence 10518, Ap	Sequence 10518, Ap	49.5	38	4	US-09-371-772B-11075	A	Sequence 11075, A

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540	10.2	48.6	20	3	US-09-167-151-4	Sequence 4, Appli	613	10.2	48.6	45	4	US-09-903-603A-305	Sequence 305, App
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ALIGNMENTS

RESULT 1
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; Sequence 12, Application US/09056052
; Patent No. 6090556
; GENERAL INFORMATION:
; APPLICANT: Kato, Kikuya
; TITLE OF INVENTION: Adaptor-Tagged Competitive PCR
; FILE REFERENCE: 07898/026001
; CURRENT APPLICATION NUMBER: US/09/056,052
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: JP88495/1997
; EARLIER FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 13
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US-09-056-052-12

Query Match 62.9%; Score 13.2; DB 3; Length 35;
Best Local Similarity 83.3%; Pred. No. 3e+02;
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; TITLE OF INVENTION: Adaptor-Tagged Competitive PCR
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; CURRENT APPLICATION NUMBER: US/09/056,052
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: JP88495/1997
; EARLIER FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(4)
; OTHER INFORMATION: 'n' can be any base A, T, G, or C
US-09-056-052-13

Query Match 62.9%; Score 13.2; DB 3; Length 39;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 CGCGTACGGTCTAATGAC 19
Db 13 CGCGTACGGTCTAATGAC 30

RESULT 3
US-09-131-028A-17
; Sequence 17, Application US/09131028A
; Patent No. 6287866
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Lemmel, Steven A.
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Chaudhary, Sunita
; TITLE OF INVENTION: BETA-CASIN EXPRESSING CONSTRUCTS
; FILE REFERENCE: 6004 US P1
; CURRENT APPLICATION NUMBER: US/09/131,028A
; CURRENT FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: US 08/064,440
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer R0204
US-09-131-028A-17

Query Match 60.0%; Score 12.6; DB 3; Length 31;
Best Local Similarity 78.9%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 CGGTACGGTCTAATGACG 21
Db 12 GAGTACTGTCTCATGACG 30

RESULT 4
US-08-207-481-29
; Sequence 29, Application US/08207481
; Patent No. 5820866
; GENERAL INFORMATION:
; APPLICANT: Kappler, John W.
; APPLICANT: Marrack, Philippa
; TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL
; TITLE OF INVENTION: REGULATION
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH
; STREET: 1700 LINCOLN STREET, SUITE 3500
; CITY: DENVER
; STATE: COLORADO
; COUNTRY: USA

```
;
;
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,481
; FILING DATE: 04-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-207-481-29

Query Match 60.0%; Score 12.6; DB 1; Length 33;
Best Local Similarity 78.9%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTTAATGACCG 21
| | | | | | | | | | | | | |
Db 2 GCGTACGACGAATGAACG 20

RESULT 5
PCT-US95-02689-31
; Sequence 31, Application PC/TUS9502689
; GENERAL INFORMATION:
; APPLICANT: National Jewish Center for Immunology and
; APPLICANT: Respiratory Medicine
; APPLICANT: Kappler, John W.
; APPLICANT: Martack, Philippa
; TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH
; STREET: 1700 LINCOLN STREET, SUITE 3500
; CITY: DENVER
; STATE: COLORADO
; COUNTRY: USA
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02689
; FILING DATE: 03-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-8-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
;
;
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US95-02689-31

Query Match 60.0%; Score 12.6; DB 5; Length 33;
Best Local Similarity 78.9%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTTAATGACCG 21
| | | | | | | | | | | | | |
Db 2 GCGTACGACGAATGAACG 20

RESULT 6
US-09-371-772B-11935/c
; Sequence 11935, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11935
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
; US-09-371-772B-11935

Query Match 60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTTAATGACC 20
| | | | | | | | | | | | | |
Db 35 TCGCNTTCGGCCTAACGCC 16

RESULT 7
US-09-371-772B-13181/c
; Sequence 13181, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
```

; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13181
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc.feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-13181

Query Match 60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 8

US-09-371-772B-13811/c
; Sequence 13811, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Favco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/138)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13811
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc.feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-13811

Query Match 60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 9

US-09-874-547-83
; Sequence 83, Application US/09874547
; Patent No. 6686154
; GENERAL INFORMATION:
; APPLICANT: No. 6686154k, Steffen
; APPLICANT: Kassner, Paul D.
; APPLICANT: Zyomyx, Inc.
; TITLE OF INVENTION: Screening of Phage Displayed Peptides Without Clearing of the Cell Culture

; FILE REFERENCE: 020144-001110US
; CURRENT APPLICATION NUMBER: US/09/874,547
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/209,503
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primers for ScFv and Fab library generation (Table 1)
; OTHER INFORMATION: I) - MVK24
US-09-874-547-83

Query Match 60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 78.9%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
Db 12 CGCGACATGTAATGACC 30

RESULT 10

US-08-373-124A-1680
; Sequence 1680, Application US/08373124A
; Patent No. 5846042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF RESTENOSIS AND CORONARY ARTERY DISEASE
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 1680:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-373-124A-1680

Query Match 59.0%; Score 12.4; DB 1; Length 38;
Best Local Similarity 64.3%; Pred. No. 8.4e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GTACGGTCTAATGA 18
|:|||||:|:|
Db 2 GUACGGUCUGAUGA 15

RESULT 11
US-08-435-628-1680
; Sequence 1680, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1680:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-1680

Query Match 59.0%; Score 12.4; DB 1; Length 38;
Best Local Similarity 64.3%; Pred. No. 8.4e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GTACGGTCTAATGA 18
|:|||||:|:|
Db 2 GUACGGUCUGAUGA 15

RESULT 12
US-09-198-452A-4954
; Sequence 4954, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffsais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4954
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4954

Query Match 58.1%; Score 12.2; DB 4; Length 20;
Best Local Similarity 82.4%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGCGTACGGTCTAATGA 18
|||||:|:|
Db 2 CGCGACGCTATAATGA 18

RESULT 13
5451502-8
; Patent No. 5451502
; APPLICANT: GEORGE JR., ALBERT L.
; TITLE OF INVENTION: RESTRICTION AMPLIFICATION ASSAY
; NUMBER OF SEQUENCES: 18
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,997
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 998,644
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: 790,174
; FILING DATE: 12-NOV-1991
; APPLICATION NUMBER: 519,146
; FILING DATE: 04-MAY-1990
; SEQ ID NO:8
; LENGTH: 21
5451502-8

Query Match 58.1%; Score 12.2; DB 6; Length 21;
Best Local Similarity 82.4%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATG 17
|||||:|:|
Db 5 TCGCATAGGTCGAATG 21

RESULT 14
US-09-313-221A-19/c
; Sequence 19, Application US/09313221A
; Patent No. 6468743
; GENERAL INFORMATION:
; APPLICANT: Thomas L. Romick (Inventor)

APPLICANT: Mark S. Fraser (Inventor)
TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL
FILE REFERENCE: HUNT-042784
CURRENT APPLICATION NUMBER: US/09/313,221A
CURRENT FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: US 60/086,025
PRIOR FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 41
TYPE: DNA
ORGANISM: Escherichia coli
US-09-313-221A-19

Query Match 58.1%; Score 12.2; DB 4; Length 41;
Best Local Similarity 82.4%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATG 17
| | | | | | | | | | | | | | | | | | | | | |
DB 24 TCGGCACGGTATATG 8

RESULT 15
US-08-860-882A-75/c
Sequence 75, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGELE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FIOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAM, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HUI
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238653
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-860-882A-75

Query Match 57.1%; Score 12; DB 2; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
| | | | | | | | | | | | | | | | | | | | | |
DB 20 TCGCGACTGGGCTTATGACC 1

RESULT 16
US-09-011-769A-61/c
Sequence 61, Application US/09011769A
Patent No. 6436691
GENERAL INFORMATION:
APPLICANT: SLATER, Anthony M.
APPLICANT: BLAXEY, David C.
APPLICANT: DAVIES, David H.
APPLICANT: HENNAM, John F.
APPLICANT: HENNEQUIN, Laurent F.A.
APPLICANT: MARSHAM, Peter R.
APPLICANT: DOWELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, LLP
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,769A
FILING DATE: 13-Feb-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
FILING DATE: 16-AUG-1995

INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-09-011-769A-61

Query Match 57.1%; Score 12; DB 4; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
| | | | | | | | | | | | | | | | | | | | | |
DB 20 TCGCGACTGGGCTTATGACC 1

RESULT 17
US-09-814-351-25/c
Sequence 25, Application US/09814351
Patent No. 6692736
GENERAL INFORMATION:


```
; APPLICANT: Yu, De-Chao
; APPLICANT: Li, Yuanhao
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
; FILE REFERENCE: 348022001700
; CURRENT APPLICATION NUMBER: US/09/814,351
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human UPII (PCR primer 127.2.1)
US-09-814-351-25

Query Match      57.1%; Score 12; DB 4; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2  CGCGTACGGTCTAATGACG 21
Db  25 CGCGGCCCTAGTAGACG 6

RESULT 18
US-09-709-103-34/c
; Sequence 34, Application US/09709103
; Patent No. 6733991
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
; FILE REFERENCE: 60388-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/709,103
; CURRENT FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe/Primer
US-09-709-103-34

Query Match      57.1%; Score 12; DB 4; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1  TCGGTACGGTCTAATGACC 20
Db  21 TCGGCCGAGTTTCATGACC 2

RESULT 19
US-09-439-410A-34/c
; Sequence 34, Application US/09439410A
; Patent No. 6746852
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS PROTEIN AND NUCLEOTIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 1919/60388-B
; CURRENT APPLICATION NUMBER: US/09/439,410A
; CURRENT FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
```

```
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Probe/Primer
US-09-439-410A-34

Query Match      57.1%; Score 12; DB 4; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1  TCGGTACGGTCTAATGACC 20
Db  21 TCGGCCGAGTTTCATGACC 2

RESULT 20
US-09-371-772B-7357/c
; Sequence 7357, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7357
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-7357

Query Match      57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1  TCGGTACGGTCTAATGACC 20
Db  35 TCGCTTCGGCCTAACGGCC 16

RESULT 21
US-09-371-772B-7797/c
; Sequence 7797, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
```

; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7797
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-7797

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCTTCGGCCTAACGGCC 16

RESULT 22

US-09-371-772B-8104/c
; Sequence 8104, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT FILING DATE: US/09/371,772B
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8104
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8104

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCTTCGGCCTAACGGCC 16

RESULT 23

US-09-371-772B-8341/c
; Sequence 8341, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT FILING DATE: US/09/371,772B
; PRIOR APPLICATION NUMBER: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8341
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8341

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCTTCGGCCTAACGGCC 16

RESULT 24

US-09-371-772B-9392/c
; Sequence 9392, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT FILING DATE: US/09/371,772B
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9392
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9392

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCTTCGGCCTAACGGCC 16

RESULT 25

US-09-371-772B-9781/c
; Sequence 9781, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974

; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9781
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9781

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCTTTCGGCCTAACGGCC 16

RESULT 26

US-09-371-772B-9974/c
; Sequence 9974, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00, 876-J (237/198)

; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9974
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9974

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCTTTCGGCCTAACGGCC 16

RESULT 27

US-09-371-772B-10321/c
; Sequence 10321, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10321
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10321

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCTTTCGGCCTAACGGCC 16

RESULT 28

US-09-371-772B-10352/c
; Sequence 10352, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00, 876-J (237/198)

; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10352
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10352

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCTTTCGGCCTAACGGCC 16

RESULT 29

US-09-371-772B-10512/c
; Sequence 10512, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam

```
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEH900,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10512
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10512

Query Match          57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTTAATGACC 20
    ||||| ||||| ||||| |||||
Db 35 TCGCTTCGGCTACGGCC 16

RESULT 30
US-09-172-045-20
; Sequence 20, Application US/09172045
; Patent No. 6277594
; GENERAL INFORMATION:
; APPLICANT: Mikoshiba, Katsuhiko
; APPLICANT: Aruga, Jun
; APPLICANT: Nagai, Takeharu
; APPLICANT: Nakata, Katsunori
; TITLE OF INVENTION: Neurogenesis Inducing Gene
; FILE REFERENCE: Hiraki-03497
; CURRENT APPLICATION NUMBER: US/09/172,045
; CURRENT FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: JP98/86979
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP98/121456
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-172-045-20

Query Match          55.2%; Score 11.6; DB 3; Length 20;
Best Local Similarity 77.8%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTTAATGAC 19
    ||||| ||||| ||||| |||||
Db 3 CTCCTTCGGTGTAAATGAC 20

RESULT 31
US-09-342-325C-20
; Sequence 20, Application US/09342325C
; Patent No. 6500637
; GENERAL INFORMATION:
; APPLICANT: Mikoshiba, Katsuhiko
```

```
; APPLICANT: Aruga, Jun
; APPLICANT: Nagai, Takeharu
; APPLICANT: Katsunori, Nakata
; TITLE OF INVENTION: Neurogenesis Inducing Gene
; FILE REFERENCE: HIRAKI-03814
; CURRENT APPLICATION NUMBER: US/09/342,325C
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: JP98/86979
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: JP98/121456
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 09/172,045
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-342-325C-20

Query Match          55.2%; Score 11.6; DB 4; Length 20;
Best Local Similarity 77.8%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTTAATGAC 19
    ||||| ||||| ||||| |||||
Db 3 CTCCTTCGGTGTAAATGAC 20

RESULT 32
US-09-056-052-10/c
; Sequence 10, Application US/09056052
; Patent No. 6090556
; GENERAL INFORMATION:
; APPLICANT: Kato, Kikuya
; TITLE OF INVENTION: Adaptor-Tagged Competitive PCR
; FILE REFERENCE: 07898/026001
; CURRENT APPLICATION NUMBER: US/09/056,052
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: JP88495/1997
; EARLIER FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-056-052-10

Query Match          55.2%; Score 11.6; DB 3; Length 35;
Best Local Similarity 77.8%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTTAATGAC 19
    ||||| ||||| ||||| |||||
Db 27 CGAGTGGCTTCTTAACGAC 10

RESULT 33
US-10-009-332-10
; Sequence 10, Application US/10009332
; Patent No. 6716613
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; APPLICANT: Kazusa DNA Research Institute
; TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING AGGREGANASE ACTIVITY
; FILE REFERENCE: Q67541
; CURRENT APPLICATION NUMBER: US/10/009,332
```

; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: JPA Hei 11-321740
; PRIOR FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: JPA 2000-144020
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-009-332-10

Query Match 55.2%; Score 11.6; DB 4; Length 37;
Best Local Similarity 77.8%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGAC 19
||| ||||| ||| |||
DB 8 CGCGCACGGCTCAGGAC 25

RESULT 34
US-09-371-772B-11413/c
; Sequence 11413, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11413
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-11413

Query Match 55.2%; Score 11.6; DB 4; Length 38;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
||| ||||| ||| |||
DB 34 CGCNTTCGGCTTAACGGCC 16

RESULT 35
US-09-371-772B-12074/c
; Sequence 12074, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12074
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-12074

Query Match 55.2%; Score 11.6; DB 4; Length 38;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
||| ||||| ||| |||
DB 34 CGCNTTCGGCTTAACGGCC 16

RESULT 36
US-09-371-772B-12155/c
; Sequence 12155, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12155
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-12155

Query Match 55.2%; Score 11.6; DB 4; Length 38;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
||| ||||| ||| |||
DB 34 CGCNTTCGGCTTAACGGCC 16

RESULT 37

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-13450

Query Match 55.2%; Score 11.6; DB 4; Length 38;
Best Local Similarity 73.7%; Pred. NO. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CGCGTAGGCTCTAATGACC 20
||| | ||| ||| |||
Db 34 CGCNTTCGGCCTAACGGCC 16

Search completed: November 23, 2004, 22:26:04
Job time : 30.3034 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 18:47:33 ; Search time 98.4719 Seconds
(without alignments)
1152.370 Million cell updates/sec

Title: US-10-087-631B-2

Perfect score: 21

Sequence: 1 tcgcgtacgtctaatgacgc 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 1987578

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications NA:*

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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	14	US-10-087-631B-2
2	21	100.0	21	14	Sequence 2, Appl
3	21	100.0	21	15	US-10-087-631B-17
4	21	100.0	21	15	Sequence 17, Appl
5	14.2	67.6	25	15	US-10-087-631B-56047
6	13.6	64.8	29	16	US-10-087-631B-218
7	13.6	64.8	29	16	US-10-087-631B-218
8	13.6	64.8	37	16	US-10-087-631B-20182
9	13.6	64.8	37	16	US-10-087-631B-20479
10	13.6	64.8	37	17	US-10-087-631B-20182
11	13.6	64.8	37	17	US-10-087-631B-20479
12	13.4	63.8	25	15	US-10-087-631B-9436

25	15	62.9	13.2	13	US-10-087-631B-88235	Sequence 88235, A
25	15	62.9	13.2	14	US-10-087-631B-88853	Sequence 88853, A
25	15	61.9	13	15	US-10-087-631B-71593	Sequence 71593, A
25	15	61.0	12.8	16	US-10-087-631B-71008	Sequence 71008, A
25	15	60.0	12.6	17	US-10-087-631B-25744	Sequence 25744, A
25	15	60.0	12.6	18	US-10-087-631B-56048	Sequence 56048, A
25	15	60.0	12.6	19	US-10-087-631B-118819	Sequence 118819, A
25	15	60.0	12.6	20	US-10-087-631B-118820	Sequence 118820, A
36	9	60.0	12.6	21	US-09-864-785-3885	Sequence 3885, Ap
37	9	60.0	12.6	22	US-09-864-785-1812	Sequence 1812, Ap
37	10	60.0	12.6	23	US-09-740-332-9583	Sequence 9583, Ap
37	10	60.0	12.6	24	US-09-817-879-9583	Sequence 9583, Ap
37	16	60.0	12.6	25	US-10-138-674-18225	Sequence 18225, A
37	16	60.0	12.6	26	US-10-138-674-18462	Sequence 18462, A
37	16	60.0	12.6	27	US-10-138-674-20525	Sequence 20525, A
37	17	60.0	12.6	28	US-10-287-949A-18225	Sequence 18225, A
37	17	60.0	12.6	29	US-10-287-949A-18462	Sequence 18462, A
37	17	60.0	12.6	30	US-10-287-949A-20525	Sequence 20525, A
37	17	60.0	12.6	31	US-10-669-841-16128	Sequence 16128, A
38	9	60.0	12.6	32	US-09-874-547-83	Sequence 83, Appl
38	9	60.0	12.6	33	US-09-864-785-1169	Sequence 1169, Ap
38	10	60.0	12.6	34	US-09-780-533A-3557	Sequence 3557, Ap
38	10	60.0	12.6	35	US-09-780-533A-3581	Sequence 3581, Ap
38	10	60.0	12.6	36	US-09-927-046-3026	Sequence 3026, Ap
38	10	60.0	12.6	37	US-09-927-046-3197	Sequence 3197, Ap
38	10	60.0	12.6	38	US-09-877-478-3764	Sequence 3764, Ap
38	10	60.0	12.6	39	US-09-848-754A-5094	Sequence 5094, Ap
38	10	60.0	12.6	40	US-09-848-754A-5300	Sequence 5300, Ap
38	15	60.0	12.6	42	US-10-230-006-911	Sequence 911, App
38	15	60.0	12.6	43	US-10-230-006-1011	Sequence 1011, Ap
38	15	60.0	12.6	44	US-10-230-006-1101	Sequence 1101, Ap
38	16	60.0	12.6	45	US-10-342-902-3468	Sequence 3468, Ap
38	16	60.0	12.6	46	US-10-342-902-3764	Sequence 3764, Ap
38	16	60.0	12.6	47	US-10-138-674-14212	Sequence 14212, A
38	16	60.0	12.6	48	US-10-138-674-15458	Sequence 15458, A
38	16	60.0	12.6	49	US-10-138-674-16088	Sequence 16088, A
38	17	60.0	12.6	50	US-10-287-949A-14212	Sequence 14212, A
38	17	60.0	12.6	51	US-10-287-949A-15458	Sequence 15458, A
38	17	60.0	12.6	52	US-10-287-949A-16088	Sequence 16088, A
38	17	60.0	12.6	53	US-10-712-672-3553	Sequence 3553, Ap
38	17	60.0	12.6	54	US-10-712-672-3746	Sequence 3746, Ap
38	17	60.0	12.6	55	US-10-712-672-4178	Sequence 4178, Ap
38	17	60.0	12.6	56	US-10-712-672-4185	Sequence 4185, Ap
38	17	60.0	12.6	57	US-10-669-841-8359	Sequence 8359, Ap
38	17	60.0	12.6	58	US-10-669-841-8655	Sequence 8655, Ap
42	9	60.0	12.6	59	US-09-101-807-5	Sequence 5, Appl
34	14	59.0	12.4	60	US-10-022-832-39	Sequence 39, Appl
38	10	59.0	12.4	61	US-09-780-533A-4554	Sequence 4554, Ap
20	16	58.1	12.2	62	US-10-289-762-4954	Sequence 4954, Ap
25	15	58.1	12.2	63	US-10-087-631B-17473	Sequence 17473, A
25	15	58.1	12.2	64	US-10-087-631B-26429	Sequence 26429, A
25	15	58.1	12.2	65	US-10-087-631B-27175	Sequence 27175, A
25	15	58.1	12.2	66	US-10-087-631B-36699	Sequence 36699, A
34	18	58.1	12.2	67	US-10-679-032-16	Sequence 16, Appl
37	10	58.1	12.2	68	US-09-927-046-3626	Sequence 3626, Ap
37	10	58.1	12.2	69	US-09-927-046-3631	Sequence 3631, Ap
37	10	58.1	12.2	70	US-09-927-046-3664	Sequence 3664, Ap
37	10	58.1	12.2	71	US-09-848-754A-5959	Sequence 5959, Ap
37	10	58.1	12.2	72	US-09-848-754A-6388	Sequence 6388, Ap
19	9	57.1	12	73	US-09-969-373-3705	Sequence 3705, Ap
25	15	57.1	12	74	US-10-308-343-2	Sequence 2, Appl
25	15	57.1	12	75	US-10-087-631B-3823	Sequence 3823, Ap
25	15	57.1	12	76	US-10-087-631B-3824	Sequence 3824, Ap
25	15	57.1	12	77	US-10-087-631B-16652	Sequence 16652, A
25	15	57.1	12	78	US-10-087-631B-68752	Sequence 68752, A
25	15	57.1	12	79	US-10-087-631B-11682	Sequence 11682, A
25	15	57.1	12	80	US-10-087-631B-12296	Sequence 12296, A
25	15	57.1	12	81	US-10-087-631B-128394	Sequence 128394, A
29	9	57.1	12	82	US-09-814-292-23	Sequence 23, Appl
29	10	57.1	12	83	US-09-814-357-25	Sequence 25, Appl
29	10	57.1	12	84	US-09-814-351-25	Sequence 25, Appl
32	17	57.1	12	85	US-10-804-491-34	Sequence 34, Appl

C 86	12	57.1	36	9	US-09-504-231A-1730	Sequence 1730, Ap	C 159	11.6	55.2	25	15	US-10-098-263B-7785	Sequence 7785, Ap
C 87	12	57.1	36	9	US-09-504-231A-1937	Sequence 1937, Ap	C 160	11.6	55.2	25	15	US-10-098-263B-33569	Sequence 33569, A
C 88	12	57.1	36	9	US-09-504-231A-1964	Sequence 1964, Ap	C 161	11.6	55.2	25	15	US-10-098-263B-46344	Sequence 46344, A
C 89	12	57.1	36	9	US-09-504-231A-2066	Sequence 2066, Ap	C 162	11.6	55.2	25	15	US-10-098-263B-53837	Sequence 53837, A
C 90	12	57.1	36	9	US-09-274-553D-1730	Sequence 1730, Ap	C 163	11.6	55.2	25	15	US-10-098-263B-72451	Sequence 72451, A
C 91	12	57.1	36	9	US-09-274-553D-1937	Sequence 1937, Ap	C 164	11.6	55.2	25	15	US-10-098-263B-77366	Sequence 77366, A
C 92	12	57.1	36	9	US-09-274-553D-1964	Sequence 1964, Ap	C 165	11.6	55.2	25	15	US-10-098-263B-77668	Sequence 77668, A
C 93	12	57.1	36	9	US-09-274-553D-2066	Sequence 2066, Ap	C 166	11.6	55.2	25	15	US-10-098-263B-88236	Sequence 88236, A
C 94	12	57.1	36	9	US-09-864-785-1970	Sequence 1970, Ap	C 167	11.6	55.2	25	15	US-10-098-263B-88854	Sequence 88854, A
C 95	12	57.1	37	10	US-09-927-046-3651	Sequence 3651, Ap	C 168	11.6	55.2	25	15	US-10-098-263B-100370	Sequence 100370, A
C 96	12	57.1	37	10	US-09-848-754A-9434	Sequence 9434, Ap	C 169	11.6	55.2	25	15	US-10-098-263B-107021	Sequence 107021, A
C 97	12	57.1	37	10	US-09-827-395A-1775	Sequence 1775, Ap	C 170	11.6	55.2	25	15	US-10-098-263B-109470	Sequence 109470, A
C 98	12	57.1	37	15	US-10-156-306-2659	Sequence 2659, Ap	C 171	11.6	55.2	25	15	US-10-098-263B-127486	Sequence 127486, A
C 99	12	57.1	37	15	US-10-156-306-2682	Sequence 2682, Ap	C 172	11.6	55.2	30	10	US-09-854-867-555	Sequence 555, App
C 100	12	57.1	37	15	US-10-156-306-6238	Sequence 6238, Ap	C 173	11.6	55.2	34	9	US-09-864-785-3884	Sequence 3884, Ap
C 101	12	57.1	37	15	US-10-430-882-1775	Sequence 1775, Ap	C 174	11.6	55.2	36	16	US-10-420-194-621	Sequence 621, App
C 102	12	57.1	37	16	US-10-138-674-20375	Sequence 20375, A	C 175	11.6	55.2	37	10	US-09-927-046-3621	Sequence 3621, Ap
C 103	12	57.1	37	16	US-10-138-674-20459	Sequence 20459, A	C 176	11.6	55.2	37	10	US-09-927-046-3682	Sequence 3682, Ap
C 104	12	57.1	37	17	US-10-287-949A-20375	Sequence 20375, A	C 177	11.6	55.2	37	10	US-09-848-754A-6416	Sequence 6416, Ap
C 105	12	57.1	37	17	US-10-287-949A-20459	Sequence 20459, A	C 178	11.6	55.2	37	15	US-10-156-306-6108	Sequence 6108, Ap
C 106	12	57.1	38	10	US-09-730-289B-2014	Sequence 2014, Ap	C 179	11.6	55.2	37	16	US-10-138-674-18325	Sequence 18325, A
C 107	12	57.1	38	10	US-09-927-046-2466	Sequence 2466, Ap	C 180	11.6	55.2	37	16	US-10-138-674-18329	Sequence 18329, A
C 108	12	57.1	38	10	US-09-877-478-2875	Sequence 2875, Ap	C 181	11.6	55.2	37	16	US-10-138-674-20309	Sequence 20309, A
C 109	12	57.1	38	10	US-09-848-754A-4055	Sequence 4055, Ap	C 182	11.6	55.2	37	16	US-10-138-674-20416	Sequence 20416, A
C 110	12	57.1	38	10	US-09-848-754A-4084	Sequence 4084, Ap	C 183	11.6	55.2	37	16	US-10-138-674-20440	Sequence 20440, A
C 111	12	57.1	38	10	US-09-848-754A-4297	Sequence 4297, Ap	C 184	11.6	55.2	37	17	US-10-287-949A-18325	Sequence 18325, A
C 112	12	57.1	38	10	US-09-930-423-1813	Sequence 1813, Ap	C 185	11.6	55.2	37	17	US-10-287-949A-18329	Sequence 18329, A
C 113	12	57.1	38	10	US-09-745-237A-1813	Sequence 1813, Ap	C 186	11.6	55.2	37	17	US-10-287-949A-20309	Sequence 20309, A
C 114	12	57.1	38	15	US-10-156-306-856	Sequence 856, App	C 187	11.6	55.2	37	17	US-10-287-949A-20416	Sequence 20416, A
C 115	12	57.1	38	15	US-10-156-306-1164	Sequence 1164, Ap	C 188	11.6	55.2	37	17	US-10-287-949A-20440	Sequence 20440, A
C 116	12	57.1	38	15	US-10-156-306-4610	Sequence 4610, Ap	C 189	11.6	55.2	37	17	US-10-763-210-10	Sequence 10, Appl
C 117	12	57.1	38	16	US-10-342-902-2875	Sequence 2875, A	C 190	11.6	55.2	38	9	US-09-864-785-856	Sequence 856, App
C 118	12	57.1	38	16	US-10-138-674-9634	Sequence 9634, Ap	C 191	11.6	55.2	38	9	US-09-864-785-859	Sequence 859, App
C 119	12	57.1	38	16	US-10-138-674-10074	Sequence 10074, A	C 192	11.6	55.2	38	9	US-09-864-785-1222	Sequence 1222, Ap
C 120	12	57.1	38	16	US-10-138-674-10381	Sequence 10381, A	C 193	11.6	55.2	38	9	US-09-864-785-1327	Sequence 1327, Ap
C 121	12	57.1	38	16	US-10-138-674-10618	Sequence 10618, A	C 194	11.6	55.2	38	10	US-09-780-533A-3460	Sequence 3460, Ap
C 122	12	57.1	38	16	US-10-138-674-11669	Sequence 11669, A	C 195	11.6	55.2	38	10	US-09-780-533A-3528	Sequence 3528, Ap
C 123	12	57.1	38	16	US-10-138-674-12058	Sequence 12058, A	C 196	11.6	55.2	38	10	US-09-780-533A-3534	Sequence 3534, Ap
C 124	12	57.1	38	16	US-10-138-674-12251	Sequence 12251, A	C 197	11.6	55.2	38	10	US-09-780-533A-3542	Sequence 3542, Ap
C 125	12	57.1	38	16	US-10-138-674-12598	Sequence 12598, A	C 198	11.6	55.2	38	10	US-09-780-533A-3570	Sequence 3570, Ap
C 126	12	57.1	38	16	US-10-138-674-12629	Sequence 12629, A	C 199	11.6	55.2	38	10	US-09-780-533A-3621	Sequence 3621, Ap
C 127	12	57.1	38	16	US-10-138-674-12789	Sequence 12789, A	C 200	11.6	55.2	38	10	US-09-780-533A-3630	Sequence 3630, Ap
C 128	12	57.1	38	17	US-10-287-949A-9634	Sequence 9634, Ap	C 201	11.6	55.2	38	10	US-09-780-533A-3642	Sequence 3642, Ap
C 129	12	57.1	38	17	US-10-287-949A-10074	Sequence 10074, A	C 202	11.6	55.2	38	10	US-09-780-533A-3781	Sequence 3781, Ap
C 130	12	57.1	38	17	US-10-287-949A-10381	Sequence 10381, A	C 203	11.6	55.2	38	10	US-09-780-533A-4158	Sequence 4158, Ap
C 131	12	57.1	38	17	US-10-287-949A-10618	Sequence 10618, A	C 204	11.6	55.2	38	10	US-09-780-533A-4200	Sequence 4200, Ap
C 132	12	57.1	38	17	US-10-287-949A-11669	Sequence 11669, A	C 205	11.6	55.2	38	10	US-09-927-046-2935	Sequence 2935, Ap
C 133	12	57.1	38	17	US-10-287-949A-12058	Sequence 12058, A	C 206	11.6	55.2	38	10	US-09-927-046-2993	Sequence 2993, Ap
C 134	12	57.1	38	17	US-10-287-949A-12251	Sequence 12251, A	C 207	11.6	55.2	38	10	US-09-927-046-3354	Sequence 3354, Ap
C 135	12	57.1	38	17	US-10-287-949A-12598	Sequence 12598, A	C 208	11.6	55.2	38	10	US-09-877-478-3450	Sequence 3450, Ap
C 136	12	57.1	38	17	US-10-287-949A-12629	Sequence 12629, A	C 209	11.6	55.2	38	10	US-09-877-478-3564	Sequence 3564, Ap
C 137	12	57.1	38	17	US-10-287-949A-12789	Sequence 12789, A	C 210	11.6	55.2	38	10	US-09-877-478-3569	Sequence 3569, Ap
C 138	12	57.1	38	17	US-10-669-841-7766	Sequence 7766, Ap	C 211	11.6	55.2	38	10	US-09-877-478-3604	Sequence 3604, Ap
C 139	12	57.1	50	15	US-10-173-730-7	Sequence 7, Appli	C 212	11.6	55.2	38	10	US-09-877-478-3684	Sequence 3684, Ap
C 140	12	57.1	50	16	US-10-662-188-193	Sequence 193, App	C 213	11.6	55.2	38	10	US-09-877-478-3836	Sequence 3836, Ap
C 141	11.8	56.2	15	9	US-09-504-231A-905	Sequence 905, App	C 214	11.6	55.2	38	10	US-09-877-478-3891	Sequence 3891, Ap
C 142	11.8	56.2	15	9	US-09-274-553D-905	Sequence 905, App	C 215	11.6	55.2	38	10	US-09-848-754A-4612	Sequence 4612, Ap
C 143	11.8	56.2	17	10	US-09-740-332-1151	Sequence 1151, Ap	C 216	11.6	55.2	38	10	US-09-848-754A-4622	Sequence 4622, Ap
C 144	11.8	56.2	17	10	US-09-817-879-1151	Sequence 1151, Ap	C 217	11.6	55.2	38	10	US-09-848-754A-4627	Sequence 4627, Ap
C 145	11.8	56.2	17	10	US-10-669-841-3744	Sequence 3744, Ap	C 218	11.6	55.2	38	10	US-09-848-754A-4630	Sequence 4630, Ap
C 146	11.8	56.2	25	15	US-10-098-263B-9435	Sequence 9435, Ap	C 219	11.6	55.2	38	10	US-09-848-754A-4632	Sequence 4632, Ap
C 147	11.8	56.2	25	15	US-10-098-263B-20460	Sequence 20460, A	C 220	11.6	55.2	38	10	US-09-848-754A-5112	Sequence 5112, Ap
C 148	11.8	56.2	25	15	US-10-098-263B-28862	Sequence 28862, A	C 221	11.6	55.2	38	10	US-09-848-754A-5174	Sequence 5174, Ap
C 149	11.8	56.2	25	15	US-10-098-263B-32872	Sequence 32872, A	C 222	11.6	55.2	38	10	US-09-848-754A-5281	Sequence 5281, Ap
C 150	11.8	56.2	25	15	US-10-098-263B-36930	Sequence 36930, A	C 223	11.6	55.2	38	10	US-09-848-754A-5395	Sequence 5395, Ap
C 151	11.8	56.2	25	15	US-10-098-263B-86994	Sequence 86994, A	C 224	11.6	55.2	38	10	US-09-848-754A-5435	Sequence 5435, Ap
C 152	11.8	56.2	25	15	US-10-098-263B-98332	Sequence 98332, A	C 225	11.6	55.2	38	10	US-09-848-754A-5519	Sequence 5519, Ap
C 153	11.8	56.2	38	10	US-09-877-478-2972	Sequence 2972, Ap	C 226	11.6	55.2	38	10	US-09-848-754A-5697	Sequence 5697, Ap
C 154	11.8	56.2	38	16	US-10-342-902-2972	Sequence 2972, Ap	C 227	11.6	55.2	38	10	US-09-930-423-2065	Sequence 2065, Ap
C 155	11.8	56.2	38	17	US-10-669-841-7863	Sequence 7863, Ap	C 228	11.6	55.2	38	10	US-09-930-423-2091	Sequence 2091, Ap
C 156	11.6	55.2	20	15	US-10-244-367-20	Sequence 20, Appl	C 229	11.6	55.2	38	10	US-09-930-423-2097	Sequence 2097, Ap
C 157	11.6	55.2	25	15	US-10-098-263B-787	Sequence 787, App	C 230	11.6	55.2	38	10	US-09-930-423-2102	Sequence 2102, Ap
C 158	11.6	55.2	25	15	US-10-098-263B-788	Sequence 788, App	C 231	11.6	55.2	38	10	US-09-930-423-2106	Sequence 2106, Ap

C 232	11.6	55.2	38	10	US-09-930-423-2119	Sequence 2119, Ap	C 305	11.6	55.2	38	17	US-10-712-672-3305	Sequence 3305, Ap
C 233	11.6	55.2	38	10	US-09-930-423-2199	Sequence 2199, Ap	C 306	11.6	55.2	38	17	US-10-712-672-3326	Sequence 3326, Ap
C 234	11.6	55.2	38	10	US-09-930-423-2248	Sequence 2248, Ap	C 307	11.6	55.2	38	17	US-10-712-672-3370	Sequence 3370, Ap
C 235	11.6	55.2	38	10	US-09-930-423-2574	Sequence 2574, Ap	C 308	11.6	55.2	38	17	US-10-712-672-3401	Sequence 3401, Ap
C 236	11.6	55.2	38	10	US-09-930-423-2595	Sequence 2595, Ap	C 309	11.6	55.2	38	17	US-10-712-672-3412	Sequence 3412, Ap
C 237	11.6	55.2	38	10	US-09-827-395A-1245	Sequence 1245, Ap	C 310	11.6	55.2	38	17	US-10-712-672-3434	Sequence 3434, Ap
C 238	11.6	55.2	38	10	US-09-827-395A-1307	Sequence 1307, Ap	C 311	11.6	55.2	38	17	US-10-712-672-3494	Sequence 3494, Ap
C 239	11.6	55.2	38	10	US-09-827-395A-1337	Sequence 1337, Ap	C 312	11.6	55.2	38	17	US-10-712-672-3559	Sequence 3559, Ap
C 240	11.6	55.2	38	10	US-09-827-395A-1379	Sequence 1379, Ap	C 313	11.6	55.2	38	17	US-10-712-672-3666	Sequence 3666, Ap
C 241	11.6	55.2	38	10	US-09-827-395A-1404	Sequence 1404, Ap	C 314	11.6	55.2	38	17	US-10-712-672-3701	Sequence 3701, Ap
C 242	11.6	55.2	38	10	US-09-827-395A-1411	Sequence 1411, Ap	C 315	11.6	55.2	38	17	US-10-712-672-3708	Sequence 3708, Ap
C 243	11.6	55.2	38	10	US-09-827-395A-1465	Sequence 1465, Ap	C 316	11.6	55.2	38	17	US-10-712-672-3729	Sequence 3729, Ap
C 244	11.6	55.2	38	10	US-09-792-818-1284	Sequence 1284, Ap	C 317	11.6	55.2	38	17	US-10-712-672-3761	Sequence 3761, Ap
C 245	11.6	55.2	38	10	US-09-792-818-1359	Sequence 1359, Ap	C 318	11.6	55.2	38	17	US-10-712-672-4076	Sequence 4076, Ap
C 246	11.6	55.2	38	10	US-09-745-237A-2065	Sequence 2065, Ap	C 319	11.6	55.2	38	17	US-10-669-841-8341	Sequence 8341, Ap
C 247	11.6	55.2	38	10	US-09-745-237A-2091	Sequence 2091, Ap	C 320	11.6	55.2	38	17	US-10-669-841-8455	Sequence 8455, Ap
C 248	11.6	55.2	38	10	US-09-745-237A-2097	Sequence 2097, Ap	C 321	11.6	55.2	38	17	US-10-669-841-8460	Sequence 8460, Ap
C 249	11.6	55.2	38	10	US-09-745-237A-2102	Sequence 2102, Ap	C 322	11.6	55.2	38	17	US-10-669-841-8495	Sequence 8495, Ap
C 250	11.6	55.2	38	10	US-09-745-237A-2106	Sequence 2106, Ap	C 323	11.6	55.2	38	17	US-10-669-841-8575	Sequence 8575, Ap
C 251	11.6	55.2	38	10	US-09-745-237A-2119	Sequence 2119, Ap	C 324	11.6	55.2	38	17	US-10-669-841-8727	Sequence 8727, Ap
C 252	11.6	55.2	38	10	US-09-745-237A-2199	Sequence 2199, Ap	C 325	11.6	55.2	38	17	US-10-669-841-8782	Sequence 8782, Ap
C 253	11.6	55.2	38	10	US-09-745-237A-2248	Sequence 2248, Ap	C 326	11.6	55.2	39	13	US-10-072-152-26	Sequence 26, Appl
C 254	11.6	55.2	38	10	US-09-745-237A-2574	Sequence 2574, Ap	C 327	11.6	55.2	39	15	US-10-277-471A-11	Sequence 11, Appl
C 255	11.6	55.2	38	10	US-09-745-237A-2595	Sequence 2595, Ap	C 328	11.6	55.2	39	15	US-10-339-674-633	Sequence 633, App
C 256	11.6	55.2	38	15	US-10-156-306-2222	Sequence 2222, Ap	C 329	11.6	55.2	39	15	US-10-339-674-6335	Sequence 2615, App
C 257	11.6	55.2	38	15	US-10-156-306-5439	Sequence 5439, Ap	C 330	11.6	55.2	39	16	US-10-655-433-26	Sequence 26, Appl
C 258	11.6	55.2	38	15	US-10-156-306-5442	Sequence 5442, Ap	C 331	11.4	54.3	15	9	US-09-504-231A-904	Sequence 904, App
C 259	11.6	55.2	38	15	US-10-156-306-5538	Sequence 5538, Ap	C 332	11.4	54.3	19	9	US-09-274-553D-904	Sequence 904, App
C 260	11.6	55.2	38	15	US-10-156-306-5615	Sequence 5615, Ap	C 333	11.4	54.3	19	9	US-09-969-373-4574	Sequence 4574, App
C 261	11.6	55.2	38	15	US-10-156-306-5717	Sequence 5717, Ap	C 334	11.4	54.3	22	15	US-10-296-995-93	Sequence 93, Appl
C 262	11.6	55.2	38	15	US-10-157-580A-88	Sequence 88, Appl	C 335	11.4	54.3	23	15	US-10-214-932-14	Sequence 14, Appl
C 263	11.6	55.2	38	15	US-10-230-006-863	Sequence 863, App	C 336	11.4	54.3	23	16	US-10-474-290-6	Sequence 6, Appl
C 264	11.6	55.2	38	15	US-10-230-006-873	Sequence 873, App	C 337	11.4	54.3	24	10	US-09-940-185-2381	Sequence 2381, Ap
C 265	11.6	55.2	38	15	US-10-230-006-887	Sequence 887, App	C 338	11.4	54.3	25	14	US-10-215-112-3435	Sequence 3435, Ap
C 266	11.6	55.2	38	15	US-10-230-006-896	Sequence 896, App	C 339	11.4	54.3	25	14	US-10-215-112-5874	Sequence 5874, Ap
C 267	11.6	55.2	38	15	US-10-230-006-930	Sequence 930, App	C 340	11.4	54.3	25	14	US-10-215-112-10677	Sequence 10677, A
C 268	11.6	55.2	38	15	US-10-230-006-970	Sequence 970, App	C 341	11.4	54.3	25	15	US-10-098-2638-34732	Sequence 34732, A
C 269	11.6	55.2	38	15	US-10-230-006-1002	Sequence 1002, Ap	C 342	11.4	54.3	25	15	US-10-098-2638-56624	Sequence 56624, A
C 270	11.6	55.2	38	15	US-10-230-006-1051	Sequence 1051, Ap	C 343	11.4	54.3	25	15	US-10-098-2638-69290	Sequence 69290, A
C 271	11.6	55.2	38	15	US-10-230-006-1058	Sequence 1058, Ap	C 344	11.4	54.3	25	15	US-10-098-2638-71594	Sequence 71594, A
C 272	11.6	55.2	38	15	US-10-230-006-1108	Sequence 1108, Ap	C 345	11.4	54.3	25	15	US-10-098-2638-89565	Sequence 89565, A
C 273	11.6	55.2	38	15	US-10-430-882-1245	Sequence 1245, Ap	C 346	11.4	54.3	25	15	US-10-098-2638-89566	Sequence 89566, A
C 274	11.6	55.2	38	15	US-10-430-882-1307	Sequence 1307, Ap	C 347	11.4	54.3	25	15	US-10-098-2638-104298	Sequence 104298, A
C 275	11.6	55.2	38	15	US-10-430-882-1337	Sequence 1337, Ap	C 348	11.4	54.3	25	15	US-10-098-2638-104438	Sequence 104438, A
C 276	11.6	55.2	38	15	US-10-430-882-1379	Sequence 1379, Ap	C 349	11.4	54.3	25	15	US-10-098-2638-110567	Sequence 110567, A
C 277	11.6	55.2	38	15	US-10-430-882-1404	Sequence 1404, Ap	C 350	11.4	54.3	25	15	US-10-098-2638-121446	Sequence 121446, A
C 278	11.6	55.2	38	15	US-10-430-882-1411	Sequence 1411, Ap	C 351	11.4	54.3	26	9	US-09-895-141-8	Sequence 8, Appl
C 279	11.6	55.2	38	15	US-10-430-882-1465	Sequence 1465, Ap	C 352	11.4	54.3	27	10	US-09-877-705A-11	Sequence 11, Appl
C 280	11.6	55.2	38	16	US-10-342-902-3450	Sequence 3450, Ap	C 353	11.4	54.3	27	10	US-09-877-705A-12	Sequence 12, Appl
C 281	11.6	55.2	38	16	US-10-342-902-3564	Sequence 3564, Ap	C 354	11.4	54.3	27	10	US-09-947-274-11	Sequence 11, Appl
C 282	11.6	55.2	38	16	US-10-342-902-3569	Sequence 3569, Ap	C 355	11.4	54.3	27	10	US-09-947-274-12	Sequence 12, Appl
C 283	11.6	55.2	38	16	US-10-342-902-3604	Sequence 3604, Ap	C 356	11.4	54.3	27	10	US-09-877-738A-11	Sequence 11, Appl
C 284	11.6	55.2	38	16	US-10-342-902-3684	Sequence 3684, Ap	C 357	11.4	54.3	27	10	US-09-877-738A-12	Sequence 12, Appl
C 285	11.6	55.2	38	16	US-10-342-902-3836	Sequence 3836, Ap	C 358	11.4	54.3	27	12	US-09-877-403A-11	Sequence 11, Appl
C 286	11.6	55.2	38	16	US-10-342-902-3891	Sequence 3891, Ap	C 359	11.4	54.3	27	12	US-09-877-403A-12	Sequence 12, Appl
C 287	11.6	55.2	38	16	US-10-138-674-13690	Sequence 13690, A	C 360	11.4	54.3	27	15	US-10-057-810-11	Sequence 11, Appl
C 288	11.6	55.2	38	16	US-10-138-674-14351	Sequence 14351, A	C 361	11.4	54.3	27	15	US-10-057-810-12	Sequence 12, Appl
C 289	11.6	55.2	38	16	US-10-138-674-14432	Sequence 14432, A	C 362	11.4	54.3	27	15	US-10-057-828-11	Sequence 11, Appl
C 290	11.6	55.2	38	16	US-10-138-674-14657	Sequence 14657, A	C 363	11.4	54.3	27	15	US-10-057-828-12	Sequence 12, Appl
C 291	11.6	55.2	38	16	US-10-138-674-14673	Sequence 14673, A	C 364	11.4	54.3	27	17	US-10-779-595-11	Sequence 11, Appl
C 292	11.6	55.2	38	16	US-10-138-674-15466	Sequence 15466, A	C 365	11.4	54.3	27	17	US-10-779-595-12	Sequence 12, Appl
C 293	11.6	55.2	38	16	US-10-138-674-15727	Sequence 15727, A	C 366	11.4	54.3	28	14	US-10-066-007-31	Sequence 31, Appl
C 294	11.6	55.2	38	17	US-10-287-949A-13690	Sequence 13690, A	C 367	11.2	53.3	18	18	US-10-740-926-406	Sequence 406, App
C 295	11.6	55.2	38	17	US-10-287-949A-14351	Sequence 14351, A	C 368	11.2	53.3	18	18	US-10-740-926-436	Sequence 436, App
C 296	11.6	55.2	38	17	US-10-287-949A-14432	Sequence 14432, A	C 369	11.2	53.3	20	17	US-10-319-914-77	Sequence 77, Appl
C 297	11.6	55.2	38	17	US-10-287-949A-14657	Sequence 14657, A	C 370	11.2	53.3	20	17	US-10-319-914-155	Sequence 155, App
C 298	11.6	55.2	38	17	US-10-287-949A-15673	Sequence 15673, A	C 371	11.2	53.3	25	17	US-10-619-739-322	Sequence 322, App
C 299	11.6	55.2	38	17	US-10-287-949A-15466	Sequence 15466, A	C 372	11.2	53.3	25	14	US-10-215-112-308	Sequence 308, App
C 300	11.6	55.2	38	17	US-10-287-949A-15727	Sequence 15727, A	C 373	11.2	53.3	25	14	US-10-215-112-8911	Sequence 8911, Ap
C 301	11.6	55.2	38	17	US-10-712-672-3204	Sequence 3204, Ap	C 374	11.2	53.3	25	14	US-10-215-112-9916	Sequence 9916, Ap
C 302	11.6	55.2	38	17	US-10-712-672-3228	Sequence 3228, Ap	C 375	11.2	53.3	25	14	US-10-215-112-10028	Sequence 10028, A
C 303	11.6	55.2	38	17	US-10-712-672-3234	Sequence 3234, Ap	C 376	11.2	53.3	25	15	US-10-098-2638-1018	Sequence 1018, Ap
C 304	11.6	55.2	38	17	US-10-712-672-3242	Sequence 3242, Ap	C 377	11.2	53.3	25	15	US-10-098-2638-2080	Sequence 2080, Ap

378	11.2	53.3	25	15	US-10-098-263B-9678	Sequence 9678, Ap	451	11	52.4	24	9	US-09-993-687-459	Sequence 459, App
c 379	11.2	53.3	25	15	US-10-098-263B-11931	Sequence 11931, A	452	11	52.4	24	10	US-09-989-734-459	Sequence 459, App
c 380	11.2	53.3	25	15	US-10-098-263B-26773	Sequence 26773, A	453	11	52.4	24	10	US-09-997-653-459	Sequence 459, App
c 381	11.2	53.3	25	15	US-10-098-263B-30572	Sequence 30572, A	454	11	52.4	24	10	US-09-989-724-459	Sequence 459, App
c 382	11.2	53.3	25	15	US-10-098-263B-34409	Sequence 34409, A	455	11	52.4	24	10	US-09-989-728-459	Sequence 459, App
c 383	11.2	53.3	25	15	US-10-098-263B-34906	Sequence 34906, A	456	11	52.4	24	10	US-09-990-441-459	Sequence 459, App
c 384	11.2	53.3	25	15	US-10-098-263B-36180	Sequence 36180, A	457	11	52.4	24	10	US-09-993-667-459	Sequence 459, App
c 385	11.2	53.3	25	15	US-10-098-263B-36180	Sequence 36180, A	458	11	52.4	24	10	US-09-997-428-459	Sequence 459, App
c 386	11.2	53.3	25	15	US-10-098-263B-44094	Sequence 44094, A	459	11	52.4	24	10	US-09-997-666-459	Sequence 459, App
c 387	11.2	53.3	25	15	US-10-098-263B-59261	Sequence 59261, A	460	11	52.4	24	10	US-09-990-438-459	Sequence 459, App
c 388	11.2	53.3	25	15	US-10-098-263B-71007	Sequence 71007, A	461	11	52.4	24	10	US-09-990-562-459	Sequence 459, App
c 389	11.2	53.3	25	15	US-10-098-263B-72284	Sequence 72284, A	462	11	52.4	24	10	US-09-990-711-459	Sequence 459, App
c 390	11.2	53.3	25	15	US-10-098-263B-75160	Sequence 75160, A	463	11	52.4	24	10	US-09-989-726-459	Sequence 459, App
c 391	11.2	53.3	25	15	US-10-098-263B-75762	Sequence 75762, A	464	11	52.4	24	10	US-09-998-156-459	Sequence 459, App
c 392	11.2	53.3	25	15	US-10-098-263B-121458	Sequence 121458, A	465	11	52.4	24	10	US-09-990-437-459	Sequence 459, App
c 393	11.2	53.3	25	15	US-10-098-263B-122026	Sequence 122026, A	466	11	52.4	24	10	US-09-991-157-459	Sequence 459, App
c 394	11.2	53.3	25	15	US-10-098-263B-128569	Sequence 128569, A	467	11	52.4	24	10	US-09-997-514-459	Sequence 459, App
c 395	11.2	53.3	25	15	US-10-098-263B-128570	Sequence 128570, A	468	11	52.4	24	10	US-09-997-573-459	Sequence 459, App
c 396	11.2	53.3	29	18	US-10-471-868-23	Sequence 23, Appl	469	11	52.4	24	10	US-09-991-172-459	Sequence 459, App
c 397	11.2	53.3	31	9	US-09-801-274-807	Sequence 807, App	470	11	52.4	24	10	US-09-990-726-459	Sequence 459, App
c 398	11.2	53.3	31	10	US-09-961-077-388	Sequence 388, App	471	11	52.4	24	10	US-09-997-559-459	Sequence 459, App
c 399	11.2	53.3	34	17	US-10-038-520-3	Sequence 3, Appl	472	11	52.4	24	10	US-09-997-601-459	Sequence 459, App
c 400	11.2	53.3	37	9	US-09-864-785-1839	Sequence 1839, Ap	473	11	52.4	24	10	US-09-990-443-459	Sequence 459, App
c 401	11.2	53.3	37	9	US-09-864-785-1919	Sequence 1919, Ap	474	11	52.4	24	10	US-09-991-854-459	Sequence 459, App
c 402	11.2	53.3	37	10	US-09-927-046-3665	Sequence 3665, Ap	475	11	52.4	24	10	US-09-997-628-459	Sequence 459, App
c 403	11.2	53.3	37	10	US-09-848-754A-6432	Sequence 6432, Ap	476	11	52.4	24	10	US-09-997-683-459	Sequence 459, App
c 404	11.2	53.3	37	16	US-09-848-754A-6516	Sequence 6516, Ap	477	11	52.4	24	10	US-09-989-729A-459	Sequence 459, App
c 405	11.2	53.3	37	16	US-10-138-674-20489	Sequence 20489, A	478	11	52.4	24	10	US-09-997-349-459	Sequence 459, App
c 406	11.2	53.3	37	16	US-10-138-674-20600	Sequence 20600, A	479	11	52.4	24	10	US-09-997-440-459	Sequence 459, App
c 407	11.2	53.3	37	16	US-10-138-674-20710	Sequence 20710, A	480	11	52.4	24	10	US-09-990-440-459	Sequence 459, App
c 408	11.2	53.3	37	17	US-10-287-949A-20489	Sequence 20489, A	481	11	52.4	24	10	US-09-997-857-459	Sequence 459, App
c 409	11.2	53.3	37	17	US-10-287-949A-20600	Sequence 20600, A	482	11	52.4	24	10	US-09-993-469-459	Sequence 459, App
c 410	11.2	53.3	38	9	US-09-874-547-65	Sequence 65, Appl	483	11	52.4	24	10	US-09-997-542-459	Sequence 459, App
c 411	11.2	53.3	39	16	US-10-345-410-2	Sequence 2, Appl	484	11	52.4	24	10	US-09-993-748-459	Sequence 459, App
c 412	11.2	53.3	40	9	US-09-815-980-3	Sequence 3, Appl	485	11	52.4	24	10	US-09-990-427-459	Sequence 459, App
c 413	11.2	53.3	40	9	US-09-815-980-4	Sequence 4, Appl	486	11	52.4	24	10	US-09-990-427-459	Sequence 459, App
c 414	11.2	53.3	45	10	US-09-791-153A-121	Sequence 121, App	487	11	52.4	24	10	US-09-989-328-459	Sequence 459, App
c 415	11.2	53.3	48	10	US-09-927-046-5230	Sequence 5230, Ap	488	11	52.4	24	10	US-09-993-583-459	Sequence 459, App
c 416	11.2	53.3	48	10	US-09-930-423-4525	Sequence 4525, Ap	489	11	52.4	24	10	US-09-941-992-459	Sequence 459, App
c 417	11.2	53.3	48	10	US-09-745-237A-4525	Sequence 4525, Ap	490	11	52.4	24	10	US-09-992-521-459	Sequence 459, App
c 418	11.2	53.3	50	16	US-10-131-827-6230	Sequence 6230, Ap	491	11	52.4	24	10	US-09-997-333-459	Sequence 459, App
c 419	11.2	53.3	50	18	US-10-690-487-43	Sequence 43, Appl	492	11	52.4	24	10	US-09-997-384-459	Sequence 459, App
c 420	11.2	53.3	50	18	US-10-690-487-44	Sequence 44, Appl	493	11	52.4	24	10	US-09-940-185-3246	Sequence 3246, Ap
c 421	11	52.4	17	16	US-10-138-674-3829	Sequence 3829, Ap	494	11	52.4	24	10	US-09-998-041-459	Sequence 459, App
c 422	11	52.4	17	16	US-10-138-674-3830	Sequence 3830, Ap	495	11	52.4	24	10	US-09-997-585-459	Sequence 459, App
c 423	11	52.4	17	17	US-10-287-949A-3829	Sequence 3829, Ap	496	11	52.4	24	10	US-09-997-614-459	Sequence 459, App
c 424	11	52.4	17	17	US-10-287-949A-3830	Sequence 3830, Ap	497	11	52.4	24	10	US-09-989-862-459	Sequence 459, App
c 425	11	52.4	20	16	US-10-349-143-6875	Sequence 6875, Ap	498	11	52.4	24	10	US-09-997-529-459	Sequence 459, App
c 426	11	52.4	20	16	US-10-289-762-5503	Sequence 5503, Ap	499	11	52.4	24	10	US-09-989-725-459	Sequence 459, App
c 427	11	52.4	22	15	US-10-270-313-4	Sequence 4, Appl	500	11	52.4	24	10	US-09-991-150-459	Sequence 459, App
c 428	11	52.4	24	9	US-09-823-936-7	Sequence 7, Appl	501	11	52.4	24	10	US-09-997-641-459	Sequence 459, App
c 429	11	52.4	24	9	US-09-823-936-8	Sequence 8, Appl	502	11	52.4	24	10	US-09-989-733-459	Sequence 459, App
c 430	11	52.4	24	9	US-09-989-722-459	Sequence 459, App	503	11	52.4	24	10	US-09-992-643-459	Sequence 459, App
c 431	11	52.4	24	9	US-09-989-723-459	Sequence 459, App	504	11	52.4	24	15	US-10-286-140-7	Sequence 7, Appl
c 432	11	52.4	24	9	US-09-989-727-459	Sequence 459, App	505	11	52.4	24	15	US-10-286-140-8	Sequence 8, Appl
c 433	11	52.4	24	9	US-09-989-727-459	Sequence 459, App	506	11	52.4	24	16	US-10-617-038-6	Sequence 6, Appl
c 434	11	52.4	24	9	US-09-989-731-459	Sequence 459, App	507	11	52.4	24	17	US-10-645-695-7	Sequence 7, Appl
c 435	11	52.4	24	9	US-09-755-836-6	Sequence 6, Appl	508	11	52.4	24	17	US-10-215-112-13237	Sequence 13237, A
c 436	11	52.4	24	9	US-09-755-836-7	Sequence 7, Appl	509	11	52.4	25	14	US-10-215-112-13363	Sequence 13363, A
c 437	11	52.4	24	9	US-09-989-732-459	Sequence 459, App	510	11	52.4	25	14	US-10-215-112-13363	Sequence 13363, A
c 438	11	52.4	24	9	US-09-991-073-459	Sequence 459, App	511	11	52.4	25	15	US-10-098-263B-4984	Sequence 4984, Ap
c 439	11	52.4	24	9	US-09-990-442-459	Sequence 459, App	512	11	52.4	25	15	US-10-098-263B-14662	Sequence 14662, A
c 440	11	52.4	24	9	US-09-991-163-459	Sequence 459, App	513	11	52.4	25	15	US-10-098-263B-16956	Sequence 16956, A
c 441	11	52.4	24	9	US-09-993-604-459	Sequence 459, App	514	11	52.4	25	15	US-10-098-263B-19771	Sequence 19771, A
c 442	11	52.4	24	9	US-09-990-456-459	Sequence 459, App	515	11	52.4	25	15	US-10-098-263B-25743	Sequence 25743, A
c 443	11	52.4	24	9	US-09-989-721-459	Sequence 459, App	516	11	52.4	25	15	US-10-098-263B-28673	Sequence 28673, A
c 444	11	52.4	24	9	US-09-992-598-459	Sequence 459, App	517	11	52.4	25	15	US-10-098-263B-28857	Sequence 28857, A
c 445	11	52.4	24	9	US-09-989-293A-459	Sequence 459, App	518	11	52.4	25	15	US-10-098-263B-31842	Sequence 31842, A
c 446	11	52.4	24	9	US-09-989-735-459	Sequence 459, App	519	11	52.4	25	15	US-10-098-263B-74355	Sequence 74355, A
c 447	11	52.4	24	9	US-09-990-444-459	Sequence 459, App	520	11	52.4	25	15	US-10-098-263B-75258	Sequence 75258, A
c 448	11	52.4	24	9	US-09-991-181-459	Sequence 459, App	521	11	52.4	25	15	US-10-098-263B-86878	Sequence 86878, A
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c 526	11	52.4	25	15	US-10-088-263B-100534	Sequence 100534, A	599	11	52.4	37	10	US-09-827-395A-1813	Sequence 1813, Ap
527	11	52.4	25	15	US-10-088-263B-112398	Sequence 112398, A	600	11	52.4	37	15	US-10-156-306-2614	Sequence 2614, Ap
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c 530	11	52.4	33	9	US-09-504-231A-3131	Sequence 3131, Ap	603	11	52.4	37	15	US-10-230-006-1551	Sequence 1551, Ap
c 531	11	52.4	33	9	US-09-274-553D-3131	Sequence 3131, Ap	604	11	52.4	37	15	US-10-230-006-1563	Sequence 1563, Ap
c 532	11	52.4	35	9	US-09-864-785-3828	Sequence 3828, Ap	605	11	52.4	37	15	US-10-230-006-1606	Sequence 1606, Ap
c 533	11	52.4	35	9	US-09-864-785-3830	Sequence 3830, Ap	606	11	52.4	37	15	US-10-430-882-1813	Sequence 1813, Ap
c 534	11	52.4	36	9	US-09-504-231A-1645	Sequence 1645, Ap	c 607	11	52.4	37	16	US-10-342-902-6277	Sequence 6277, Ap
c 535	11	52.4	36	9	US-09-504-231A-1682	Sequence 1682, Ap	c 608	11	52.4	37	16	US-10-342-902-6373	Sequence 6373, Ap
c 536	11	52.4	36	9	US-09-504-231A-1808	Sequence 1808, Ap	c 609	11	52.4	37	16	US-10-138-674-18727	Sequence 18727, A
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c 539	11	52.4	36	9	US-09-504-231A-2001	Sequence 2001, Ap	612	11	52.4	37	16	US-10-138-674-20186	Sequence 20186, A
c 540	11	52.4	36	9	US-09-504-231A-2052	Sequence 2052, Ap	613	11	52.4	37	16	US-10-138-674-20624	Sequence 20624, A
c 541	11	52.4	36	9	US-09-504-231A-2101	Sequence 2101, Ap	614	11	52.4	37	16	US-10-138-674-20731	Sequence 20731, A
c 542	11	52.4	36	9	US-09-504-231A-2174	Sequence 2174, Ap	615	11	52.4	37	16	US-10-138-674-20743	Sequence 20743, A
c 543	11	52.4	36	9	US-09-504-231A-2184	Sequence 2184, Ap	616	11	52.4	37	16	US-10-138-674-20759	Sequence 20759, A
c 544	11	52.4	36	9	US-09-504-231A-2186	Sequence 2186, Ap	617	11	52.4	37	17	US-10-287-949A-18727	Sequence 18727, A
c 545	11	52.4	36	9	US-09-504-231A-2190	Sequence 2190, Ap	618	11	52.4	37	17	US-10-287-949A-18872	Sequence 18872, A
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c 548	11	52.4	36	9	US-09-504-231A-2458	Sequence 2458, Ap	621	11	52.4	37	17	US-10-287-949A-20624	Sequence 20624, A
c 549	11	52.4	36	9	US-09-504-231A-2513	Sequence 2487, Ap	622	11	52.4	37	17	US-10-287-949A-20731	Sequence 20731, A
c 550	11	52.4	36	9	US-09-504-231A-2513	Sequence 2513, Ap	623	11	52.4	37	17	US-10-287-949A-20743	Sequence 20743, A
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c 555	11	52.4	36	9	US-09-274-553D-1894	Sequence 1894, Ap	628	11	52.4	38	9	US-09-874-547-79	Sequence 79, Appl
c 556	11	52.4	36	9	US-09-274-553D-2001	Sequence 1980, Ap	629	11	52.4	38	9	US-09-874-547-84	Sequence 84, Appl
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c 558	11	52.4	36	9	US-09-274-553D-2052	Sequence 2052, Ap	c 631	11	52.4	38	9	US-09-864-785-771	Sequence 771, App
c 559	11	52.4	36	9	US-09-274-553D-2101	Sequence 2101, Ap	c 632	11	52.4	38	9	US-09-864-785-775	Sequence 775, App
c 560	11	52.4	36	9	US-09-274-553D-2174	Sequence 2174, Ap	c 633	11	52.4	38	9	US-09-864-785-787	Sequence 787, App
c 561	11	52.4	36	9	US-09-274-553D-2184	Sequence 2184, Ap	c 634	11	52.4	38	9	US-09-864-785-910	Sequence 910, App
c 562	11	52.4	36	9	US-09-274-553D-2186	Sequence 2186, Ap	c 635	11	52.4	38	9	US-09-864-785-932	Sequence 932, App
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c 564	11	52.4	36	9	US-09-274-553D-2378	Sequence 2378, Ap	c 637	11	52.4	38	9	US-09-864-785-990	Sequence 990, App
c 565	11	52.4	36	9	US-09-274-553D-2384	Sequence 2384, Ap	c 638	11	52.4	38	9	US-09-864-785-1027	Sequence 1027, App
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c 568	11	52.4	36	9	US-09-274-553D-2513	Sequence 2513, Ap	c 641	11	52.4	38	9	US-09-864-785-1066	Sequence 1066, App
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c 575	11	52.4	36	16	US-10-420-194-585	Sequence 585, App	c 648	11	52.4	38	9	US-09-864-785-1205	Sequence 1205, App
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c 595	11	52.4	37	10	US-09-848-754A-5984	Sequence 5984, Ap	c 668	11	52.4	38	10	US-09-780-533A-2792	Sequence 2792, App
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c 677	11	52.4	38	10	US-09-780-533A-3599	Sequence 3599, Ap	c 750	11	52.4	38	10	US-09-848-754A-3795	Sequence 3795, Ap
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c 690	11	52.4	38	10	US-09-780-533A-4020	Sequence 4020, Ap	c 763	11	52.4	38	10	US-09-848-754A-4996	Sequence 4996, Ap
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c 693	11	52.4	38	10	US-09-780-533A-4068	Sequence 4068, Ap	c 766	11	52.4	38	10	US-09-848-754A-5107	Sequence 5107, Ap
c 694	11	52.4	38	10	US-09-780-533A-4086	Sequence 4086, Ap	c 767	11	52.4	38	10	US-09-848-754A-5143	Sequence 5143, Ap
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C 879	11	52.4	38	10	US-09-745-237A-2150	Sequence 2150, Ap	C 952	11	52.4	38	15	US-10-230-006-302	Sequence 302, App
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c 984      11 52.4      38 15 US-10-230-006-1114      Sequence 1114, Ap
c 985      11 52.4      38 15 US-10-230-006-1117      Sequence 1117, Ap
c 986      11 52.4      38 15 US-10-230-006-1120      Sequence 1120, Ap
c 987      11 52.4      38 15 US-10-230-006-1123      Sequence 1123, Ap
c 988      11 52.4      38 15 US-10-230-006-1126      Sequence 1126, Ap
c 989      11 52.4      38 15 US-10-230-006-1129      Sequence 1129, Ap
c 990      11 52.4      38 15 US-10-230-006-1132      Sequence 1132, Ap
c 991      11 52.4      38 15 US-10-230-006-1135      Sequence 1135, Ap
c 992      11 52.4      38 15 US-10-230-006-1138      Sequence 1138, Ap
c 993      11 52.4      38 15 US-10-230-006-1141      Sequence 1141, Ap
c 994      11 52.4      38 15 US-10-230-006-1144      Sequence 1144, Ap
c 995      11 52.4      38 15 US-10-230-006-1147      Sequence 1147, Ap
c 996      11 52.4      38 15 US-10-230-006-1150      Sequence 1150, Ap
c 997      11 52.4      38 15 US-10-230-006-1153      Sequence 1153, Ap
c 998      11 52.4      38 15 US-10-230-006-1156      Sequence 1156, Ap
c 999      11 52.4      38 15 US-10-230-006-1159      Sequence 1159, Ap
c1000     11 52.4      38 15 US-10-230-006-1162      Sequence 1162, Ap
```

ALIGNMENTS

```
RESULT 1
US-10-087-631B-2
; Sequence 2, Application US/10087631B
; Publication No. US20030054372A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial sequence to exemplify
; OTHER INFORMATION: principle
US-10-087-631B-2
Query Match      100.0%; Score 21; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 TCGCGTACGGTCTTAATGACCG 21
Db      1 TCGCGTACGGTCTTAATGACCG 21
```

RESULT 2

```
US-10-087-631B-17/c
; Sequence 17, Application US/10087631B
; Publication No. US20030054372A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence to exemplify principle
US-10-087-631B-17
Query Match      100.0%; Score 21; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 TCGCGTACGGTCTTAATGACCG 21
```

```
Db      1 TCGCGTACGGTCTTAATGACCG 1
```

RESULT 3

```
US-10-419-022-2
; Sequence 2, Application US/10419022
; Publication No. US20030165982A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT FILING DATE: 2003-04-17
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial sequence to exemplify
; OTHER INFORMATION: principle
US-10-419-022-2
Query Match      100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 TCGCGTACGGTCTTAATGACCG 21
```

```
Db      1 TCGCGTACGGTCTTAATGACCG 21
```

RESULT 4

```
US-10-419-022-17/c
; Sequence 17, Application US/10419022
; Publication No. US20030165982A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; OTHER INFORMATION: principle
US-10-419-022-17/c
Query Match      100.0%; Score 21; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 TCGCGTACGGTCTTAATGACCG 21
```

```
Db      1 TCGCGTACGGTCTTAATGACCG 21
```


FILE REFERENCE: 1803-335-999
CURRENT APPLICATION NUMBER: US/10/419,022
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US/10/087,631B
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Sequence to exemplify principle
US-10-419-022-17

Query Match 100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0

Qy 1 TCGCGTACGGTCTAATGACCG 21
|||||
Db 21 TCGCGTACGGTCTAATGACCG 1

RESULT 5

US-10-098-263B-56047/c
Sequence 56047, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 56047
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-56047

Query Match 67.6%; Score 14.2; DB 15; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGAC 19
|||
Db 24 TCGACACGGTCTAATGAC 6

RESULT 6

US-09-374-046A-218/c
Sequence 218, Application US/09374046A
Publication No. US20030096951A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

FILE REFERENCE: GI 6075-83A
CURRENT APPLICATION NUMBER: US/09/374,046A
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 218
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)
OTHER INFORMATION: biotinylated phosphoramidite residue
US-09-374-046A-218

Query Match 64.8%; Score 13.6; DB 10; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
|||
Db 24 TGGAGTACTGCTTATGACC 5

RESULT 7

US-10-616-263-218/c
Sequence 218, Application US/10616263
Publication No. US20040038276A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 00766.000103.5
CURRENT APPLICATION NUMBER: US/10/616,263
CURRENT FILING DATE: 2003-07-08
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 218
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)
OTHER INFORMATION: biotinylated phosphoramidite residue
US-10-616-263-218

Query Match 64.8%; Score 13.6; DB 16; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
|||
Db 24 TGGAGTACTGCTTATGACC 5

RESULT 8

```
US-10-138-674-20182
; Sequence 20182, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20182
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-20182

Query Match          64.8%; Score 13.6; DB 16; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACCG 21
DB 18 CGAGUGAGGUCUACUGACCG 37

RESULT 9
US-10-138-674-20479
; Sequence 20479, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20479
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-20479

Query Match          64.8%; Score 13.6; DB 16; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACCG 21
DB 18 CGAGUGAGGUCUACUGACCG 37

RESULT 10
US-10-287-949A-20182
; Sequence 20182, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
```

```
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20182
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-20182

Query Match          64.8%; Score 13.6; DB 17; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACCG 21
DB 18 CGAGUGAGGUCUACUGACCG 37

RESULT 11
US-10-287-949A-20479
; Sequence 20479, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20479
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-20479

Query Match          64.8%; Score 13.6; DB 17; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACCG 21
DB 18 CGAGUGAGGUCUACUGACCG 37

RESULT 12
US-10-098-263B-9436
; Sequence 9436, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
```

; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 9436
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-9436

Query Match 63.8%; Score 13.4; DB 15; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GTACGGTCTAATGAC 19
||| |||||
Db 4 GTACAGTCTAATGAC 18

RESULT 13
US-10-098-263B-88235/c
; Sequence 88235, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 88235
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-88235

Query Match 62.9%; Score 13.2; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGA 18
||| |||||
Db 24 TCCCGTAAGGCTATTGA 7

RESULT 14
US-10-098-263B-88853/c
; Sequence 88853, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 88853
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-88853

Query Match 62.9%; Score 13.2; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGA 18
||| |||||

Db 25 TCCCGTAAGGCTATTGA 8
RESULT 15
US-10-098-263B-71593
; Sequence 71593, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 71593
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-71593

Query Match 61.9%; Score 13; DB 15; Length 25;
Best Local Similarity 76.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACCG 21
||| |||||
Db 1 TCTCGTACGACTACCCACCG 21

RESULT 16
US-10-098-263B-71008/c
; Sequence 71008, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 71008
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-71008

Query Match 61.0%; Score 12.8; DB 15; Length 25;
Best Local Similarity 87.5%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CGTACGGTCTAATGAC 19
||| |||||
Db 20 CGTACGGTCTAATGAC 5

RESULT 17
US-10-098-263B-25744/c
; Sequence 25744, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 25744
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-25744

Query Match 60.0%; Score 12.6; DB 15; Length 25;
Best Local Similarity 78.9%; Pred. No. 6.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCGTACGGTCTTAATGACCG 21
||| ||||| |||
DB 25 GCGTTCGGTCTAAGGACG 7
||| ||||| |||

RESULT 18

US-10-098-263B-56048/c
; Sequence 56048, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 56048
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-56048

Query Match 60.0%; Score 12.6; DB 15; Length 25;
Best Local Similarity 78.9%; Pred. No. 6.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGGTACGGTCTTAATGAC 19
||| ||||| |||||
DB 24 TCGAACACGGTGTAAATGAC 6
||| ||||| |||||

RESULT 19

US-10-098-263B-118819
; Sequence 11819, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118819
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118819

Query Match 60.0%; Score 12.6; DB 15; Length 25;
Best Local Similarity 78.9%; Pred. No. 6.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCGTACGGTCTTAATGACCG 21
||| ||||| |||||
DB 3 GTGTGCGGTCCGATGACAG 21
||| ||||| |||||

RESULT 20

US-10-098-263B-118820
; Sequence 11820, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118820
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118820

Query Match 60.0%; Score 12.6; DB 15; Length 25;
Best Local Similarity 78.9%; Pred. No. 6.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCGTACGGTCTTAATGACCG 21
||| ||||| |||||
DB 3 GTGTGCGGTCCGATGACAG 21
||| ||||| |||||

RESULT 21

US-09-864-785-3885
; Sequence 3885, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:

; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MEH800-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3885
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (1)..(4)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; NAME/KEY: misc feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (18)..(23)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (25)..(26)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (28)..(35)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-Amino
; NAME/KEY: misc feature
; LOCATION: (27)..(27)

; OTHER INFORMATION: 2'-deoxy-2'-Amino
; NAME/KEY: misc_feature
; LOCATION: (36)..(36)
; OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-864-785-3885

Query Match 60.0%; Score 12.6; DB 9; Length 36;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTTAATGACC 20
|||.|||.|||.|||
DB 17 CGAGUGAGGUCUAUGGCC 35

RESULT 22

US-09-864-785-1812
; Sequence 1812, Application US/09864785
; Patent No. US20020177568A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Draper, Ken

; APPLICANT: McSwiggen, Jim

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

; FILE REFERENCE: Levels of NF-Kappa B

; FILE REFERENCE: 400/022 (MBH800-812-D)

; CURRENT APPLICATION NUMBER: US/09/864,785

; CURRENT FILING DATE: 2001-05-23

; NUMBER OF SEQ ID NOS: 3929

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1812

; LENGTH: 37

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-09-864-785-1812

Query Match 60.0%; Score 12.6; DB 9; Length 37;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTTAATGACC 20
|||.|||.|||.|||
DB 18 CGAGUGAGGUCUAUGGCC 36

RESULT 23

US-09-740-332-9583/c
; Sequence 9583, Application US/09740332
; Publication No. US20030125270A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals Inc.

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

; FILE REFERENCE: Hepatitis C Virus Infection

; FILE REFERENCE: RPI 400/003

; CURRENT APPLICATION NUMBER: US/09/740,332

; CURRENT FILING DATE: 2001-03-26

; NUMBER OF SEQ ID NOS: 9704

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9583

; LENGTH: 37

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (37)..(37)

; OTHER INFORMATION: n is an inverted deoxyabasic moiety

; NAME/KEY: misc_feature

; LOCATION: (30)..(30)

; OTHER INFORMATION: n is inosine

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; LOCATION: (1)..(7)
; OTHER INFORMATION: 2'-O-methyl derivative
; NAME/KEY: misc_feature
; LOCATION: (15)..(26)
; OTHER INFORMATION: 2'-O-methyl derivative
; NAME/KEY: misc_feature
; LOCATION: (31)..(36)
; OTHER INFORMATION: 2'-O-methyl derivative
US-09-740-332-9583

Query Match 60.0%; Score 12.6; DB 10; Length 37;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTTAATGACC 20
||||| ||||| ||||| |||||
DB 34 TCGCNTTCGGCCTAACGCC 15

RESULT 24

US-09-817-879-9583/c

; Sequence 9583, Application US/09817879

; Publication No. US20030171311A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals Inc.

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

; FILE REFERENCE: Hepatitis C Virus Infection

; CURRENT APPLICATION NUMBER: US/09/817,879

; CURRENT FILING DATE: 2001-03-26

; NUMBER OF SEQ ID NOS: 9703

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9583

; LENGTH: 37

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (37)..(37)

; OTHER INFORMATION: n is an inverted deoxyabasic moiety

; NAME/KEY: misc_feature

; LOCATION: (30)..(30)

; OTHER INFORMATION: n is inosine

; NAME/KEY: misc_feature

; LOCATION: (1)..(7)

; OTHER INFORMATION: 2'-O-methyl derivative

; NAME/KEY: misc_feature

; LOCATION: (15)..(26)

; OTHER INFORMATION: 2'-O-methyl derivative

; NAME/KEY: misc_feature

; LOCATION: (31)..(36)

; OTHER INFORMATION: 2'-O-methyl derivative

US-09-817-879-9583

Query Match 60.0%; Score 12.6; DB 10; Length 37;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTTAATGACC 20
||||| ||||| ||||| |||||
DB 34 TCGCNTTCGGCCTAACGCC 15

RESULT 25

US-10-138-674-18225

; Sequence 18225, Application US/10138674

; Publication No. US20040077565A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

```
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-N (400/049)
/ CURRENT APPLICATION NUMBER: US/10/138,674
/ CURRENT FILING DATE: 2002-05-03
/ NUMBER OF SEQ ID NOS: 20822
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 18225
/ LENGTH: 37
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-18225

Query Match          60.0%; Score 12.6; DB 16; Length 37;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      2 CGCGTACGGTCTAATGACC 20
        ||| | | | | | | | | |
Db      18 CGAGUGAGGCUAAAGACC 36

RESULT 26
US-10-138-674-18462
/ Sequence 18462, Application US/10138674
/ Publication No. US20040077565A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-N (400/049)
/ CURRENT APPLICATION NUMBER: US/10/138,674
/ CURRENT FILING DATE: 2002-05-03
/ NUMBER OF SEQ ID NOS: 20822
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 18462
/ LENGTH: 37
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-18462

Query Match          60.0%; Score 12.6; DB 16; Length 37;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      2 CGCGTACGGTCTAATGACC 20
        ||| | | | | | | | | |
Db      18 CGAGUGAGGCUAAAGACC 36

RESULT 27
US-10-138-674-20525
/ Sequence 20525, Application US/10138674
/ Publication No. US20040077565A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-N (400/049)
/ CURRENT APPLICATION NUMBER: US/10/138,674
/ CURRENT FILING DATE: 2002-05-03
```

```
/ NUMBER OF SEQ ID NOS: 20822
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 20525
/ LENGTH: 37
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-20525

Query Match          60.0%; Score 12.6; DB 16; Length 37;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      2 CGCGTACGGTCTAATGACC 20
        ||| | | | | | | | | |
Db      18 CGAGUGAGGCUAAAGACC 36

RESULT 28
US-10-287-949A-18225
/ Sequence 18225, Application US/10287949A
/ Publication No. US20040102389A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-N (400/049)
/ CURRENT APPLICATION NUMBER: US/10/287,949A
/ CURRENT FILING DATE: 2003-04-11
/ NUMBER OF SEQ ID NOS: 20822
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 18225
/ LENGTH: 37
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-18225

Query Match          60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 63.2%; Pred. No. 6.5e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      2 CGCGTACGGTCTAATGACC 20
        ||| | | | | | | | | |
Db      18 CGAGUGAGGCUAAAGACC 36

RESULT 29
US-10-287-949A-18462
/ Sequence 18462, Application US/10287949A
/ Publication No. US20040102389A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-N (400/049)
/ CURRENT APPLICATION NUMBER: US/10/287,949A
/ CURRENT FILING DATE: 2003-04-11
/ NUMBER OF SEQ ID NOS: 20822
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 18462
/ LENGTH: 37
/ TYPE: RNA
```

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-18462

Query Match 60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGCGTACGGTCTAATGACC 20
Db 18 CGAGUGAGGCUAAUACACC 36

RESULT 30
US-10-287-949A-20525
Sequence 20525, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MHB00-876-N (400/049)
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20525
LENGTH: 37
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-20525

Query Match 60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGCGTACGGTCTAATGACC 20
Db 18 CGAGUGAGGCUAAUACACC 36

RESULT 31
US-10-669-841-16128/c
Sequence 16128, Application US/10669841
Publication No. US20040127446A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
APPLICANT: James, McSwiggen
APPLICANT: David, Morrissey
APPLICANT: Pamela, Pavco
APPLICANT: Patrice, Lee
APPLICANT: Kenneth, Draper
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
FILE REFERENCE: 400/042US (MHB02-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: PCT/US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: US 60/337,055
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 09/817,879
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/740,332
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 16207
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16128
LENGTH: 37
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (37)..(37)
OTHER INFORMATION: n stands for inverted deoxyabasic derivative
NAME/KEY: misc_feature
LOCATION: (30)..(30)
OTHER INFORMATION: n is inosine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(7)
OTHER INFORMATION: 2'-O-Methyl
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)..(26)
OTHER INFORMATION: 2'-O-Methyl
FEATURE:
NAME/KEY: misc_feature
LOCATION: (31)..(36)
OTHER INFORMATION: 2'-O-Methyl
US-10-669-841-16128

Query Match 60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
Db 34 TCGCNTTCGGCCTAACGGCC 15

RESULT 32
US-09-874-547-83
Sequence 83, Application US/09874547
Patent No. US20020058269A1
GENERAL INFORMATION:
APPLICANT: No. US20020058269A1k, Steffen
APPLICANT: Kassner, Paul D.
APPLICANT: Zyomyx, Inc.
TITLE OF INVENTION: Screening of Phage Displayed Peptides
FILE REFERENCE: 020144-001110US
CURRENT APPLICATION NUMBER: US/09/874,547
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/209,503
PRIOR FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 83
LENGTH: 38

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: Primers for ScFv and Fab library generation (Table I) - MVK24
; OTHER INFORMATION: n stands for inosine
US-09-874-547-83

Query Match          60.0%; Score 12.6; DB 9; Length 38;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCGGTACGGTCTAATGACC 20
    ||||| ||| ||| ||| |||
Db 12 CGCGGACATTGTAATGACC 30

RESULT 33
US-09-864-785-1169/c
; Sequence 1169, Application US/09864785
; Patent No. US20020177569A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MEHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1169
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-864-785-1169

Query Match          60.0%; Score 12.6; DB 9; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGGTACGGTCTAATGACC 20
    ||||| ||| ||| ||| |||
Db 35 TCGCNTTCGGCCTAAGGCC 16

RESULT 34
US-09-780-533A-3557/c
; Sequence 3557, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEHB00, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO.3557
; LENGTH: 38
; TYPE: RNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-780-533A-3557

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGGTACGGTCTAATGACC 20
    ||||| ||| ||| ||| |||
Db 35 TCGCNTTCGGCCTAAGGCC 16

RESULT 35
US-09-780-533A-3581/c
; Sequence 3581, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEHB00, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3581
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-780-533A-3581

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGGTACGGTCTAATGACC 20
    ||||| ||| ||| ||| |||
Db 35 TCGCNTTCGGCCTAAGGCC 16

RESULT 36
US-09-927-046-3026/c
; Sequence 3026, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
```



```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3026
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-927-046-3026

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
    ||||| ||||| ||||| |||||
Db 35 TCGCNTTCGGCCCTAACGCC 16

RESULT 37
US-09-927-046-3197/c
; Sequence 3197, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwigen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3197
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-927-046-3197

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
    ||||| ||||| ||||| |||||
Db 35 TCGCNTTCGGCCCTAACGCC 16

RESULT 38
US-09-927-478-3468/c
; Sequence 3468, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
```

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; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3468
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-877-478-3468

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
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Db 35 TCGCNTTCGGCCCTAACGCC 16

RESULT 39
US-09-877-478-3764/c
; Sequence 3764, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3764
; LENGTH: 38
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; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-877-478-3764

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Query Match	60.0%;	Score 12.6;	DB 10;	Length 38;
Best Local Similarity	75.0%;	Pred. No. 6.5e+03;		
Matches 15;	Conservative	0;	Mismatches 5;	Indels 0;
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Qy 1 TCGCGTACGGTCTAATGACC 20
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RESULT 40
US-09-848-754A-5094/c
; Sequence 5094, Application US/09848754A
; Publication NO. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (406/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5094
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-848-754A-5094

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Query Match	60.0%;	Score 12.6;	DB 10;	Length 38;
Best Local Similarity	75.0%;	Pred. No. 6.5e+03;		
Matches	15;	Conservative	0;	Mismatches 5;
				Indels 0;
				Gaps 0;

Qy
1 TCGCGTACGGTCTAATGACC 20
35 TCGCNTTCGGCCTAACGGCC 16

Search completed: November 24, 2004, 03:42:04
Job time : 108.572 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1006.82 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-2

Perfect score: 21
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : EST:
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2: gb_est2:*
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7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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24	10.8	51.4	45	9	AG192385

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46	8	BZ379971	SALK 1143
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37	8	BZ383634	SALK 1342
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100	9.8	46.7	39	8	BZ289706	BZ289706	SALK_0231	c 173	9.4	44.8	31	9	AL947428	AL947428	ARabidops
101	9.8	46.7	39	8	CC053623	CC053623	SALK_0458	c 174	9.4	44.8	33	9	EX530768	EX530768	ARabidops
102	9.8	46.7	40	5	BX564806	BX564806	EX564806	c 175	9.4	44.8	34	1	AI168400	AI168400	qa2se03.s
103	9.8	46.7	40	8	BZ287846	BZ287846	SALK_0212	c 176	9.4	44.8	34	1	AI185295	AI185295	qa35b09.s
104	9.8	46.7	40	9	AL759372	AL759372	ARabidops	c 177	9.4	44.8	34	1	AU007062	AU007062	AU007062
105	9.8	46.7	41	8	BH863752	BH863752	SALK_0944	c 178	9.4	44.8	34	8	BH911674	BH911674	SALK_0714
106	9.8	46.7	41	8	BH863753	BH863753	SALK_0944	c 179	9.4	44.8	35	8	AZ591995	AZ591995	1M0402F06
107	9.8	46.7	41	8	BH864990	BH864990	SALK_0972	c 180	9.4	44.8	35	8	AZ591995	AZ591995	1M0402F06
108	9.8	46.7	42	6	CD530457	CD530457	06G12_Ara	c 181	9.4	44.8	35	9	CG709475	CG709475	1119013C1
109	9.8	46.7	43	1	AI196640	AI196640	ui53d01.y	c 182	9.4	44.8	36	9	BX535278	BX535278	ARabidops
110	9.8	46.7	44	9	TA30E12Q	TA30E12Q	T. brucei	c 183	9.4	44.8	36	9	TA38H05P	TA38H05P	T. brucei
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115	9.8	46.7	46	8	BZ770587	BZ770587	SALK_1435	c 188	9.4	44.8	38	9	CNS07FAG	CNS07FAG	Anopheles
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118	9.8	46.7	48	1	AI313698	AI313698	EST010_Mo	c 191	9.4	44.8	39	9	CG796635	CG796635	SALK_1362
119	9.8	46.7	49	1	AI359268	AI359268	qy27c06.x	c 192	9.4	44.8	40	8	BH900955	BH900955	KG07812-3
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123	9.8	46.7	49	9	CR402941	CR402941	ARabidops	c 196	9.4	44.8	42	9	TA157C05P	TA157C05P	T. brucei
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126	9.8	46.7	50	1	AU105980	AU105980	AU105980	c 199	9.4	44.8	43	2	BF163929	BF163929	601772256
127	9.8	46.7	50	1	AU106625	AU106625	AU106625	c 200	9.4	44.8	44	4	B1829988	B1829988	603080234
128	9.8	46.7	50	9	BX945487	BX945487	ARabidops	c 201	9.4	44.8	44	8	AZ622559	AZ622559	1M0459P24
129	9.8	46.7	24	4	BM397712	BM397712	5009-0-35	c 202	9.4	44.8	44	8	CC455081	CC455081	SALK_0476
130	9.6	45.7	25	8	CC458426	CC458426	SALK_1187	c 203	9.4	44.8	44	9	AJ622264	AJ622264	Drosophil
131	9.6	45.7	27	9	TA143H1P	TA143H1P	T. brucei	c 204	9.4	44.8	44	9	CG797754	CG797754	SALK_1453
132	9.6	45.7	30	8	BH849994	BH849994	SALK_0706	c 205	9.4	44.8	45	1	AV970560	AV970560	AV970560
133	9.6	45.7	31	1	AU258240	AU258240	AU258240	c 206	9.4	44.8	45	8	BH908303	BH908303	SALK_0471
134	9.6	45.7	31	7	D18722	D18722	MUSGS01784	c 207	9.4	44.8	46	8	BH902367	BH902367	SALK_0917
135	9.6	45.7	31	8	BH810158	BH810158	SALK_0414	c 208	9.4	44.8	47	6	CB305190	CB305190	3'EST-NF1
136	9.6	45.7	34	9	TA124F07P	TA124F07P	T. brucei	c 209	9.4	44.8	47	9	CG466461	CG466461	01S0600-0
137	9.6	45.7	35	2	BE275280	BE275280	601122119	c 210	9.4	44.8	48	2	B738353	B738353	601572748
138	9.6	45.7	38	8	BH613959	BH613959	SALK_0352	c 211	9.4	44.8	48	4	B083470	B083470	BJ083470
139	9.6	45.7	40	8	BJ060137	BJ060137	BJ060137	c 212	9.4	44.8	48	5	B0582005	B0582005	195_Oryct
140	9.6	45.7	40	8	BH911408	BH911408	SALK_0684	c 213	9.4	44.8	48	7	CO789074	CO789074	NT005D_H0
141	9.6	45.7	40	9	TA17C08Q	TA17C08Q	T. brucei	c 214	9.4	44.8	48	8	AQ026317	AQ026317	13J3A6
142	9.6	45.7	41	7	CN755514	CN755514	ID0AA16A	c 215	9.4	44.8	48	8	BH865457	BH865457	SALK_0985
143	9.6	45.7	41	8	BH908133	BH908133	SALK_0458	c 216	9.4	44.8	48	8	BH866365	BH866365	SALK_1012
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145	9.6	45.7	42	9	AL763403	AL763403	ARabidops	c 218	9.4	44.8	48	9	CR399068	CR399068	ARabidops
146	9.6	45.7	43	9	AG217405	AG217405	Drosophil	c 219	9.4	44.8	48	9	CG808438	CG808438	1118092D1
147	9.6	45.7	44	8	BH172536	BH172536	SALK_0058	c 220	9.4	44.8	49	4	BJ040441	BJ040441	BJ040441
148	9.6	45.7	44	8	BH214294	BH214294	SALK_0105	c 221	9.4	44.8	49	9	AL771898	AL771898	ARabidops
149	9.6	45.7	44	8	BH252344	BH252344	SALK_0131	c 222	9.4	44.8	49	9	TA101C02Q	TA101C02Q	T. brucei
150	9.6	45.7	44	8	BH612495	BH612495	SALK_0328	c 223	9.4	44.8	49	9	CG705752	CG705752	01S0585-0
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152	9.6	45.7	44	8	BH752299	BH752299	SALK_0140	c 225	9.4	44.8	50	1	AU103418	AU103418	AU103418
153	9.6	45.7	44	9	DR102GGS	DR102GGS	Danio rer	c 226	9.4	44.8	50	1	AU103989	AU103989	AU103989
154	9.6	45.7	45	8	CC023725	CC023725	3591_1_36	c 227	9.4	44.8	50	1	AU104834	AU104834	AU104834
155	9.6	45.7	46	7	CN758478	CN758478	ID0AA22B	c 228	9.4	44.8	50	1	AU104848	AU104848	AU104848
156	9.6	45.7	46	8	BH610910	BH610910	SALK_0182	c 229	9.4	44.8	50	1	AU106578	AU106578	AU106578
157	9.6	45.7	46	9	AB081994	AB081994	Drosophil	c 230	9.4	44.8	50	1	AU106591	AU106591	AU106591
158	9.6	45.7	47	9	CL523386	CL523386	SNOWD03_F	c 231	9.4	44.8	50	1	AU107230	AU107230	AU107230
159	9.6	45.7	48	8	BH253356	BH253356	602362952	c 232	9.4	44.8	50	2	AW630853	AW630853	h88e007.y
160	9.6	45.7	48	8	BH251093	BH251093	SALK_0109	c 233	9.4	44.8	50	4	BI708333	BI708333	ft46c02.y
161	9.6	45.7	48	8	BH611118	BH611118	SALK_0299	c 234	9.4	44.8	50	7	CF641166	CF641166	D36_E05_F
162	9.6	45.7	48	9	TA194C12Q	TA194C12Q	T. brucei	c 235	9.4	44.8	50	9	AJ588199	AJ588199	ARabidops
163	9.6	45.7	50	1	AU102458	AU102458	AU102458	c 236	9.4	44.8	50	9	TA154F10Q	TA154F10Q	T. brucei
164	9.6	45.7	50	1	AU103408	AU103408	AU103408	c 237	9.2	43.8	22	8	AZ372259	AZ372259	1M0124J02
165	9.6	45.7	50	1	AU106624	AU106624	AU106624	c 238	9.2	43.8	22	8	AZ496170	AZ496170	1M0332N13
166	9.6	45.7	50	1	AV969171	AV969171	AV969171	c 239	9.2	43.8	23	8	AZ840154	AZ840154	2M0136N05
167	9.6	45.7	50	4	BG222716	BG222716	nah37e07.	c 240	9.2	43.8	25	1	AI000280	AI000280	ov10e04.s
168	9.4	44.8	27	8	AZ794090	AZ794090	2M0047O09	c 241	9.2	43.8	26	9	AJ595210	AJ595210	ARabidops
169	9.4	44.8	27	8	BZ378105	BZ378105	SALK_1071	c 242	9.2	43.8	27	1	AU254174	AU254174	AU254174
170	9.4	44.8	29	1	AU007063	AU007063	AU007063	c 243	9.2	43.8	27	7	D18735	D18735	MUSGS01797

C 244	9.2	43.8	27	8	A2427088	AZ427088	1M0208B24	317	9.2	43.8	50	1	AU105480	AU105480
C 245	9.2	43.8	27	8	A2810485	AZ810485	2M0076H05	318	9.2	43.8	50	1	AU108048	AU108048
C 246	9.2	43.8	28	8	A2441205	AZ441205	1M0232B10	319	9.2	43.8	50	5	BX722422	BX722422
C 247	9.2	43.8	29	1	AJ674160	AJ674160	AJ674160	C 320	9.2	43.8	50	7	CR437050	CR437050
C 248	9.2	43.8	29	9	AJ594026	AJ594026	Arabidops	321	9.2	43.8	50	9	BX977848	BX977848
C 249	9.2	43.8	29	9	AG198112	AG198112	Pan trogl	322	9.2	43.8	50	9	CR209280	CR209280
C 250	9.2	43.8	30	7	CF543220	CF543220	S014680-0	323	9.2	43.8	50	9	CL519142	CL519142
C 251	9.2	43.8	30	8	AZ431038	AZ431038	1M0215I15	C 324	9.2	43.8	50	9	CL519142	CL519142
C 252	9.2	43.8	30	8	BZ762449	BZ762449	SALK 1047	325	9.2	43.8	50	21	AZ592202	AZ592202
C 253	9.2	43.8	30	9	CG714388	CG714388	1119036D1	C 326	9.2	43.8	50	21	TA39002P	TA39002P
C 254	9.2	43.8	32	8	AZ765095	AZ765095	1M0561A22	327	9.2	43.8	50	23	AZ818662	AZ818662
C 255	9.2	43.8	33	9	DME545578	DME545578	Drsoephil	328	9.2	43.8	50	23	AZ826455	AZ826455
C 256	9.2	43.8	34	1	AI125992	AI125992	qc4ed12.x	329	9.2	43.8	50	24	CO785230	CO785230
C 257	9.2	43.8	34	8	BH907363	BH907363	SALK 0397	330	9.2	43.8	50	25	AZ605844	AZ605844
C 258	9.2	43.8	34	8	BZ288240	BZ288240	SALK 0216	331	9.2	43.8	50	25	AZ655084	AZ655084
C 259	9.2	43.8	35	8	AZ820699	AZ820699	2M0093L02	332	9.2	43.8	50	25	CG1714033	CG1714033
C 260	9.2	43.8	35	9	TA103A09Q	TA103A09Q	T. brucei	333	9.2	43.8	50	25	CG723016	CG723016
C 261	9.2	43.8	37	9	DR10838	DR10838	Danio rer	334	9.2	43.8	50	27	AZ8331609	AZ8331609
C 262	9.2	43.8	38	1	AU260238	AU260238	AU260238	C 335	9.2	43.8	50	27	AJ587528	AJ587528
C 263	9.2	43.8	38	8	AZ659279	AZ659279	1M0536L02	336	9.2	43.8	50	27	TA383D12Q	TA383D12Q
C 264	9.2	43.8	39	8	BH809708	BH809708	SALK 0050	337	9.2	43.8	50	28	AI573848	AI573848
C 265	9.2	43.8	39	8	BH908228	BH908228	SALK 0465	338	9.2	43.8	50	28	AJ795430	AJ795430
C 266	9.2	43.8	40	8	BZ589975	BZ589975	3590_1_73	C 339	9.2	43.8	50	28	AZ780159	AZ780159
C 267	9.2	43.8	40	9	CU523373	CU523373	DA12H04 F	C 340	9.2	43.8	50	28	BH846511	BH846511
C 268	9.2	43.8	41	1	AA253540	AA253540	SWMPCAI43	C 341	9.2	43.8	50	31	AI346598	AI346598
C 269	9.2	43.8	41	8	AZ774470	AZ774470	2M0003P13	342	9.2	43.8	50	31	AU266417	AU266417
C 270	9.2	43.8	41	8	BZ765629	BZ765629	SALK 1319	C 343	9.2	43.8	50	31	CF335931	CF335931
C 271	9.2	43.8	41	9	TA151G10Q	TA151G10Q	T. brucei	344	9.2	43.8	50	31	BZ382978	BZ382978
C 272	9.2	43.8	42	8	AZ666806	AZ666806	1M0549N10	C 345	9.2	43.8	50	31	EX893918	EX893918
C 273	9.2	43.8	43	1	AA815634	AA815634	vt03d02.r	C 346	9.2	43.8	50	31	TA65601Q	TA65601Q
C 274	9.2	43.8	43	1	AA921653	AA921653	VY22d03.r	347	9.2	43.8	50	32	CD534487	CD534487
C 275	9.2	43.8	44	8	AZ646714	AZ646714	1M0512D21	C 348	9.2	43.8	50	32	AZ491344	AZ491344
C 276	9.2	43.8	45	9	TA372A04P	TA372A04P	T. brucei	349	9.2	43.8	50	32	AZ799655	AZ799655
C 277	9.2	43.8	45	9	CG892752	CG892752	01S0617-0	C 350	9.2	43.8	50	32	BZ358744	BZ358744
C 278	9.2	43.8	46	1	AA1884160	AA1884160	fc74e12.x	C 351	9.2	43.8	50	32	AJ590509	AJ590509
C 279	9.2	43.8	46	1	AA625631	AA625631	adi0d01.s	C 352	9.2	43.8	50	33	AJ647516	AJ647516
C 280	9.2	43.8	46	9	AJ591587	AJ591587	Arabidops	C 353	9.2	43.8	50	33	BH849814	BH849814
C 281	9.2	43.8	46	9	CR360032	CR360032	Arabidops	354	9.2	43.8	50	33	CG722737	CG722737
C 282	9.2	43.8	47	4	BI089840	BI089840	602855085	355	9.2	43.8	50	33	BH251010	BH251010
C 283	9.2	43.8	47	8	AQ026076	AQ026076	1(2)k1420	356	9.2	43.8	50	35	BH253542	BH253542
C 284	9.2	43.8	47	8	BH813914	BH813914	SALK 0654	357	9.2	43.8	50	35	BH613670	BH613670
C 285	9.2	43.8	47	8	BH846892	BH846892	SALK_0110	358	9.2	43.8	50	35	BH617331	BH617331
C 286	9.2	43.8	47	9	DME545407	DME545407	Drsoephil	359	9.2	43.8	50	35	BH617681	BH617681
C 287	9.2	43.8	47	9	AG197950	AG197950	Pan trogl	360	9.2	43.8	50	35	BH618593	BH618593
C 288	9.2	43.8	48	4	BJ083470	BJ083470	Arabidops	361	9.2	43.8	50	35	BH751605	BH751605
C 289	9.2	43.8	48	9	CR358002	CR358002	Arabidops	362	9.2	43.8	50	35	BH753496	BH753496
C 290	9.2	43.8	49	1	AA109169	AA109169	mp38f04.r	C 363	9.2	43.8	50	35	BH854633	BH854633
C 291	9.2	43.8	49	4	BG292262	BG292262	602386710	C 364	9.2	43.8	50	35	TA248D10Q	TA248D10Q
C 292	9.2	43.8	49	4	BI760726	BI760726	603044726	C 365	9.2	43.8	50	36	T61825	T61825
C 293	9.2	43.8	49	8	CG325828	CG325828	RRG292 Ba	366	9.2	43.8	50	36	BH751713	BH751713
C 294	9.2	43.8	49	9	CG779221	CG779221	1123032D0	367	9.2	43.8	50	36	CG713884	CG713884
C 295	9.2	43.8	49	9	AG190566	AG190566	Pan trogl	368	9.2	43.8	50	36	CG714202	CG714202
C 296	9.2	43.8	49	1	AJ920149	AJ920149	1679 Pine	369	9.2	43.8	50	36	CG714303	CG714303
C 297	9.2	43.8	50	1	AU102923	AU102923	AU102923	370	9.2	43.8	50	37	AU010468	AU010468
C 298	9.2	43.8	50	1	AU102930	AU102930	AU102930	371	9.2	43.8	50	37	AU010469	AU010469
C 299	9.2	43.8	50	1	AU102933	AU102933	AU102933	372	9.2	43.8	50	37	BH211687	BH211687
C 300	9.2	43.8	50	1	AU102934	AU102934	AU102934	373	9.2	43.8	50	37	BH212711	BH212711
C 301	9.2	43.8	50	1	AU102935	AU102935	AU102935	374	9.2	43.8	50	37	BH213109	BH213109
C 302	9.2	43.8	50	1	AU102936	AU102936	AU102936	375	9.2	43.8	50	37	BH254171	BH254171
C 303	9.2	43.8	50	1	AU102937	AU102937	AU102937	376	9.2	43.8	50	37	BH612755	BH612755
C 304	9.2	43.8	50	1	AU102947	AU102947	AU102947	377	9.2	43.8	50	37	BH613685	BH613685
C 305	9.2	43.8	50	1	AU102948	AU102948	AU102948	378	9.2	43.8	50	37	BH613909	BH613909
C 306	9.2	43.8	50	1	AU102954	AU102954	AU102954	379	9.2	43.8	50	37	BH613940	BH613940
C 307	9.2	43.8	50	1	AU103589	AU103589	AU103589	380	9.2	43.8	50	37	BH617568	BH617568
C 308	9.2	43.8	50	1	AU104153	AU104153	AU104153	381	9.2	43.8	50	37	BH617569	BH617569
C 309	9.2	43.8	50	1	AU104179	AU104179	AU104179	382	9.2	43.8	50	37	BH633214	BH633214
C 310	9.2	43.8	50	1	AU104207	AU104207	AU104207	383	9.2	43.8	50	37	BH751779	BH751779
C 311	9.2	43.8	50	1	AU105472	AU105472	AU105472	384	9.2	43.8	50	37	BH751802	BH751802
C 312	9.2	43.8	50	1	AU105473	AU105473	AU105473	385	9.2	43.8	50	37	BH791757	BH791757
C 313	9.2	43.8	50	1	AU105474	AU105474	AU105474	386	9.2	43.8	50	37	CG711288	CG711288
C 314	9.2	43.8	50	1	AU105475	AU105475	AU105475	C 387	9.2	43.8	50	37	CG713746	CG713746
C 315	9.2	43.8	50	1	AU105476	AU105476	AU105476	388	9.2	43.8	50	37	CG722734	CG722734
C 316	9.2	43.8	50	1	AU105479	AU105479	AU105479	389	9.2	43.8	50	37	CG722734	CG722734

390	9	42.9	37	9	CG724536	CG724536	1119081F0	463	9	42.9	44	8	BH172646	BH172646	SALK_0059
391	9	42.9	38	4	BM400755	BM400755	5009-0-78	464	9	42.9	44	8	BH172689	BH172689	SALK_0060
392	9	42.9	38	8	BH170263	BH170263	SALK_0026	465	9	42.9	44	8	BH173144	BH173144	SALK_0070
393	9	42.9	38	8	BH611224	BH611224	SALK_0304	466	9	42.9	44	8	BH212259	BH212259	SALK_0073
394	9	42.9	38	8	BH612424	BH612424	SALK_0326	467	9	42.9	44	8	BH212377	BH212377	SALK_0075
395	9	42.9	38	8	BH792093	BH792093	SALK_0626	468	9	42.9	44	8	BH212514	BH212514	SALK_0076
396	9	42.9	38	9	BX287919	BX287919	Arabidops	469	9	42.9	44	8	BH213282	BH213282	SALK_0090
397	9	42.9	38	9	CG729929	CG729929	1119116B0	470	9	42.9	44	8	BH251475	BH251475	SALK_0116
398	9	42.9	39	4	BG112163	BG112163	602283080	471	9	42.9	44	8	BH251575	BH251575	SALK_0118
399	9	42.9	39	4	BI660394	BI660394	603302045	472	9	42.9	44	8	BH251615	BH251615	SALK_0118
400	9	42.9	39	8	BH212311	BH212311	SALK_0074	473	9	42.9	44	8	BH251830	BH251830	SALK_0121
401	9	42.9	39	8	BH212359	BH212359	SALK_0074	474	9	42.9	44	8	BH251946	BH251946	SALK_0123
402	9	42.9	39	8	BH751820	BH751820	SALK_0506	475	9	42.9	44	8	BH252164	BH252164	SALK_0128
403	9	42.9	39	9	CG713365	CG713365	1119032D0	476	9	42.9	44	8	BH252206	BH252206	SALK_0129
404	9	42.9	40	1	AI613042	AI613042	ty06h09.X	477	9	42.9	44	8	BH252225	BH252225	SALK_0129
405	9	42.9	40	1	AI805437	AI805437	tx96e03.X	478	9	42.9	44	8	BH252323	BH252323	SALK_0130
406	9	42.9	40	8	BH212182	BH212182	SALK_0072	479	9	42.9	44	8	BH252360	BH252360	SALK_0130
407	9	42.9	40	8	BH212218	BH212218	SALK_0072	480	9	42.9	44	8	BH252506	BH252506	SALK_0135
408	9	42.9	40	8	BH613805	BH613805	SALK_0349	481	9	42.9	44	8	BH252718	BH252718	SALK_0137
409	9	42.9	40	8	BH751640	BH751640	SALK_0504	482	9	42.9	44	8	BH252765	BH252765	SALK_0138
410	9	42.9	40	9	BX572583	BX572583	Arabidops	483	9	42.9	44	8	BH252848	BH252848	SALK_0139
411	9	42.9	40	9	CG796357	CG796357	SALK_1294	484	9	42.9	44	8	BH252865	BH252865	SALK_0139
412	9	42.9	40	9	CG729877	CG729877	1119116B0	485	9	42.9	44	8	BH253523	BH253523	SALK_0150
413	9	42.9	41	1	AV834393	AV834393	AV834393	486	9	42.9	44	8	BH253838	BH253838	SALK_0155
414	9	42.9	41	8	AQ025324	AQ025324	EP(X)0362	487	9	42.9	44	8	BH254181	BH254181	SALK_0161
415	9	42.9	41	8	AZ454047	AZ454047	1M0255015	488	9	42.9	44	8	BH254446	BH254446	SALK_0165
416	9	42.9	41	8	AZ475800	AZ475800	1M0294G10	489	9	42.9	44	8	BH254727	BH254727	SALK_0171
417	9	42.9	41	8	AZ773365	AZ773365	1M0584A20	490	9	42.9	44	8	BH611523	BH611523	SALK_0310
418	9	42.9	41	8	BH252552	BH252552	SALK_0135	491	9	42.9	44	8	BH611569	BH611569	SALK_0311
419	9	42.9	41	8	BH254298	BH254298	SALK_0163	492	9	42.9	44	8	BH611657	BH611657	SALK_0315
420	9	42.9	41	8	BH610796	BH610796	SALK_0180	493	9	42.9	44	8	BH611723	BH611723	SALK_0316
421	9	42.9	41	8	BH611601	BH611601	SALK_0312	494	9	42.9	44	8	BH611974	BH611974	SALK_0319
422	9	42.9	41	8	BH614048	BH614048	SALK_0353	495	9	42.9	44	8	BH612122	BH612122	SALK_0321
423	9	42.9	41	8	BH749252	BH749252	SALK_0475	496	9	42.9	44	8	BH612168	BH612168	SALK_0322
424	9	42.9	41	8	BH749713	BH749713	SALK_0286	497	9	42.9	44	8	BH612218	BH612218	SALK_0323
425	9	42.9	41	8	BH751659	BH751659	SALK_0504	498	9	42.9	44	8	BH612350	BH612350	SALK_0325
426	9	42.9	41	8	BZ663233	BZ663233	SALK_0268	499	9	42.9	44	8	BH612910	BH612910	SALK_0334
427	9	42.9	41	9	DM547498	DM547498	T. brucei	500	9	42.9	44	8	BH613025	BH613025	SALK_0336
428	9	42.9	41	9	TA131C04P	TA131C04P	AL465339	501	9	42.9	44	8	BH613027	BH613027	SALK_0336
429	9	42.9	42	8	BH611542	BH611542	SALK_0311	502	9	42.9	44	8	BH613209	BH613209	SALK_0339
430	9	42.9	42	8	BH624495	BH624495	1007078G0	503	9	42.9	44	8	BH613233	BH613233	SALK_0339
431	9	42.9	42	8	BH750272	BH750272	SALK_0376	504	9	42.9	44	8	BH613425	BH613425	SALK_0342
432	9	42.9	42	8	BH751578	BH751578	SALK_0503	505	9	42.9	44	8	BH613572	BH613572	SALK_0344
433	9	42.9	42	9	AL765989	AL765989	Arabidops	506	9	42.9	44	8	BH617039	BH617039	SALK_0358
434	9	42.9	42	9	CG729941	CG729941	1119116F0	507	9	42.9	44	8	BH617095	BH617095	SALK_0359
435	9	42.9	42	9	CL705862	CL705862	EY00848-3	508	9	42.9	44	8	BH617247	BH617247	SALK_0361
436	9	42.9	43	1	AA928331	AA928331	cm76c12.S	509	9	42.9	44	8	BH617442	BH617442	SALK_0365
437	9	42.9	43	1	AI657864	AI657864	fc14e05.Y	510	9	42.9	44	8	BH617453	BH617453	SALK_0365
438	9	42.9	43	1	AA241931	AA241931	mx26a04.r	511	9	42.9	44	8	BH617506	BH617506	SALK_0371
439	9	42.9	43	1	AA549203	AA549203	VK85d08.S	512	9	42.9	44	8	BH617771	BH617771	SALK_0377
440	9	42.9	43	8	BH173048	BH173048	SALK_0014	513	9	42.9	44	8	BH617921	BH617921	SALK_0381
441	9	42.9	43	8	BH254096	BH254096	SALK_0159	514	9	42.9	44	8	BH617944	BH617944	SALK_0381
442	9	42.9	43	8	BH611286	BH611286	SALK_0306	515	9	42.9	44	8	BH618166	BH618166	SALK_0386
443	9	42.9	43	8	BH611477	BH611477	SALK_0309	516	9	42.9	44	8	BH618486	BH618486	SALK_0391
444	9	42.9	43	8	BH612999	BH612999	SALK_0336	517	9	42.9	44	8	BH618549	BH618549	SALK_0392
445	9	42.9	43	8	BH613221	BH613221	SALK_0339	518	9	42.9	44	8	BH618610	BH618610	SALK_0394
446	9	42.9	43	8	BH617226	BH617226	SALK_0361	519	9	42.9	44	8	BH633222	BH633222	SALK_0410
447	9	42.9	43	8	BH617444	BH617444	SALK_0365	520	9	42.9	44	8	BH634244	BH634244	SALK_0449
448	9	42.9	43	8	BH750703	BH750703	SALK_0422	521	9	42.9	44	8	BH750166	BH750166	SALK_0371
449	9	42.9	44	8	BH168728	BH168728	SALK_0001	522	9	42.9	44	8	BH750554	BH750554	SALK_0416
450	9	42.9	44	8	BH168811	BH168811	SALK_0002	523	9	42.9	44	8	BH751355	BH751355	SALK_0500
451	9	42.9	44	8	BH168944	BH168944	SALK_0003	524	9	42.9	44	8	BH752016	BH752016	SALK_0516
452	9	42.9	44	8	BH168955	BH168955	SALK_0004	525	9	42.9	44	8	BH752121	BH752121	SALK_0517
453	9	42.9	44	8	BH169147	BH169147	SALK_0007	526	9	42.9	44	8	BH752301	BH752301	SALK_0140
454	9	42.9	44	8	BH169189	BH169189	SALK_0007	527	9	42.9	44	8	BH752319	BH752319	SALK_0140
455	9	42.9	44	8	BH169506	BH169506	SALK_0014	528	9	42.9	44	8	BH752350	BH752350	SALK_0141
456	9	42.9	44	8	BH169809	BH169809	SALK_0019	529	9	42.9	44	8	BH752481	BH752481	SALK_0187
457	9	42.9	44	8	BH169920	BH169920	SALK_0020	530	9	42.9	44	8	BH752619	BH752619	SALK_0189
458	9	42.9	44	8	BH170451	BH170451	SALK_0029	531	9	42.9	44	8	BH908840	BH908840	SALK_0507
459	9	42.9	44	8	BH171381	BH171381	SALK_0041	532	9	42.9	44	9	AL757126	AL757126	Arabidops
460	9	42.9	44	8	BH171826	BH171826	SALK_0048	533	9	42.9	44	9	CG714300	CG714300	1119036A0
461	9	42.9	44	8	BH172056	BH172056	SALK_0051	534	9	42.9	44	9	CG724480	CG724480	1119081D0
462	9	42.9	44	8	BH172538	BH172538	SALK_0058	535	9	42.9	45	8	AZ815371	AZ815371	2M0083M04

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536	9	42.9	45	8	BH168809	BH168809 SALK_0002	609	9	42.9	48	8	BH172074	BH172074 SALK_0052
537	9	42.9	45	8	BH169016	BH169016 SALK_0004	610	9	42.9	48	8	BH172483	BH172483 SALK_0057
538	9	42.9	45	8	BH169715	BH169715 SALK_0017	611	9	42.9	48	8	BH173104	BH173104 SALK_0013
539	9	42.9	45	8	BH170991	BH170991 SALK_0036	612	9	42.9	48	8	BH211911	BH211911 SALK_0068
540	9	42.9	45	8	BH171160	BH171160 SALK_0038	613	9	42.9	48	8	BH212124	BH212124 SALK_0071
541	9	42.9	45	8	BH172480	BH172480 SALK_0057	614	9	42.9	48	8	BH212192	BH212192 SALK_0072
542	9	42.9	45	8	BH251855	BH251855 SALK_0122	615	9	42.9	48	8	BH212362	BH212362 SALK_0074
543	9	42.9	45	8	BH252041	BH252041 SALK_0124	616	9	42.9	48	8	BH213362	BH213362 SALK_0091
544	9	42.9	45	8	BH252624	BH252624 SALK_0136	617	9	42.9	48	8	BH213445	BH213445 SALK_0092
545	9	42.9	45	8	BH253683	BH253683 SALK_0152	618	9	42.9	48	8	BH213559	BH213559 SALK_0093
546	9	42.9	45	8	BH610643	BH610643 SALK_0177	619	9	42.9	48	8	BH214012	BH214012 SALK_0100
547	9	42.9	45	8	BH613489	BH613489 SALK_0343	620	9	42.9	48	8	BH214058	BH214058 SALK_0101
548	9	42.9	45	8	BH617238	BH617238 SALK_0361	621	9	42.9	48	8	BH251827	BH251827 SALK_0121
549	9	42.9	45	8	BH617343	BH617343 SALK_0363	622	9	42.9	48	8	BH252179	BH252179 SALK_0128
550	9	42.9	45	8	BH617375	BH617375 SALK_0364	623	9	42.9	48	8	BH252272	BH252272 SALK_0130
551	9	42.9	45	8	BH617528	BH617528 SALK_0372	624	9	42.9	48	8	BH253038	BH253038 SALK_0143
552	9	42.9	45	8	BH618005	BH618005 SALK_0383	625	9	42.9	48	8	BH253184	BH253184 SALK_0145
553	9	42.9	45	8	BH618006	BH618006 SALK_0383	626	9	42.9	48	8	BH253291	BH253291 SALK_0147
554	9	42.9	45	8	BH618252	BH618252 SALK_0387	627	9	42.9	48	8	BH253306	BH253306 SALK_0147
555	9	42.9	45	8	BH619123	BH619123 SALK_0402	628	9	42.9	48	8	BH253358	BH253358 SALK_0148
556	9	42.9	45	8	BH749090	BH749090 SALK_0472	629	9	42.9	48	8	BH253833	BH253833 SALK_0155
557	9	42.9	45	8	BH790393	BH790393 SALK_0569	630	9	42.9	48	8	BH254186	BH254186 SALK_0161
558	9	42.9	46	1	A1735034	A1735034 as6bh04.x	631	9	42.9	48	8	BH254463	BH254463 SALK_0165
559	9	42.9	46	1	A1399336	A1399336 zt49c12.x	632	9	42.9	48	8	BH254917	BH254917 SALK_0174
560	9	42.9	46	7	H52294	H52294 CHR220233.C	633	9	42.9	48	8	BH610731	BH610731 SALK_0179
561	9	42.9	46	8	BH168816	BH168816 SALK_0002	634	9	42.9	48	8	BH610835	BH610835 SALK_0181
562	9	42.9	46	8	BH169680	BH169680 SALK_0017	635	9	42.9	48	8	BH610916	BH610916 SALK_0182
563	9	42.9	46	8	BH172748	BH172748 SALK_0061	636	9	42.9	48	8	BH611306	BH611306 SALK_0309
564	9	42.9	46	8	BH212329	BH212329 SALK_0074	637	9	42.9	48	8	BH611439	BH611439 SALK_0309
565	9	42.9	46	8	BH213521	BH213521 SALK_0093	638	9	42.9	48	8	BH611499	BH611499 SALK_0310
566	9	42.9	46	8	BH252530	BH252530 SALK_0135	639	9	42.9	48	8	BH611861	BH611861 SALK_0318
567	9	42.9	46	8	BH611610	BH611610 SALK_0312	640	9	42.9	48	8	BH612357	BH612357 SALK_0325
568	9	42.9	46	8	BH618888	BH618888 SALK_0399	641	9	42.9	48	8	BH613342	BH613342 SALK_0341
569	9	42.9	46	8	BH641999	BH641999 1008052B0	642	9	42.9	48	8	BH614164	BH614164 SALK_0355
570	9	42.9	46	8	BH747763	BH747763 SALK_0340	643	9	42.9	48	8	BH617377	BH617377 SALK_0364
571	9	42.9	46	8	BH751055	BH751055 SALK_0487	644	9	42.9	48	8	BH617696	BH617696 SALK_0374
572	9	42.9	46	8	BH910540	BH910540 SALK_0601	645	9	42.9	48	8	BH633587	BH633587 SALK_0428
573	9	42.9	46	9	CC887473	CC887473 SALK_1502	646	9	42.9	48	8	BH748267	BH748267 SALK_0450
574	9	42.9	46	9	CG782542	CG782542 1123050H0	647	9	42.9	48	8	BH748292	BH748292 SALK_0451
575	9	42.9	47	8	A2623246	A2623246 1M0460C17	648	9	42.9	48	8	BH748882	BH748882 SALK_0469
576	9	42.9	47	8	A2779546	A2779546 2M0016C09	649	9	42.9	48	8	BH749772	BH749772 SALK_0302
577	9	42.9	47	8	BH169602	BH169602 SALK_0016	650	9	42.9	48	8	BH749892	BH749892 SALK_0303
578	9	42.9	47	8	BH172194	BH172194 SALK_0053	651	9	42.9	48	8	BH750103	BH750103 SALK_0347
579	9	42.9	47	8	BH172688	BH172688 SALK_0060	652	9	42.9	48	8	BH751416	BH751416 SALK_0501
580	9	42.9	47	8	BH213222	BH213222 SALK_0089	653	9	42.9	48	8	BH753224	BH753224 SALK_0199
581	9	42.9	47	8	BH213678	BH213678 SALK_0095	654	9	42.9	48	8	BH753678	BH753678 SALK_0294
582	9	42.9	47	8	BH214187	BH214187 SALK_0103	655	9	42.9	48	8	BH902361	BH902361 SALK_0917
583	9	42.9	47	8	BH252265	BH252265 SALK_0130	656	9	42.9	48	8	BZ382688	BZ382688 SALK_1186
584	9	42.9	47	8	BH252797	BH252797 SALK_0138	657	9	42.9	48	9	BX286631	BX286631 Arabidops
585	9	42.9	47	8	BH253337	BH253337 SALK_0147	658	9	42.9	49	1	AA706582	AA706582 ah27b06.8
586	9	42.9	47	8	BH253852	BH253852 SALK_0155	659	9	42.9	49	1	AA726836	AA726836 vu94gl2.r
587	9	42.9	47	8	BH611281	BH611281 SALK_0306	660	9	42.9	49	1	AI558595	AI558595 fb68a10.y
588	9	42.9	47	8	BH611531	BH611531 SALK_0310	661	9	42.9	49	1	AI584385	AI584385 fb92h12.x
589	9	42.9	47	8	BH612570	BH612570 SALK_0329	662	9	42.9	49	1	AI883392	AI883392 fc63c06.y
590	9	42.9	47	8	BH617563	BH617563 SALK_0372	663	9	42.9	49	1	AU013938	AU013938 AU013938
591	9	42.9	47	8	BH618704	BH618704 SALK_0395	664	9	42.9	49	5	BQ587334	BQ587334 E012340w-
592	9	42.9	47	8	BH747945	BH747945 SALK_0397	665	9	42.9	49	5	BQ587752	BQ587752 E012340-0
593	9	42.9	47	8	BH748581	BH748581 SALK_0461	666	9	42.9	49	7	X98140	X98140 MMEST49.Mou
594	9	42.9	47	8	BH752651	BH752651 SALK_0189	667	9	42.9	49	8	BH168986	BH168986 SALK_0004
595	9	42.9	47	8	BH753401	BH753401 SALK_0287	668	9	42.9	49	8	BH169475	BH169475 SALK_0014
596	9	42.9	47	8	BH851673	BH851673 SALK_0733	669	9	42.9	49	8	BH170166	BH170166 SALK_0024
597	9	42.9	47	9	AL946412	AL946412 Arabidops	670	9	42.9	49	8	BH170234	BH170234 SALK_0025
598	9	42.9	47	9	CG714468	CG714468 1119036H0	671	9	42.9	49	8	BH172398	BH172398 SALK_0056
599	9	42.9	48	1	AV967257	AV967257 AV967257	672	9	42.9	49	8	BH212186	BH212186 SALK_0072
600	9	42.9	48	8	BH169127	BH169127 SALK_0006	673	9	42.9	49	8	BH212189	BH212189 SALK_0072
601	9	42.9	48	8	BH169913	BH169913 SALK_0020	674	9	42.9	49	8	BH213269	BH213269 SALK_0089
602	9	42.9	48	8	BH170421	BH170421 SALK_0028	675	9	42.9	49	8	BH251862	BH251862 SALK_0122
603	9	42.9	48	8	BH170455	BH170455 SALK_0029	676	9	42.9	49	8	BH252868	BH252868 SALK_0139
604	9	42.9	48	8	BH170532	BH170532 SALK_0030	677	9	42.9	49	8	BH253161	BH253161 SALK_0145
605	9	42.9	48	8	BH170799	BH170799 SALK_0033	678	9	42.9	49	8	BH253743	BH253743 SALK_0153
606	9	42.9	48	8	BH171310	BH171310 SALK_0040	679	9	42.9	49	8	BH253938	BH253938 SALK_0157
607	9	42.9	48	8	BH171340	BH171340 SALK_0041	680	9	42.9	49	8	BH614128	BH614128 SALK_0355
608	9	42.9	48	8	BH171719	BH171719 SALK_0047	681	9	42.9	49	8	BH748794	BH748794 SALK_0467

682	9	42.9	49	8	BH752698	SALK_0192	755	8.8	41.9	31	9	AG194290	AG194290	Pan trogl
683	9	42.9	49	8	BH753750	SALK_0295	756	8.8	41.9	32	8	AZ485865	AZ485865	IM0313H02
684	9	42.9	49	9	AJ596083	Arabidops	c 757	8.8	41.9	32	8	AZ583239	IM0378K08	
685	9	42.9	49	9	CNS07F9C	Arabidops	758	8.8	41.9	32	8	BZ381666	SALK_1170	
686	9	42.9	49	9	CR400023	Arabidops	759	8.8	41.9	32	8	BZ383892	SALK_1347	
687	9	42.9	50	1	AL802196	AL802196	760	8.8	41.9	32	9	EX656781	Arabidops	
688	9	42.9	50	1	AUI02484	AUI02484	c 761	8.8	41.9	32	9	CR359095	Arabidops	
689	9	42.9	50	1	AUI04254	AUI04254	c 762	8.8	41.9	32	9	CR359095	Arabidops	
690	9	42.9	50	1	AUI05296	AUI05296	c 763	8.8	41.9	32	9	DMES45221	Drosophil	
691	9	42.9	50	1	AUI07262	AUI07262	c 764	8.8	41.9	33	1	AV834380	AV834380	
692	9	42.9	50	1	AUI07263	AUI07263	c 765	8.8	41.9	33	4	BI656215	603283594	
693	9	42.9	50	1	AUI07510	AUI07510	c 766	8.8	41.9	33	7	T89682	Y099F02.s1	
694	9	42.9	50	1	AUI07860	AUI07860	c 767	8.8	41.9	33	8	AZ316728	IM0035A15	
695	9	42.9	50	1	AUI07968	AUI07968	c 768	8.8	41.9	33	8	BZ380694	SALK_1155	
696	9	42.9	50	1	AZ108799	AZ108799	c 769	8.8	41.9	33	8	BZ382892	SALK_1190	
697	9	42.9	50	8	BH211702	BH211702	c 770	8.8	41.9	33	8	CC049737	0190506-0	
698	9	42.9	50	8	BH213709	BH213709	c 771	8.8	41.9	33	9	AJ599597	Arabidops	
699	9	42.9	50	8	BH253148	BH253148	772	8.8	41.9	34	8	BZ377896	SALK_1063	
700	9	42.9	50	8	BH611167	BH611167	773	8.8	41.9	34	8	BZ380603	SALK_1153	
701	9	42.9	50	8	BH612727	BH612727	774	8.8	41.9	34	9	CG723116	1119074G1	
702	9	42.9	50	8	BH617293	BH617293	775	8.8	41.9	35	8	AZ838159	2M0133C15	
703	9	42.9	50	8	BH617418	BH617418	c 776	8.8	41.9	35	8	BH847051	SALK_0129	
704	9	42.9	50	8	BH747393	BH747393	777	8.8	41.9	35	8	BH852456	SALK_0746	
705	9	42.9	50	8	BH750106	BH750106	778	8.8	41.9	35	8	BZ378301	SALK_1079	
706	9	42.9	50	8	BH753469	BH753469	779	8.8	41.9	35	8	BZ380621	SALK_1154	
707	9	42.9	50	9	BS572281	Arabidops	780	8.8	41.9	35	8	BZ380790	SALK_1156	
708	9	42.9	50	9	CC547498	CH240_430	781	8.8	41.9	35	8	BZ383613	SALK_1341	
709	9	42.9	50	9	CG711376	CG711376	782	8.8	41.9	35	8	BZ763321	SALK_1162	
710	9	42.9	50	9	CG713887	CG713887	783	8.8	41.9	35	9	AL947040	Arabidops	
711	9	42.9	50	9	CG894689	CG894689	784	8.8	41.9	35	9	DR31814T	Arabidops	
712	8.8	41.9	20	1	AU258084	AU258084	c 785	8.8	41.9	36	8	AQ073401	EP(2)_2212	
713	8.8	41.9	21	5	BS566484	BS566484	786	8.8	41.9	36	8	BZ380578	SALK_1153	
714	8.8	41.9	21	8	AZ309721	AZ309721	787	8.8	41.9	36	9	TA126A03P	TA126A03P	
715	8.8	41.9	22	9	TA290E03P	TA290E03P	788	8.8	41.9	37	1	AA977326	Cq72C02.s	
716	8.8	41.9	22	9	CL438518	CL438518	789	8.8	41.9	37	1	AA984865	am62b07.s	
717	8.8	41.9	22	9	CL670198	CL670198	790	8.8	41.9	37	1	AI142601	ok35d07.s	
718	8.8	41.9	22	9	AG195487	AG195487	791	8.8	41.9	37	2	BF122604	BF122604	
719	8.8	41.9	23	8	AZ805705	AZ805705	c 792	8.8	41.9	37	4	BJ049420	BJ049420	
720	8.8	41.9	24	7	L32029	L32029	c 793	8.8	41.9	37	8	AZ653729	IM0527103	
721	8.8	41.9	24	8	AZ469511	AZ469511	c 794	8.8	41.9	37	8	AZ789498	2M0037N16	
722	8.8	41.9	24	8	AZ475486	AZ475486	c 795	8.8	41.9	37	8	AZ863572	2M0171E07	
723	8.8	41.9	25	1	AJ679528	AJ679528	c 796	8.8	41.9	37	8	AZ863572	2M0171E07	
724	8.8	41.9	25	8	AZ654827	AZ654827	797	8.8	41.9	37	8	BZ377641	SALK_0986	
725	8.8	41.9	26	1	AU011509	AU011509	798	8.8	41.9	37	8	BZ377654	SALK_0987	
726	8.8	41.9	26	8	AZ427547	AZ427547	799	8.8	41.9	37	8	BZ377657	SALK_0987	
727	8.8	41.9	26	8	AZ623173	AZ623173	800	8.8	41.9	37	8	BZ377658	SALK_0987	
728	8.8	41.9	26	8	AZ821460	AZ821460	801	8.8	41.9	37	8	BZ377667	SALK_0987	
729	8.8	41.9	26	9	TA252D07Q	TA252D07Q	802	8.8	41.9	37	8	BZ377667	SALK_0987	
730	8.8	41.9	27	8	AZ347928	AZ347928	803	8.8	41.9	37	8	BZ377667	SALK_0987	
731	8.8	41.9	27	9	TA354A04Q	TA354A04Q	804	8.8	41.9	37	8	BZ377667	SALK_0987	
732	8.8	41.9	28	1	AI076131	AI076131	805	8.8	41.9	37	8	BZ377667	SALK_0987	
733	8.8	41.9	28	8	AZ780159	AZ780159	806	8.8	41.9	37	8	BZ377667	SALK_0987	
734	8.8	41.9	28	8	AZ783515	AZ783515	807	8.8	41.9	37	8	BZ377667	SALK_0987	
735	8.8	41.9	28	9	TA300B03Q	TA300B03Q	808	8.8	41.9	37	8	BZ377667	SALK_0987	
736	8.8	41.9	29	5	BQ595553	BQ595553	809	8.8	41.9	37	8	BZ377667	SALK_0987	
737	8.8	41.9	29	8	AQ025252	AQ025252	810	8.8	41.9	37	8	BZ377667	SALK_0987	
738	8.8	41.9	29	8	AZ775915	AZ775915	811	8.8	41.9	37	8	BZ377667	SALK_0987	
739	8.8	41.9	29	8	BH906395	BH906395	812	8.8	41.9	37	8	BZ377667	SALK_0987	
740	8.8	41.9	29	8	BZ380586	BZ380586	813	8.8	41.9	37	8	BZ377667	SALK_0987	
741	8.8	41.9	29	8	BZ380648	BZ380648	814	8.8	41.9	37	8	BZ377667	SALK_0987	
742	8.8	41.9	29	8	BZ380770	BZ380770	815	8.8	41.9	37	8	BZ377667	SALK_0987	
743	8.8	41.9	29	8	BZ384011	BZ384011	816	8.8	41.9	37	8	BZ377667	SALK_0987	
744	8.8	41.9	29	8	BZ765533	BZ765533	817	8.8	41.9	37	8	BZ377667	SALK_0987	
745	8.8	41.9	30	9	AX289793	AX289793	818	8.8	41.9	37	8	BZ377667	SALK_0987	
746	8.8	41.9	31	1	AA781776	AA781776	819	8.8	41.9	37	8	BZ377667	SALK_0987	
747	8.8	41.9	31	1	AA78844	AA78844	820	8.8	41.9	37	8	BZ377667	SALK_0987	
748	8.8	41.9	31	1	AA590433	AA590433	821	8.8	41.9	37	8	BZ377667	SALK_0987	
749	8.8	41.9	31	4	EG432088	EG432088	822	8.8	41.9	37	8	BZ377667	SALK_0987	
750	8.8	41.9	31	7	CO782526	CO782526	823	8.8	41.9	37	8	BZ377667	SALK_0987	
751	8.8	41.9	31	8	AZ318049	AZ318049	824	8.8	41.9	37	8	BZ377667	SALK_0987	
752	8.8	41.9	31	8	AZ318049	AZ318049	825	8.8	41.9	37	8	BZ377667	SALK_0987	
753	8.8	41.9	31	8	BZ381518	BZ381518	826	8.8	41.9	37	8	BZ377667	SALK_0987	
754	8.8	41.9	31	9	BZ383871	BZ383871	827	8.8	41.9	37	8	BZ377667	SALK_0987	

828	8.8	41.9	37	8	B2381631	B2381631	SALK_1170	901	8.8	41.9	45	8	BH908303	BH908303	SALK_0471
829	8.8	41.9	37	8	B2381688	B2381688	SALK_1171	c 902	8.8	41.9	45	8	CC178546	CC178546	NPX482 Ba
830	8.8	41.9	37	8	B2381722	B2381722	SALK_1171	c 903	8.8	41.9	45	9	AL764750	AL764750	ArabiDops
831	8.8	41.9	37	8	B2381723	B2381723	SALK_1171	904	8.8	41.9	46	1	AV834157	AV834157	AV834157
832	8.8	41.9	37	8	B2381736	B2381736	SALK_1171	905	8.8	41.9	46	1	AA616469	AA616469	vn66d10.1
833	8.8	41.9	37	8	B2383575	B2383575	SALK_1341	906	8.8	41.9	45	8	BH861568	BH861568	SALK_0818
834	8.8	41.9	37	8	B2383596	B2383596	SALK_1341	907	8.8	41.9	46	8	BZ287326	BZ287326	SALK_0206
835	8.8	41.9	37	8	B2383623	B2383623	SALK_1341	908	8.8	41.9	46	8	BZ383801	BZ383801	SALK_1345
836	8.8	41.9	37	8	B2383627	B2383627	SALK_1341	909	8.8	41.9	46	9	AJ622642	AJ622642	Drosophil
837	8.8	41.9	37	8	B2383631	B2383631	SALK_1342	910	8.8	41.9	46	9	AL758842	AL758842	ArabiDops
838	8.8	41.9	37	8	B2383632	B2383632	SALK_1342	911	8.8	41.9	47	6	CF329526	CF329526	NACL_-04-
839	8.8	41.9	37	8	B2383659	B2383659	SALK_1342	912	8.8	41.9	47	8	AZ856490	AZ856490	2M0160K22
840	8.8	41.9	37	8	B2383661	B2383661	SALK_1342	913	8.8	41.9	47	8	CC039002	CC039002	3591_1_99
841	8.8	41.9	37	8	B2383666	B2383666	SALK_1342	914	8.8	41.9	48	1	AI749566	AI749566	at30f01.x
842	8.8	41.9	37	8	B2383686	B2383686	SALK_1342	c 915	8.8	41.9	48	7	D19123	D19123	MUSGS01337
843	8.8	41.9	37	8	B2383862	B2383862	SALK_1346	916	8.8	41.9	48	8	AZ458771	AZ458771	1M0263H10
844	8.8	41.9	37	8	B2383914	B2383914	SALK_1347	917	8.8	41.9	48	8	AZ503560	AZ503560	1M0343R21
845	8.8	41.9	37	8	B2766033	B2766033	SALK_1365	c 918	8.8	41.9	48	8	CC179090	CC179090	SALK_0582
846	8.8	41.9	37	8	BH857421	BH857421	SALK_0748	c 919	8.8	41.9	48	9	EX122790	EX122790	Danio_per
847	8.8	41.9	38	8	BZ380646	BZ380646	SALK_1154	920	8.8	41.9	48	9	CG778060	CG778060	1123025E0
c 848	8.8	41.9	38	8	BZ768853	BZ768853	SALK_1408	c 921	8.8	41.9	48	9	CG918667	CG918667	01S0556-0
c 849	8.8	41.9	38	9	AL942413	AL942413	ArabiDops	c 922	8.8	41.9	48	9	CL528747	CL528747	ASV7F07.f
850	8.8	41.9	38	9	BX287148	BX287148	ArabiDops	923	8.8	41.9	49	1	AA657082	AA657082	vs23c09.1
c 851	8.8	41.9	38	9	AG217395	AG217395	Drosophil	c 924	8.8	41.9	49	1	AA948394	AA948394	ons2b09.s
c 852	8.8	41.9	39	8	AZ595333	AZ595333	1M0407F23	c 925	8.8	41.9	49	1	AI004508	AI004508	ot66g10.s
c 853	8.8	41.9	39	8	AZ773859	AZ773859	2M0001I10	c 926	8.8	41.9	49	1	AI359268	AI359268	gy27c06.x
c 854	8.8	41.9	39	9	AG261161	AG261161	Lotus cor	927	8.8	41.9	49	1	AI444171	AI444171	fb43b07.y
855	8.8	41.9	40	1	A1219362	A1219362	qg14e08.x	c 928	8.8	41.9	49	1	AI638467	AI638467	tt07d10.x
c 856	8.8	41.9	40	1	A1433170	A1433170	ti46a06.x	929	8.8	41.9	49	1	AI738824	AI738824	wi39d04.x
c 857	8.8	41.9	40	6	CF305521	CF305521	CLD1--01-	930	8.8	41.9	49	4	BI525053	BI525053	602925110
858	8.8	41.9	40	8	BZ782376	BZ782376	1M0583011	931	8.8	41.9	49	6	CB337845	CB337845	laa29h07.
859	8.8	41.9	40	8	BZ385044	BZ385044	SALK_1363	c 932	8.8	41.9	49	6	CD681046	CD681046	tab67e02.
c 860	8.8	41.9	40	8	CC040316	CC040316	3591_1_13	c 933	8.8	41.9	49	8	AZ405394	AZ405394	1M0174N07
c 861	8.8	41.9	40	9	BX893447	BX893447	ArabiDops	934	8.8	41.9	49	8	AQ254822	AQ254822	EP(2)1132
c 862	8.8	41.9	40	9	AG189131	AG189131	Pan trogl	c 935	8.8	41.9	49	8	BZ383782	BZ383782	SALK_1344
c 863	8.8	41.9	41	1	AU266348	AU266348	ArabiDops	936	8.8	41.9	49	8	CC045158	CC045158	3591_1_17
c 864	8.8	41.9	41	7	CO732377	CO732377	SILL01B01	c 937	8.8	41.9	49	8	CC060297	CC060297	EY04028-5
865	8.8	41.9	41	7	H89001	H89001	Yw26b07.r1	c 938	8.8	41.9	49	9	AJ599619	AJ599619	ArabiDops
866	8.8	41.9	41	7	T17567	T17567	mps v288.Th	939	8.8	41.9	49	9	CG718294	CG718294	1119052D0
c 867	8.8	41.9	41	9	AJ600758	AJ600758	ArabiDops	940	8.8	41.9	49	9	CL213029	CL213029	G030H04.G
c 868	8.8	41.9	41	9	AL756926	AL756926	ArabiDops	941	8.8	41.9	50	1	AA116917	AA116917	mq25g06.x
c 869	8.8	41.9	41	9	DME547050	DME547050	ArabiDops	c 942	8.8	41.9	50	1	AU102357	AU102357	AU102357
c 870	8.8	41.9	41	9	CG799936	CG799936	01S0783-0	c 943	8.8	41.9	50	1	AU102880	AU102880	AU102880
c 871	8.8	41.9	41	9	CC884734	CC884734	SALK_1350	944	8.8	41.9	50	1	AU102957	AU102957	AU102957
c 872	8.8	41.9	41	9	AB081895	AB081895	Drosophil	945	8.8	41.9	50	1	AU103632	AU103632	AU103632
c 873	8.8	41.9	42	7	H07866	H07866	Y186508.s1	946	8.8	41.9	50	1	AU103633	AU103633	AU103633
c 874	8.8	41.9	42	8	BH000535	BH000535	2M028B805	947	8.8	41.9	50	1	AU103633	AU103633	AU103633
c 875	8.8	41.9	42	8	BH799740	BH799740	1008109H1	948	8.8	41.9	50	1	AU103997	AU103997	AU103997
c 876	8.8	41.9	42	9	AL763435	AL763435	ArabiDops	949	8.8	41.9	50	1	AU104135	AU104135	AU104135
c 877	8.8	41.9	42	9	DME545209	DME545209	ArabiDops	950	8.8	41.9	50	1	AU104175	AU104175	AU104175
c 878	8.8	41.9	43	1	AA948203	AA948203	op99h09.s	951	8.8	41.9	50	1	AU104448	AU104448	AU104448
c 879	8.8	41.9	43	1	AA976713	AA976713	qo6d06.s	c 952	8.8	41.9	50	1	AU104885	AU104885	AU104885
c 880	8.8	41.9	43	1	AA976713	AA976713	qo6d06.s	c 953	8.8	41.9	50	1	AU104953	AU104953	AU104953
c 881	8.8	41.9	43	1	AL115342	AL115342	uh84a06.r	c 954	8.8	41.9	50	1	AU105325	AU105325	AU105325
c 882	8.8	41.9	43	1	AJ666206	AJ666206	AJ666206	955	8.8	41.9	50	1	AU105434	AU105434	AU105434
883	8.8	41.9	43	4	B1333375	B1333375	602996772	c 956	8.8	41.9	50	1	AU105452	AU105452	AU105452
884	8.8	41.9	43	5	BX551512	BX551512	EX551512	957	8.8	41.9	50	1	AU105954	AU105954	AU105954
885	8.8	41.9	43	6	CF321300	CF321300	HD--12-I0	958	8.8	41.9	50	1	AU106291	AU106291	AU106291
c 886	8.8	41.9	43	7	W38487	W38487	zb19b07.r1	c 959	8.8	41.9	50	1	AU107257	AU107257	AU107257
c 887	8.8	41.9	43	8	BH643347	BH643347	1008057B0	c 960	8.8	41.9	50	1	AU107258	AU107258	AU107258
c 888	8.8	41.9	43	9	EX892893	EX892893	ArabiDops	c 961	8.8	41.9	50	1	AU107260	AU107260	AU107260
c 889	8.8	41.9	44	6	CF315888	CF315888	HD--04-F1	c 962	8.8	41.9	50	1	AU107261	AU107261	AU107261
c 890	8.8	41.9	44	7	T17569	T17569	mps v3 The	963	8.8	41.9	50	1	AU107612	AU107612	AU107612
c 891	8.8	41.9	44	8	BH905113	BH905113	SALK_1056	c 964	8.8	41.9	50	1	AU107636	AU107636	AU107636
c 892	8.8	41.9	44	8	BZ384007	BZ384007	SALK_1349	965	8.8	41.9	50	1	AU107648	AU107648	AU107648
c 893	8.8	41.9	44	8	BZ384717	BZ384717	SALK_1359	966	8.8	41.9	50	1	AU107652	AU107652	AU107652
894	8.8	41.9	44	9	CC455081	CC455081	SALK_0476	967	8.8	41.9	50	1	AU107653	AU107653	AU107653
c 895	8.8	41.9	44	9	CC795527	CC795527	SALK_0814	968	8.8	41.9	50	1	AU107654	AU107654	AU107654
c 896	8.8	41.9	45	8	AZ345886	AZ345886	1M0080P17	969	8.8	41.9	50	1	AU107892	AU107892	AU107892
c 897	8.8	41.9	45	8	AZ605963	AZ605963	1M0427A12	970	8.8	41.9	50	1	AU108020	AU108020	AU108020
898	8.8	41.9	45	8	BH638406	BH638406	1008022D0	971	8.8	41.9	50	1	AU108057	AU108057	AU108057
899	8.8	41.9	45	8	BH759240	BH759240	KG00542-3	c 972	8.8	41.9	50	1	AV836264	AV836264	AV836264
900	8.8	41.9	45	8	BH789424	BH789424	SALK_0293	c 973	8.8	41.9	50	2	BE732496	BE732496	601567696

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974      8.8 41.9 50 2 BE978663
975      8.8 41.9 50 6 CD422372
976      8.8 41.9 50 7 CK984500
977      8.8 41.9 50 8 AZ446391
978      8.8 41.9 50 8 BZ664163
979      8.8 41.9 50 8 CC325469
980      8.8 41.9 50 9 BX659110
981      8.8 41.9 50 9 CR105452
982      8.8 41.9 50 9 CR397867
983      8.8 41.9 50 9 TA300F12Q
984      8.8 41.9 50 9 CT794988
985      8.6 41.0 20 1 AF683142
986      8.6 41.0 20 6 CF337542
987      8.6 41.0 20 8 AZ989202
988      8.6 41.0 20 9 AG201749
989      8.6 41.0 21 7 CO785256
990      8.6 41.0 21 8 AZ352290
991      8.6 41.0 22 1 AA991491
992      8.6 41.0 22 8 AZ824852
993      8.6 41.0 23 9 TA184F06Q
994      8.6 41.0 23 9 TA270S01Q
995      8.6 41.0 24 4 BM396768
996      8.6 41.0 24 9 AJ587571
997      8.6 41.0 25 6 CA850879
998      8.6 41.0 25 8 AZ591086
999      8.6 41.0 25 8 AZ806433
1000     8.6 41.0 25 9 AJ588696

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ALIGNMENTS

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RESULT 1
TA199C08P
LOCUS      32 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 199c08, forward sequence,
            genomic survey sequence.
ACCESSION  AL475986
VERSION     AL475986.1 GI:11842726
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
            Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 32)
AUTHORS    Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.B., Rajandream,M.A. and Barrell,B.G.
TITLE       Direct Submission
JOURNAL     Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.

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FEATURES

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            source
            Location/Qualifiers
                1..32
                /organism="Trypanosoma brucei"
                /mol_type="genomic DNA"
                /strain="TREU927"
                /db_xref="taxon:5691"
                /clone="199c08"

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ORIGIN

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Query Match      60.0%;      Score 12.6;      DB 9;      Length 32;
Best Local Similarity 78.9%;      Pred. No. 3.3e+04;
Matches 15;      Conservative 0;      Mismatches 4;      Indels 0;      Gaps 0;

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QY      2  CGCGTACGGTCTTAATGACC 20
        ||||| ||||| |||||
DB      7  CGCGTACGGTCTTAATGACC 25

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RESULT 2
AW004201/c
LOCUS      50 bp      mRNA      linear      EST 08-SEP-1999
DEFINITION 701550260 A. thaliana, Columbia Col-0, inflorescence-2 Arabidopsis
            thaliana cDNA clone 701550260, mRNA sequence.
ACCESSION  AW004201
VERSION     AW004201.1 GI:5851230
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
            Arabidopsis thaliana

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```

            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
            1 (bases 1 to 50)
AUTHORS     Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D.,
            Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P.,
            Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D.,
            Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C.,
            Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S.,
            Nobrega,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and
            Hanson,D.

```

TITLE Arabidopsis thaliana Gene Expression MicroArray

```

JOURNAL     Unpublished (1999)
COMMENT     Contact: David Smoller, Ph.D.
            Genome Systems, Inc., a wholly owned subsidiary of Incyte
            Pharmaceuticals, Inc., 4633 World Parkway Circle, St. Louis, MO 63134, USA
            Tel: 877-577-2733
            Fax: 314-427-3324
            Email: service@genomesystems.com.

```

FEATURES

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            source
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            /organism="Arabidopsis thaliana"
            /mol_type="mRNA"
            /ecotye="Col-0"
            /db_xref="taxon:3702"
            /clone="701550260"
            /tissue type="inflorescence"
            /dev stage="4 - 7 weeks"
            /clone lib="A. thaliana, Columbia Col-0, inflorescence-2"
            /note="vector: pSPORT; Site 1: NotI; Site 2: SalI; CDNA
            library was derived from untreated inflorescence tissue
            from Arabidopsis thaliana, Columbia Col-0, at 4 - 7
            weeks. Plants were grown in 1:1:1 peat
            moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C
            under constant light, and watered with fertilizer. cDNA
            synthesis was initiated using a NotI-oligo(dT) primer.
            Double-stranded cDNA was blunted, ligated to SalI
            adaptors, digested with NotI, size-selected, and cloned
            into the NotI and SalI sites of the pSPORT vector."

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ORIGIN

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Query Match      58.1%;      Score 12.2;      DB 1;      Length 50;
Best Local Similarity 82.4%;      Pred. No. 5.6e+04;
Matches 14;      Conservative 0;      Mismatches 3;      Indels 0;      Gaps 0;

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QY      2  CGCGTACGGTCTTAATGCA 18
        ||||| ||||| |||||
DB      47  CGCGTACGGTATATTGA 31

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RESULT 3
CF338319

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LOCUS
DEFINITION CF338319 33 bp mRNA linear EST 18-AUG-2003
 RC11--01-F04.g1 Regenerated callus lambda phage cDNA library (RCL1)
 Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-F04,
 mRNA sequence.

ACCESSION CF338319
VERSION CF338319.1 GI:33825024
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS 1 (bases 1 to 33)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Mahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongui University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 Location/Qualifiers
 1..33
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--01-F04"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

ORIGIN
 Query Match 57.1%; Score 12; DB 6; Length 33;
 Best Local Similarity 75.0%; Pred. No. 7.3e+04;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACC 20
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Db 8 TCAAGTAGTGTCTAATTACC 27
 |||||

RESULT 4
BQ592384
LOCUS BQ592384 36 bp mRNA linear EST 06-DEC-2002
DEFINITION E012681-024-020-N04-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
 cDNA clone 024-020-N04 5-PRIME, mRNA sequence.

ACCESSION BQ592384
VERSION BQ592384.1 GI:26121967
KEYWORDS EST.

SOURCE
ORGANISM Beta vulgaris
 Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS 1 (bases 1 to 36)
 Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
 and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189

12472698
PUBMED
COMMENT Contact: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 36 Std Error: 0.00
 Plate: 20 row: N column: 04
 Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES
 Location/Qualifiers
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 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
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 /db_xref="taxon:161934"
 /db_xref="GABI:190371"
 /clone="024-020-N04"
 /tissue_type="developing root"
 /lab_host="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-developing root"
 /note="Vector: pCMVSPORT6; Site 1: SstI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SstI-NotI, primer sites and
 orientation:
 SP6-SstI-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
 Query Match 55.2%; Score 11.6; DB 5; Length 36;
 Best Local Similarity 77.8%; Pred. No. 1.2e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGCGTACGGTCTAATGAC 19
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Db 5 CGCGTACGATTATTATAC 22
 |||||

RESULT 5
BH903257
LOCUS BH903257 43 bp DNA linear GSS 04-SEP-2002
DEFINITION SALK_102332.18 30.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_102332.18.30.x, genomic
 survey sequence.

ACCESSION BH903257
VERSION BH903257.1 GI:22714417
KEYWORDS GSS.

SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
AUTHORS 1 (bases 1 to 43)
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.

```

Class: TDNA tagged.
FEATURES
    source
        1. .43
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /scot_type="Col-0"
            /db_xref="taxon:3702"
            /clone="GALK 102332.18.30.x"
            /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"
            /note="each of which contains one or more TDNA insertion"
            /note="elements. The resultant fragment for each line was"
            /note="directly sequenced to determine the genomic sequence at"
            /note="the site of insertion. Details of the protocols used can"
            /note="be found at http://signal.salk.edu/tdna\_protocols.html"
ORIGIN
    Query Match      55.2%; Score 11.6; DB 8; Length 43;
    Best Local Similarity 77.8%; Pred. No. 1.2e+05;
    Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 GCGTACGGTCTATGACC 20
    |||||
Db 13 GCGTTGGTCTGATAACC 30
    |||||

RESULT 6
LOCUS CL660557
DEFINITION PRI0137b_H04 - PRI0137b.B21 (29) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL660557
GSS CL660557.1 GI:50146000
VERSION Pristionchus pacificus
KEYWORDS Pristionchus pacificus
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppADB: An AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES
    source
        1. .29
            /organism="Pristionchus pacificus"
            /mol_type="genomic DNA"
            /strain="California"
            /db_xref="taxon:54126"
            /clone_lib="Mixed stage fosmid library of P. pacificus"
            /var. "California"
            /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN
    Query Match      54.3%; Score 11.4; DB 9; Length 29;
    Best Local Similarity 92.3%; Pred. No. 1.6e+05;
    Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 ACGGTCTTATGAC 19
    |||||
Db 16 ACGATCTATGAC 28
    |||||

Class: TDNA tagged.
FEATURES
    source
        1. .43
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /scot_type="Col-0"
            /db_xref="taxon:3702"
            /clone="GALK 102332.18.30.x"
            /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"
            /note="each of which contains one or more TDNA insertion"
            /note="elements. The resultant fragment for each line was"
            /note="directly sequenced to determine the genomic sequence at"
            /note="the site of insertion. Details of the protocols used can"
            /note="be found at http://signal.salk.edu/tdna\_protocols.html"
ORIGIN
    Query Match      55.2%; Score 11.6; DB 8; Length 43;
    Best Local Similarity 77.8%; Pred. No. 1.2e+05;
    Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 GCGTACGGTCTATGACC 20
    |||||
Db 13 GCGTTGGTCTGATAACC 30
    |||||

RESULT 7
LOCUS CL293866/c
DEFINITION CL293866
ACCESSION CL293866
VERSION CL293866
KEYWORDS CL293866.1 GI:42541995
SOURCE GSS.
ORGANISM Zea mays
Ze mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE Latschew,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
AUTHORS Sequence tagged transposon insertions from the UniformMu maize
TITLE population
JOURNAL Unpublished (2003)
COMMENT Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drm@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
02S0349-08, Primer set: A
Class: transposon insertion site.
FEATURES
    source
        1. .39
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /strain="W22 (ACR, bz1-m9)"
            /cultivar="UniformMu"
            /db_xref="taxon:4577"
            /clone="02S0349-08A1-E04"
            /clone_lib="UniformMu MuTAIL Library"
            /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
            insertions in Mu inactive lines were extracted from the
            UniformMu maize population by the thermo asymmetric
            interlaced PCR (TAIL) protocol using primers specific for
            the Mu terminal inverted repeat and a set of 16 arbitrary
            primers. Amplicons were size enriched using Sepharose 400
            spin columns and cloned into the TOPO PCR4 vector."
ORIGIN
    Query Match      54.3%; Score 11.4; DB 9; Length 39;
    Best Local Similarity 71.4%; Pred. No. 1.6e+05;
    Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 TCGGTACGGTCTATGACCG 21
    |||||
Db 34 TCACCTCGGTATATATCCCG 14
    |||||

RESULT 8
LOCUS AU106620/c
DEFINITION AU106620 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT06186, mRNA sequence.
ACCESSION AU106620
VERSION AU106620.1 GI:13556141
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale

```

mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT06186"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 54.3%; Score 11.4; DB 1; Length 50;
Best Local Similarity 71.4%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTTAATGACCG 21
||| ||||| ||||| |||||
Db 22 TCCCTATGCTCTCATGTCAG 2

RESULT 9
AUI06626/c
LOCUS
DEFINITION
AUI06626 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT11544, mRNA sequence.
AUI06626
AUI06626.1 GI:13556147
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT11544"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 54.3%; Score 11.4; DB 1; Length 50;
Best Local Similarity 71.4%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

JOURNAL
MEDLINE
PUBMED
COMMENT

QY 1 TCGCGTACGGTCTTAATGACCG 21
||| ||||| ||||| |||||
Db 30 TCCCTATGCTCTCATGTCG 10

RESULT 10
BH615074/c
LOCUS
DEFINITION
BH615074 Prime Drosophila melanogaster P(SUPor-P) P element
insertion lines Drosophila melanogaster genomic Sequence recovered
from 5' end of P element, genomic survey sequence.
BH615074
BH615074.1 GI:18379762
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 31)
Levis, R., Hoskins, R., Liao, G., Mozden, N., Taang, G., He, Y.,
Karpen, G., Bellen, H., Rubin, G. and Spradling, A.
The Berkeley Drosophila Genome Project Gene Disruption Project
Unpublished (2001)
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element
The P element insertion position is base 24 in the 31 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon-tagged.
Location/Qualifiers
1..31
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster P(SUPor-P) P element
insertion lines"
/note="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P(SUPor-P) P-element transposon insertion. The resultant
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
http://www.fruitfly.org/about/methods/inverse.pcr.html."

ORIGIN
Query Match 53.3%; Score 11.2; DB 8; Length 31;
Best Local Similarity 81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TACGGTCTTAATGACCG 21
||| ||||| ||||| |||||
Db 17 TACGGCCCAATGACCG 2

RESULT 11
CL303319/c
LOCUS
DEFINITION
CL303319 GGTC Gene Trap Library GV03C04 Mus musculus cDNA clone
W130C02, mRNA sequence.
CL303319
CL303319.2 GI:49489549
GSS.
Mus musculus (house mouse)
Mus musculus
Mus musculus

ORIGIN
Query Match 53.3%; Score 11.2; DB 8; Length 31;
Best Local Similarity 81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

JOURNAL
MEDLINE
PUBMED
COMMENT

QY 1 TCGCGTACGGTCTTAATGACCG 21
||| ||||| ||||| |||||
Db 30 TCCCTATGCTCTCATGTCG 10

RESULT 10
BH615074/c
LOCUS
DEFINITION
BH615074 Prime Drosophila melanogaster P(SUPor-P) P element
insertion lines Drosophila melanogaster genomic Sequence recovered
from 5' end of P element, genomic survey sequence.
BH615074
BH615074.1 GI:18379762
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 31)
Levis, R., Hoskins, R., Liao, G., Mozden, N., Taang, G., He, Y.,
Karpen, G., Bellen, H., Rubin, G. and Spradling, A.
The Berkeley Drosophila Genome Project Gene Disruption Project
Unpublished (2001)
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element
The P element insertion position is base 24 in the 31 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon-tagged.
Location/Qualifiers
1..31
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster P(SUPor-P) P element
insertion lines"
/note="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P(SUPor-P) P-element transposon insertion. The resultant
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
http://www.fruitfly.org/about/methods/inverse.pcr.html."

ORIGIN
Query Match 53.3%; Score 11.2; DB 8; Length 31;
Best Local Similarity 81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TACGGTCTTAATGACCG 21
||| ||||| ||||| |||||
Db 17 TACGGCCCAATGACCG 2

RESULT 11
CL303319/c
LOCUS
DEFINITION
CL303319 GGTC Gene Trap Library GV03C04 Mus musculus cDNA clone
W130C02, mRNA sequence.
CL303319
CL303319.2 GI:49489549
GSS.
Mus musculus (house mouse)
Mus musculus
Mus musculus

ORIGIN
Query Match 53.3%; Score 11.2; DB 8; Length 31;
Best Local Similarity 81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

JOURNAL
MEDLINE
PUBMED
COMMENT

QY 1 TCGCGTACGGTCTTAATGACCG 21
||| ||||| ||||| |||||
Db 30 TCCCTATGCTCTCATGTCG 10

RESULT 10
BH615074/c
LOCUS
DEFINITION
BH615074 Prime Drosophila melanogaster P(SUPor-P) P element
insertion lines Drosophila melanogaster genomic Sequence recovered
from 5' end of P element, genomic survey sequence.
BH615074
BH615074.1 GI:18379762
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 31)
Levis, R., Hoskins, R., Liao, G., Mozden, N., Taang, G., He, Y.,
Karpen, G., Bellen, H., Rubin, G. and Spradling, A.
The Berkeley Drosophila Genome Project Gene Disruption Project
Unpublished (2001)
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element
The P element insertion position is base 24 in the 31 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon-tagged.
Location/Qualifiers
1..31
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster P(SUPor-P) P element
insertion lines"
/note="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P(SUPor-P) P-element transposon insertion. The resultant
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
http://www.fruitfly.org/about/methods/inverse.pcr.html."

ORIGIN
Query Match 53.3%; Score 11.2; DB 8; Length 31;
Best

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 43)

REFERENCE
AUTHORS
Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, P., Arnold, H.H., Schmutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)

JOURNAL
MEDLINE
22810117

PUBMED
12904583

COMMENT
On Jun 30, 2004 this sequence version replaced gi:42744159.
Contact: GGC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
pTibetago gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=W130C02'. ES cell line harboring insertion mutation of target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm'
1' Inhouse Sequence Identifier: 08816
Class: Gene Trap.

FEATURES source
Location/Qualifiers
1..43
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="W130C02"
/sex="Male"
/cell_type="Embryonic stem cell"
/note="ES cells 129S2 (formerly 129/SvPas)"
/clone_lib="GGTC Gene Trap Library GV03C04"
/note="Vector: pTibetago"

ORIGIN

Query Match 53.3%; Score 11.2; DB 9; Length 43;
Best Local Similarity 72.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CGTACGGTCTAATGACCG 21
||||| ||| ||| ||| |||
Db 38 CGTACGTTNNTAAACCG 21

RESULT 12
BX287629
LOCUS
Arabidopsis thaliana T-DNA flanking sequence GK-403C11-017864,
Genomic survey sequence.
BX287629.1 GI:28886625
ACCESSION
BX287629
VERSION
BX287629.1
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL
MEDLINE
22755829
PUBMED
12874060

REFERENCE
AUTHORS
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
JOURNAL
MEDLINE
23117147

14756321
REFERENCE
3
AUTHORS
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weisshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
BioTechniques 35 (6), 1164-1168 (2003)

JOURNAL
MEDLINE
14682050

PUBMED
14682050

REFERENCE
4 (bases 1 to 45)
AUTHORS
Rosso, M.G., Li, Y., Strizhov, N. and Weisshaar, B.
TITLE
Direct Submission
JOURNAL
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
It indicates an insertion within the locus defined by BAC clone
T12C14. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES source
Location/Qualifiers
1..45
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-403C11-017864"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match 53.3%; Score 11.2; DB 9; Length 45;
Best Local Similarity 81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAAT 16
||||| ||| ||| ||| |||
Db 23 TCGGTACGTCTACT 38

RESULT 13
BX650703
LOCUS
Arabidopsis thaliana T-DNA flanking sequence GK-551H04-022301,
Genomic survey sequence.
BX650703.1 GI:37607091
ACCESSION
BX650703
VERSION
BX650703.1
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL
MEDLINE
22755829
PUBMED
12874060

REFERENCE
2
AUTHORS
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
14756321

3 Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weishaar,B.
Weishaar,B.
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050

4 (bases 1 to 45)
Rosso,M.G., Li,Y., Strizhov,N. and Weishaar,B.
Direct Submission
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuchtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g53580.
Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source
1..45
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-551H04-022301"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 53.3%; Score 11.2; DB 9; Length 45;
Best Local Similarity 81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGCGTACGCTCTAATG 17
| | | | | | | | | | | | | | | | | | | | |
Db 13 CGCATAGTGTCTAATG 28

RESULT 14
AZ583945
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ583945 46 bp DNA linear GSS 13-DEC-2000
1M038107F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0388107 F, genomic survey sequence.
AZ583945
AZ583945.1 GI:11704336
GSS
Mus musculus (house mouse)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0388 row: I column: 07
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 46.
Location/Qualifiers
1..46
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0388107"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source
1..46
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0388107"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.3%; Score 11.2; DB 8; Length 46;
Best Local Similarity 81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 TACGCTCTAATGACCG 21
| | | | | | | | | | | | | | | | | | | | |
Db 4 TAGGACTAATGACAG 19

RESULT 15
CG774856/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CG774856 49 bp DNA linear GSS 29-OCT-2003
1123021C02.1BL.xl 1123 - RescueMu Grid L Zea mays genomic, genomic survey sequence.
CG774856
CG774856.1 GI:38031309
GSS.
Zea mays
Zea mays

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 49)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227

Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1123021 row: 16
Class: transposon-tagged.
Location/Qualifiers
1. .49
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1123 - RescueMu Grid L"
/note="Organ: Leaf; Vector: RescueMu (engineered from plusScript backbone); Site1: BamHI; Site2: BglII; RescueMu is a 4.9 Kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.znadb.iastate.edu' and follow the links for 'RescueMu.' Grid L was grown in Molokai in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

FEATURES
source
1. .49
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strains="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="GK-055D02-012479"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ517514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 53.3%; Score 11.2; DB 9; Length 49;
Best Local Similarity 81.2%; Pred. NO. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GCGTACGGTCTAATGA 18
Db 36 GCGTATGGTCGAATAA 21

RESULT 16
AL754718
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-055D02-012479,
genomic survey sequence.
AL754718.1 GI:21487216
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weissshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE
PUBMED
12874060
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weissshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
MEDLINE
PUBMED
14756321
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weissshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines

Biotechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 42)
Li, Y., Rosso, M.G., Strizhov, N. and Weissshaar, B.
Direct Submission
Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At1g78560.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1. .42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strains="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="GK-055D02-012479"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ517514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match 52.4%; Score 11; DB 9; Length 42;
Best Local Similarity 73.7%; Pred. NO. 2.7e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TCGCGTACGGTCTAATGAC 19
Db 11 TCGATTGCTATCTAATGAC 29

RESULT 17
AL939959
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-243C02-014389,
genomic survey sequence.
AL939959.1 GI:24396408
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weissshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE
PUBMED
12874060
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weissshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
MEDLINE
PUBMED
14756321
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weissshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines

WEISSHAAR, B.
 High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 Biotechniques 35 (6), 1164-1168 (2003)
 14682050
 4 (bases 1 to 47)
 Rosso, M.G., Strizhov, N., Li, Y. and Weishaar, B.
 Direct Submission
 Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion within the locus defined by BAC clone
 K14B15. Details on the protocols used for generation of the
 sequence are described in References 1-3. The sequences are
 generated at the MPI for Plant Breeding Research in the context of
 the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
 program designated 'GABI'. Information on line availability can be
 found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
 Location/Qualifiers
 1. .47
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-243C02-014389"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161 (GenBank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."
 ORIGIN
 Query Match 52.4%; Score 11; DB 9; Length 47;
 Best Local Similarity 73.7%; Pred. No. 2.7e+05;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 2 CGCGTACGGTCTAATGACC 20
 ||||| ||||| ||||| |||||
 Db 5 CGCGTGACGTTTAAACACC 23
 ||||| ||||| ||||| |||||
 RESULT 18
 BH895527 48 bp DNA linear GSS 14-AUG-2002
 LOCUS 3526_1_34_1_F09_2EL_x1 3526 - RescueMu Grid K Zea mays genomic,
 DEFINITION genomic survey sequence.
 ACCESSION BH895527
 VERSION BH895527.1 GI:22229580
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 48)
 Walbot, V.
 Maize genomic sequences found using engineered RescueMu transposon
 Unpublished (2001)
 CONTACT Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 3526_1_34_1 row: 3
 Class: transposon-tagged.

FEATURES
 source
 1. .48
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="3526 - RescueMu Grid K"
 /note="Organ: leaf; Vector: RescueMu (engineered from
 pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
 RescueMu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on RescueMu, go to the web
 site 'www.zmdb.iastate.edu' and follow the links for
 'RescueMu.' Grid K was grown at Molokai, Hawaii in Winter
 2000-2001. DNA was extracted from leaf punches, double
 digested using BamHI and BglII, and ligated to form
 circular plasmids. DH10B cells, and ligated to form
 screened on LB plates with ampicillin."
 ORIGIN
 Query Match 52.4%; Score 11; DB 8; Length 48;
 Best Local Similarity 73.7%; Pred. No. 2.7e+05;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 3 CGGTACGGTCTAATGACCG 21
 ||||| ||||| ||||| |||||
 Db 2 CGGACCATCTAGTGCCCG 20
 ||||| ||||| ||||| |||||
 RESULT 19
 BI223057 32 bp mRNA linear EST 11-JUL-2001
 LOCUS 602942007F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5105088 5',
 DEFINITION mRNA sequence.
 ACCESSION BI223057
 VERSION BI223057.1 GI:14676501
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 32)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11253 row: n column: 01
 High quality sequence stop: 32.
 Location/Qualifiers
 1. .32
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5105088"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_12"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

ORIGIN

Query Match 51.4%; Score 10.8; DB 4; Length 32;
 Best Local Similarity 85.7%; Pred. No. 3.6e+05;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAA 15
 |||||
 Db 4 CGCGTACGGTGCAA 17
 |||||

RESULT 20

BH810122
 LOCUS SALK_040987 Arabidopsis thaliana DNA linear GSS 02-MAY-2002
 DEFINITION thaliana genomic clone SALK_040987, genomic survey sequence.

ACCESSION BH810122

VERSION BH810122.1 GI:20387940

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 36)

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

FEATURES

source

Class: TDNA tagged.
 Location/Qualifiers
 1..36
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_040987"
 /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 51.4%; Score 10.8; DB 8; Length 36;
 Best Local Similarity 85.7%; Pred. No. 3.6e+05;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TACGGTCTAATGAC 19
 |||||
 Db 9 TACGGTATAATAAC 22
 |||||

RESULT 21

BH810143
 LOCUS SALK_041377 Arabidopsis thaliana DNA linear GSS 02-MAY-2002
 DEFINITION thaliana genomic clone SALK_041377, genomic survey sequence.

ACCESSION BH810143

VERSION BH810143.1 GI:20387961

KEYWORDS

SOURCE

ORGANISM

GSS.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

FEATURES

source

Class: TDNA tagged.
 Location/Qualifiers
 1..36
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_041377"
 /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 51.4%; Score 10.8; DB 8; Length 36;
 Best Local Similarity 85.7%; Pred. No. 3.6e+05;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TACGGTCTAATGAC 19
 |||||
 Db 9 TACGGTATAATAAC 22
 |||||

RESULT 22

CR360542/c

LOCUS CR360542

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-821B07-025531,

genomic survey sequence.

ACCESSION CR360542

VERSION CR360542.1 GI:45543464

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

TITLE

Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weishaar,B.
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis

thaliana

Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE 22755829

PUBMED 12874060

REFERENCE 2

AUTHORS

TITLE

Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
 Weishaar,B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for

flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
14756321

REFERENCE
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weishaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL BioTechniques 35 (6), 1164-1168 (2003)

REFERENCE 14682050

4 (bases 1 to 36)

Strizhov, N., Rosso, M.G., Li, Y. and Weishaar, B.

Direct Submission

Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene Atg10350.

Details on the protocols used for generation of the sequence are

described in References 1-3. The sequences are generated at the MPI

for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated

'GABI'. Information on line availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1. .36

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/clone="GK-821B07-025531"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana

plants (T1) which were transformed with the T-DNA from

vector PAC106 (GenBank accession number: AJ537513). The

lines contain one or more T-DNA insertions. The DNA

fragment(s) resulting from the PCR were directly sequenced

to determine the genomic sequence flanking the insertion.

T-DNA derived sequences were removed."

ORIGIN

Query Match 51.4%; Score 10.8; DB 9; Length 36;

Best Local Similarity 85.7%; Pred. No. 3.6e+05;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TACGGTCTAATGAC 19

|||||

36 TACGCTCAATGAC 23

CL524591

CL524591.1 GI:46151391

GSS.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 44)

Sallaud, C., Gay, C., Larmande, P., Bes, M., Piffanelli, P., Piegou, B.,

Droc, G., Regad, F., Bourgeois, E., Meynard, D., Perin, C.,

Ghesquiere, A., Delseny, M., Glaszmann, J.C. and Guiderdoni, E.

High throughput T-DNA insertion mutagenesis in rice: A first step

towards in silico reverse genetics

Plant J. (2004) In press

Contact: Guiderdoni

TITLE

JOURNAL

COMMENT

REFERENCE

AUTHORS

CL524591/c

LOCUS

DEFINITION

CL524591

CL524591.1 GI:46151391

GSS.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 44)

Sallaud, C., Gay, C., Larmande, P., Bes, M., Piffanelli, P., Piegou, B.,

Droc, G., Regad, F., Bourgeois, E., Meynard, D., Perin, C.,

UMR PIA Biotrop program

CIRAD

TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE

Tel: 33467615629

Fax: 33467615605

Email: emmanuel.guiderdoni@cirad.fr

Class: TDNA tagged.

Location/Qualifiers

1. .44

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="genomic DNA"

/cultivar="Nipponbare"

/db_xref="taxon:3994"

/clone_lib="Flanking Sequence Tag of Oryza sativa T-DNA

insertion lines"

/note="PCR was performed on DNA of primary transformants

of Oryza sativa plants. The DNA fragment(s) resulting of

PCR were directly sequenced from the left border to

determine the genomic sequence flanking the insertion.

T-DNA derived sequences were removed. Information to order

the corresponding mutant line and a link to a database

providing a graphical display is available from June 2004

at http://genoplante-info.infobiogen.fr/oryzatagline/.

This sequence has been generated in the framework of the

French plant genomics program Genoplante

(http://www.genoplante.org and

http://genoplante-info.infobiogen.fr)."

ORIGIN

Query Match 51.4%; Score 10.8; DB 9; Length 44;

Best Local Similarity 85.7%; Pred. No. 3.6e+05;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CGTACGGTCTAATG 17

|||||

36 CGGACGGTCAATG 23

AG192385

AG192385.1 GI:45224561

GSS.

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,

Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

BAC end sequences of Library RP-43

Unpublished

2 (bases 1 to 45)

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,

Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

Direct Submission

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of

Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);

52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea

(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/.

Tel:82-42-866-7181, Fax:82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC

end was generated during the R&D process and may have higher chance

of clone tracking errors.

PRIMERS

Sequencing: TJ

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI.

COMMENT

```

FEATURES
  source
    Location/Qualifiers
      1..45
        /organism="Pan troglodytes"
        /mol_type="genomic DNA"
        /db_xref="taxon:9598"
        /clone="RP43-068014.TJ"
        /sex="male"
        /cell_type="lymphocytes"
        /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN
  Query Match      51.4%; Score 10.8; DB 9; Length 45;
  Best Local Similarity 85.7%; Pred. No. 3.6e+05;
  Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 2 CGCGTACGGTCTAA 15
  Db 2 CGCATAGGATATNA 15
  RESULT 25
  AUI02564/c
  LOCUS
  DEFINITION
    AUI02564 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
    HEP07440, mRNA sequence.
  ACCESSION
    AUI02564
  VERSION
    AUI02564.1 GI:13552085
  KEYWORDS
    EST.
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
  REFERENCE
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  AUTHORS
    Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
    Hata,H., Oca,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
    Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE
    Diverse transcriptional initiation revealed by fine, large-scale
    mapping of mRNA start sites
  JOURNAL
    EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE
    21270072
  PUBMED
    11375929
  COMMENT
    Contact: Yutaka Suzuki
    Department of Virology
    Institute of Medical Science, University of Tokyo
    4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
    Email: ysuzuki@ims.u-tokyo.ac.jp
    Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
    Sugano,S. Construction and characterization of a full
    length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
    149-156 (1997).
FEATURES
  source
    Location/Qualifiers
      1..50
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="HEP07440"
        /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
  Query Match      51.4%; Score 10.8; DB 1; Length 50;
  Best Local Similarity 85.7%; Pred. No. 3.6e+05;
  Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 5 GTACCGTCTAATGA 18
  Db 15 GCACCGTCTAATGA 2
  RESULT 26
  BZ358744
  LOCUS
  DEFINITION
    SALK_133243.27.05.x Arabidopsis thaliana TDNA insertion lines
    Arabidopsis thaliana genomic clone SALK_133243.27.05.x, genomic
  survey sequence.
  accession
    BZ358744
  version
    BZ358744.1 GI:24951173
  keywords
    GSS
  source
    Arabidopsis thaliana (thale cress)
    Arabidopsis thaliana
    Arabidopsis thaliana
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
  reference
    Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
    Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
    Shinn,P., Zimmerman,J. and Ecker,J.R.
  title
    A Sequence-Indexed Library of Insertion Mutations in the
    Arabidopsis Genome
  journal
    Unpublished (2001)
  comment
    Contact: Joseph R. Ecker
    Salk Institute Genomic Analysis Laboratory (SIGNAL)
    The Salk Institute for Biological Studies
    10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
    Tel: 858 453 4100 x1752
    Fax: 858 558 6379
    Email: eckersalk.edu
    This is single pass sequence recovered from the left border of
    TDNA.
  features
    Class: TDNA tagged.
    Location/Qualifiers
      1..32
        /organism="Arabidopsis thaliana"
        /mol_type="genomic DNA"
        /ecotype="Col-0"
        /db_xref="taxon:3702"
        /clone="SALK_133243.27.05.x"
        /clone_lib="Arabidopsis thaliana TDNA insertion lines"
        /note="PCR was performed on Arabidopsis thaliana lines
        each of which contains one or more TDNA insertion
        elements. The resultant fragment for each line was
        directly sequenced to determine the genomic sequence at
        the site of insertion. Details of the protocols used can
        be found at http://signal.salk.edu/tdna_protocols.html"
  origin
    Query Match      50.5%; Score 10.6; DB 8; Length 32;
    Best Local Similarity 76.5%; Pred. No. 4.7e+05;
    Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
    QY 4 CGTACGGTCTAATGACC 20
    Db 12 CGTACGGACATGAGC 28
  result
    RESULT 27
    A2492641/c
    LOCUS
    DEFINITION
      A2492641 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
      clone UUGC1M0326D24 R, genomic survey sequence.
    accession
      A2492641
    version
      A2492641.1 GI:10665556
    keywords
      GSS
    source
      Mus musculus (house mouse)
    organism
      Mus musculus
  reference
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  authors
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D., Weiss,R.
  title
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
  journal
    Unpublished (2000)
  comment
    Contact: Robert B. Weiss
    University of Utah Genome Center

```

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0326 row: D column: 24
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.

FEATURES
source
1..38
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0326D24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 50.5%; Score 10.6; DB 8; Length 38;
Best Local Similarity 76.5%; Pred. No. 4.7e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGCGTACGGTCTAATGA 18
| ||||| |||||
Db 34 CCCGTGCACTCTAATGA 18

RESULT 28
DME545378
LOCUS 39 bp DNA linear GSS 24-FEB-2003
DEFINITION Drosophila melanogaster flanking sequence of RS P element insertion P[RS5]5-SZ-3505, clone library P[RS5], genomic survey sequence.
ACCESSION AJ545378
VERSION AJ545378.1 GI:28553187
KEYWORDS GSS; genome survey sequence.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
1
AUTHORS Ryder, E.J., Ashburner, M., Baguna, J.J., Blows, F., Bucheton, A., Coulson, D., Dickson, B., Drummond, J., Glover, D., Gunton, N., Hafen, E., Hall, S., Heisenberg, M., Lepesant, J.A., Maroy, P., Mechler, B., O'Kane, C., Pflugfelder, G., Rasmuson-Lestander, A., Reuter, G., Roote, J., Szidonya, J., Wang, S., Webster, J. and Russell, S.
TITLE Mapping of RS P element insertions in *Drosophila melanogaster* for the DrosDel second generation deficiency kit

Unpublished
2 (bases 1 to 39)
Ryder, E.J.
Direct Submission
Submitted (17-FEB-2003) Ryder E.J., Department of Genetics, University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM
The insertion point of the P element is before base 1 of the sequence. Further information about this P element insertion line can be found at <http://www.flyseq.org.uk> and <http://www.drosdel.org.uk>.

FEATURES
source
1..39
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/chromosome="3L"
/clone="P[RS5]5-SZ-3505"
/clone_lib="P[RS5]"
/note="read=5' end"

misc_feature
1..39
/note="P element insertion in the 5' to 3' orientation"

ORIGIN
Query Match 50.5%; Score 10.6; DB 9; Length 39;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGCGTACGGTCTAATGA 18
| ||||| |||||
Db 2 CACGTAATGTTAATGA 18

RESULT 29
BH213213
LOCUS 43 bp DNA linear GSS 24-OCT-2001
DEFINITION SALK 008917 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_008917, genomic survey sequence.
ACCESSION BH213213
VERSION BH213213.1 GI:16394927
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1 (bases 1 to 43)
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..43
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_008917"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

```

ORIGIN
Query Match      50.5%; Score 10.6; DB 8; Length 43;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGA 18
||||| |||||
Db 25 CGCGTACGGTCTAATGA 41

RESULT 30
AA441847/c
LOCUS
DEFINITION
ZM6204.1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:774630 5' similar to TR:G558458 G558458 ACIDIC 82 KDA
PROTEIN. i, mRNA sequence.
ACCESSION
AA441847
VERSION
AA441847.1 GI:2153731
SOURCE
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 46)
AUTHORS
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wyllie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES
source
1..46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:774630"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/clone_lib="Soares total_fetus_Nb2HF8_9w"
/notes="Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pTT3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match      50.5%; Score 10.6; DB 1; Length 46;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GTACGGTCTAATGACCG 21
||| ||| |||||

```

```

Db 43 GTCAGGTGTAATGACGG 27

RESULT 31
AZ769367
LOCUS
DEFINITION
1M0569021R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0569021 R, genomic survey sequence.
ACCESSION
AZ769367
VERSION
AZ769367.1 GI:12889428
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 46)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0569 row: 0 column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 46.
FEATURES
source
1..46
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0569021"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      50.5%; Score 10.6; DB 8; Length 46;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGGTACGGTCTAATG 17
||||| |||||

```

Db	5	TCGGTGCCCTCTCTG	21
RESULT 32	BZ379971	46 bp DNA linear	GSS 26-NOV-2002
LOCUS	SALK_114399.18.50.x	Arabidopsis thaliana TDNA insertion lines	
DEFINITION	Arabidopsis thaliana genomic clone SALK_114399.18.50.x, genomic survey sequence.		
ACCESSION	BZ379971		
VERSION	BZ379971.1	GI:25472355	
KEYWORDS	GSS		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	1 (bases 1 to 46)		
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednits,L., Shinn,P., Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379 Email: ecker@salk.edu This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g03070. Class: TDNA tagged.		
FEATURES	Location/Qualifiers		
source	1..46		
	/organism="Arabidopsis thaliana"		
	/mol_type="genomic DNA"		
	/ecotype="Col-0"		
	/db_xref="taxon:3702"		
	/clone="SALK_114399.18.50.x"		
	/clone_lib="Arabidopsis thaliana TDNA insertion lines"		
	/notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html "		
ORIGIN			
Query Match	50.5%;	Score 10.6;	DB 8; Length 46;
Best Local Similarity	76.5%;	Pred. No. 4.6e+05;	
Matches	13; Conservative	0; Mismatches	4; Indels 0; Gaps 0;
Qy	1	TCGGTACGGTCTAATG	17
Db	23	TCGGTAAAGGTAATG	39
RESULT 33	AL753413	46 bp DNA linear	GSS 01-APR-2004
LOCUS	Arabidopsis thaliana T-DNA flanking sequence GK-049H07-013871,		
DEFINITION	genomic survey sequence.		
ACCESSION	AL753413		
VERSION	AL753413.1	GI:21485911	
KEYWORDS	GSS		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	1		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Arabidopsis.		

AUTHORS	Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.		
TITLE	GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana		
JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)		
MEDLINE	22755829		
PUBMED	12874060		
REFERENCE	2		
AUTHORS	Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.		
TITLE	An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics		
JOURNAL	Plant Mol. Biol. 53 (1-2), 247-259 (2003)		
MEDLINE	23117147		
PUBMED	14756321		
REFERENCE	3		
AUTHORS	Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.		
TITLE	High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines		
JOURNAL	BioTechniques 35 (6), 1164-1168 (2003)		
MEDLINE	14682050		
PUBMED			
REFERENCE	4 (bases 1 to 46)		
AUTHORS	Li, Y., Rosso, M.G., Strizhov, N. and Weisshaar, B.		
TITLE	Direct Submission		
JOURNAL			
COMMENT	Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone F26G5. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/ .		
FEATURES	Location/Qualifiers		
source	1..46		
	/organism="Arabidopsis thaliana"		
	/mol_type="genomic DNA"		
	/strain="Columbia 0"		
	/db_xref="taxon:3702"		
	/clone="GK-049H07-013871"		
	/clone_lib="Arabidopsis thaliana T-DNA insertion lines"		
	/ecotype="Col-0"		
	/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."		
ORIGIN			
Query Match	50.5%;	Score 10.6;	DB 9; Length 46;
Best Local Similarity	76.5%;	Pred. No. 4.6e+05;	
Matches	13; Conservative	0; Mismatches	4; Indels 0; Gaps 0;
Qy	2	CGGTACGGTCTAATGA	18
Db	40	CGGTACGGTCTAATGA	24
RESULT 34	H50401	49 bp mRNA linear	EST 18-SEP-1995
LOCUS	yc29h01.r1 Soares adult brain N25HB551 Homo sapiens cDNA clone IMAGE:179377 5' similar to SP:A45072 A45072 TYPE L K+ CHANNEL, KV3.1 - HUMAN ;, mRNA sequence.		
DEFINITION	H50401		
ACCESSION	H50401		
VERSION	H50401.1	GI:990242	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0036 row: K column: 16
Seq primer: CACACGGAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 30:
Location/Qualifiers
1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0036K16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pPW42 (gil4732114[gb]|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 49.5%; Score 10.4; DB 8; Length 30;
Best Local Similarity 70.0%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCACGTCACGCTCTAATGACC 20
|||||
Db 1 TCACCTCGGTCGATGACC 20
|||||

RESULT 37
AZ381857/c

LOCUS
AZ381857 30 bp DNA linear GSS 02-OCT-2000

DEFINITION
IM0138A10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0138A10 R, genomic survey sequence.

ACCESSION
A2381857

VERSION
A2381857.1 GI:10495557

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingle, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 1.

FEATURES

source

1. .37
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1301547"
/tissue type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP GCBI"

/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IGD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCTCAATTTTTTTTTTTT-3', 1. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 49.5%; Score 10.4; DB 1; Length 37;
Best Local Similarity 70.0%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY

2 CGCGTACGCTCTAATGACCG 21

DB

33 CGCGCAGCGTCATCGGAGCG 14

RESULT 39

BZ377768

LOCUS

DEFINITION BZ377768 37 bp DNA linear GSS 26-NOV-2002
SALK 106163.28.55.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_106163.28.55.n, genomic survey sequence.

ACCESSION

BZ377768

VERSION

BZ377768.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 37)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

FEATURES

source

1. .37
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"

/clone="SALK_106163.28.55.n"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 49.5%; Score 10.4; DB 8; Length 37;
Best Local Similarity 91.7%; Pred. No. 6.1e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

7 ACGGCTCTAATGA 18

DB

13 ACGGCTCTAATGA 24

RESULT 40

BZ383634

LOCUS

DEFINITION BZ383634 37 bp DNA linear GSS 26-NOV-2002
SALK 134205.28.00.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_134205.28.00.n, genomic survey sequence.

ACCESSION

BZ383634

VERSION

BZ383634.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 37)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

TITLE

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 37)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@alk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At2g25610.

Class: TDNA tagged.

Location/Qualifiers

1. .37

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_106163.28.55.n"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 49.5%; Score 10.4; DB 8; Length 37;
Best Local Similarity 91.7%; Pred. NO. 6.1e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 ACGGCTCTAATGA 18
||| |||||
Db 13 ACGGCTCTAATGA 24

Search completed: November 23, 2004, 22:21:54
Job time : 1040.82 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 594.247 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631B-3

Perfect score: 33

Sequence: 1 cgggtactaccgttcgcagaccactatggc 33

Scoring table:

IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745.residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	93.9	31	6	AX802289 Sequence
2	30.4	92.1	36	6	AS2660 Sequence 5
3	27.4	83.0	29	6	A68291 Sequence 12
4	22	66.7	34	6	BD181364 A method
5	22	66.7	34	6	AX523944 Sequence
6	22	66.7	34	6	AX524842 Sequence
7	22	66.7	41	6	BD171248 Method of
8	21	63.6	41	6	E25774 Method for
9	20.4	61.8	26	6	AR411540 Sequence
10	20.4	61.8	26	6	BD000266 Oligonucle
11	20.4	61.8	28	6	AR094968 Sequence
12	20.4	61.8	28	6	BD183050 Nucleic a
13	20.4	61.8	36	6	A70977 Sequence 31
14	20.4	61.8	36	6	BD244766 Isolation
15	20.4	61.8	36	6	AR255272 Sequence
16	20	60.6	32	6	AX147026 Sequence
17	20	60.6	37	6	E25770 Method for
18	20	60.6	38	6	I17519 Sequence.9
19	20	60.6	38	6	I17520 Sequence 10

19.4	58.8	30	6	AR080402 Sequence
19.4	58.8	30	6	AR118787 Sequence
19.4	58.8	30	6	E51970 Diagnostic
19.4	58.8	30	6	I70136 Sequence 3
19.4	58.8	30	6	BD004842 Method fo
19	57.6	22	6	E07367 PCR primer
19	57.6	22	6	E07369 PCR primer
19	57.6	24	6	AX250662 Sequence
19	57.6	25	6	AR400912 Sequence
19	57.6	25	6	AR400921 Sequence
19	57.6	25	6	AR411538 Sequence
19	57.6	25	6	AX571897 Sequence
19	57.6	25	6	BD000246 Oligonucle
19	57.6	25	6	BD000255 Oligonucle
19	57.6	25	6	BD000264 Oligonucle
18.4	55.8	20	6	A49280 Sequence 6
18.4	55.8	20	6	A64953 Sequence 7
18.4	55.8	20	6	AR020188 Sequence
18.4	55.8	20	6	AR301416 Sequence
18.4	55.8	20	6	AX004406 Sequence
18.4	55.8	20	6	BD077112 Hepatitis
18.4	55.8	26	6	A68290 Sequence 11
18.4	55.8	26	6	C0759765 Sequence
18.4	55.8	26	6	I17521 Sequence 11
18.4	55.8	26	6	I22184 Sequence 43
18	54.5	18	6	AX555048 Sequence
18	54.5	18	6	AX556788 Sequence
18	54.5	20	6	E08193 Primer. 9/1
18	54.5	21	6	BD062362 Cells and
18	54.5	21	6	BD102078 Cells and
18	54.5	46	6	BD175035 Method fo
18	54.5	46	6	BD102535 Method fo
17.8	53.9	25	6	E07744 Primer. 9/1
17.8	53.9	25	6	E07745 Primer. 9/1
17.4	52.7	20	6	AR167033 Sequence
17.4	52.7	20	6	AR210688 Sequence
17	51.5	17	6	A68289 Sequence 10
17	51.5	22	6	BD017181 Method fo
17	51.5	22	6	BD095630 Genotype
17	51.5	24	6	AX419900 Sequence
17	51.5	50	6	E44269 Oligo-DNA s
16.4	49.7	20	6	A68292 Sequence 13
16	48.5	16	6	AR234355 Sequence
16	48.5	16	6	AR285652 Sequence
16	48.5	16	6	AR397643 Sequence
16	48.5	16	6	AR004392 Sequence
16	48.5	33	6	AR064954 Sequence
16	48.5	33	6	AR097184 Sequence
16	48.5	33	6	AR130682 Sequence
16	48.5	33	6	AR172031 Sequence
16	48.5	33	6	BD189148 HCV Genom
16	48.5	33	6	BD189295 HCV Genom
16	48.5	33	6	BD189442 HCV Genom
16	48.5	33	6	I82867 Sequence 46
16	48.5	39	6	AR179035 Sequence
15.4	46.7	18	6	AR131559 Sequence
15.4	46.7	18	6	AR199493 Sequence
15.4	46.7	18	6	AR200964 Sequence
15.4	46.7	18	6	AR488724 Sequence
15.4	46.7	18	6	AX419715 Sequence
15.4	46.7	18	6	BD084977 Target-de
15.4	46.7	38	6	AR059771 Sequence
15.4	46.7	48	6	BD081885 Method fo
15.2	46.1	33	6	AR147751 Sequence
15.2	46.1	33	6	AR159773 Sequence
15.2	46.1	33	6	AR160465 Sequence
15.2	46.1	33	6	AR199704 Sequence
15.2	46.1	33	6	AR202421 Sequence
15.2	46.1	33	6	AR235998 Sequence
15.2	46.1	38	6	AR168755 Sequence
15.2	46.1	38	6	AR168757 Sequence
15.2	46.1	38	6	AR205494 Sequence
15.2	46.1	38	6	AR205496 Sequence

93	15.2	46.1	38	6	AR391943	Sequence	166	14.4	43.6	36	6	AX061258	Sequence
94	15.2	46.1	38	6	AR391945	Sequence	c 167	14.4	43.6	41	6	AR109120	Sequence
95	15.2	46.1	38	6	AX076510	Sequence	c 168	14.4	43.6	41	6	AR200775	Sequence
96	15.2	46.1	38	6	AX076512	Sequence	c 169	14.2	43.0	21	6	AX134096	Sequence
97	15.2	46.1	38	6	AX076644	Sequence	c 170	14.2	43.0	21	6	AX189705	Sequence
98	15.2	46.1	38	6	AX076646	Sequence	c 171	14.2	43.0	21	6	AX189705	Sequence
99	15.2	46.1	38	6	AX076648	Sequence	c 172	14.2	43.0	30	6	AX491621	Sequence
100	15.2	46.1	38	6	AX076650	Sequence	c 173	14.2	43.0	30	6	BD074883	Group A s
101	15.2	46.1	40	6	E01694	DNA encodin	c 174	14.2	43.0	33	6	AX323171	Sequence
c 102	15.2	46.1	46	6	CQ54922	Sequence	c 175	14.2	43.0	36	9	HSTCARB25	Sequence
c 103	15	45.5	15	6	AR033238	Sequence	c 176	14.2	43.0	36	9	HSTCARB46	Sequence
c 104	15	45.5	15	6	AR113060	Sequence	177	14	42.4	20	6	E08281	Sequence
c 105	15	45.5	15	6	BD206416	Enzymatic	178	14	42.4	25	6	BD222531	Methods f
c 106	15	45.5	15	6	BD206971	Enzymatic	179	14	42.4	25	6	BD222532	Methods f
c 107	15	45.5	15	6	E17467	Sequence 4	c 180	14	42.4	25	6	BD222533	Methods f
c 108	15	45.5	18	6	BD142099	A method	c 181	14	42.4	25	6	BD222534	Methods f
c 109	15	45.5	18	6	BD142136	A method	c 182	14	42.4	26	6	AR428913	Sequence
c 110	15	45.5	18	6	BD171237	Method of	c 183	14	42.4	26	6	AX696021	Sequence
c 111	15	45.5	21	6	A68285	Sequence 6	c 184	14	42.4	26	6	AX720385	Sequence
c 112	15	45.5	25	6	E44264	Sequence	c 185	14	42.4	26	6	AX720389	Sequence
c 113	15	45.5	26	6	AR488116	Sequence	c 186	14	42.4	26	6	AX814300	Sequence
c 114	15	45.5	26	6	AX472309	Sequence	c 187	14	42.4	26	6	AX814303	Sequence
c 115	15	45.5	37	6	AR050591	Sequence	c 188	14	42.4	37	6	AX351559	Sequence
c 116	15	45.5	50	6	E44268	Sequence	c 189	14	42.4	38	6	AR286735	Sequence
c 117	14.8	44.8	18	6	A68282	Sequence 3	c 190	14	42.4	38	6	AR398725	Sequence
c 118	14.8	44.8	19	6	A64951	Sequence 5	c 191	14	42.4	42	6	A68288	Sequence 9
c 119	14.8	44.8	21	6	AR166996	Sequence	c 192	14	42.4	42	6	AX003364	Sequence
c 120	14.8	44.8	21	6	AR210651	Sequence	c 193	14	42.4	47	6	AR237984	Sequence
c 121	14.8	44.8	23	6	AX098832	Sequence	194	13.8	41.8	20	6	AR167034	Sequence
c 122	14.8	44.8	25	6	AR089855	Sequence	195	13.8	41.8	20	6	AR210689	Sequence
c 123	14.8	44.8	25	6	E09662	Primer for	196	13.8	41.8	23	6	AX805796	Sequence
c 124	14.8	44.8	25	6	I93330	Sequence 4	c 197	13.8	41.8	25	6	CQ626245	Sequence
c 125	14.8	44.8	25	6	AR308955	Sequence	c 198	13.8	41.8	25	6	AR467308	Sequence
c 126	14.8	44.8	25	6	AR317086	Sequence	c 199	13.8	41.8	28	6	AX404625	Sequence
c 127	14.8	44.8	25	6	AX555526	Sequence	c 200	13.8	41.8	31	6	AX248737	Sequence
c 128	14.8	44.8	25	6	BD095878	Sequence	c 201	13.8	41.8	34	6	AR126133	Sequence
c 129	14.8	44.8	26	6	I46685	FEN-1 end	c 202	13.8	41.8	36	6	CQ784496	Sequence
c 130	14.8	44.8	28	6	AR094969	Sequence 66	c 203	13.8	41.8	37	6	AR122589	Sequence
c 131	14.8	44.8	28	6	AR094995	Sequence	c 204	13.8	41.8	40	6	A99066	Sequence 74
c 132	14.8	44.8	32	6	AX746459	Sequence	c 205	13.8	41.8	40	6	BD235443	Translati
c 133	14.8	44.8	32	6	AX763805	Sequence	c 206	13.8	41.8	40	6	AR195381	Sequence
c 134	14.8	44.8	33	6	AR004393	Sequence	c 207	13.8	41.8	40	6	AX001472	Sequence
c 135	14.8	44.8	33	6	AR064955	Sequence	c 208	13.8	41.8	42	6	E06011	A part of s
c 136	14.8	44.8	33	6	AR097185	Sequence	c 209	13.8	41.8	43	6	AX554432	Sequence
c 137	14.8	44.8	33	6	AR130683	Sequence	c 210	13.8	41.8	45	9	S80711	gamma delta
c 138	14.8	44.8	33	6	AR131570	Sequence	c 211	13.8	41.8	48	6	BD081886	Method fo
c 139	14.8	44.8	33	6	AR172032	Sequence	c 212	13.8	41.8	50	6	CQ003759	Sequence
c 140	14.8	44.8	33	6	BD189449	HCV Genom	c 213	13.6	41.2	38	6	AX220482	Sequence
c 141	14.8	44.8	33	6	BD189296	HCV Genom	c 214	13.6	41.2	38	6	AX223143	Sequence
c 142	14.8	44.8	33	6	BD189443	HCV Genom	c 215	13.6	41.2	48	6	AR307709	Sequence
c 143	14.8	44.8	33	6	I82868	Sequence 47	c 216	13.6	41.2	48	6	BD076359	Ligand ho
c 144	14.8	44.8	33	6	AR199504	Sequence	c 217	13.6	41.2	48	10	AB001358	Mus muscu
c 145	14.8	44.8	33	6	AR200975	Sequence	c 218	13.6	41.2	50	6	AX199460	Sequence
c 146	14.8	44.8	33	6	AR488734	Sequence	c 219	13.4	40.6	23	6	CQ840432	Sequence
c 147	14.8	44.8	33	6	AX419726	Sequence	c 220	13.4	40.6	27	6	CQ840432	Sequence
c 148	14.8	44.8	33	6	BD084988	Target-de	c 221	13.4	40.6	33	6	BD238547	Expressio
c 149	14.8	44.8	46	6	I49767	Sequence 12	c 222	13.4	40.6	39	6	I09580	Sequence 15
c 150	14.8	44.8	50	6	AX397950	Sequence	c 223	13.4	40.6	47	6	AR290168	Sequence
c 151	14.8	44.8	50	6	AX397958	Sequence	c 224	13.4	40.6	48	6	AX181923	Sequence
c 152	14.4	43.6	18	6	AX469411	Sequence	c 225	13.4	40.6	48	6	BD077303	Method an
c 153	14.4	43.6	18	6	AX470910	Sequence	c 226	13.4	40.6	50	6	CQ008965	Sequence
c 154	14.4	43.6	18	6	BD001051	Method an	c 227	13.4	40.6	50	6	CQ008987	Sequence
c 155	14.4	43.6	18	6	BD001480	Method an	c 228	13.2	40.0	24	6	AR474765	Sequence
c 156	14.4	43.6	22	6	AR124658	Sequence	c 229	13.2	40.0	26	6	AR090276	Sequence
c 157	14.4	43.6	22	6	AR242411	Sequence	c 230	13.2	40.0	26	6	AR197311	Sequence
c 158	14.4	43.6	22	6	AX540622	Sequence	c 231	13.2	40.0	26	6	AR259465	Sequence
c 159	14.4	43.6	26	6	E58847	Method for	c 232	13.2	40.0	29	6	A32376	Synthetic 1
c 160	14.4	43.6	26	6	AR411539	Sequence	c 233	13.2	40.0	29	6	AX712192	Sequence
c 161	14.4	43.6	26	6	BD000265	Oligonucl	c 234	13.2	40.0	32	6	AX180384	Sequence
c 162	14.4	43.6	35	6	BD175039	Method fo	c 235	13.2	40.0	33	6	AX839492	Sequence
c 163	14.4	43.6	36	6	AX061253	Sequence	c 236	13.2	40.0	41	6	AX515871	Sequence
c 164	14.4	43.6	36	6	AX061254	Sequence	c 237	13.2	40.0	41	6	AX521128	Sequence
c 165	14.4	43.6	36	6	AX061257	Sequence	c 238	13.2	40.0	45	6	A69002	Sequence 26

239	13.2	40.0	45	6	ARI39228	ARI39228 Sequence	C 312	13	39.4	50	6	E50439	E50439 Method for
240	13.2	40.0	45	6	AR30984	AR30984 Sequence	C 313	13	39.4	50	6	AR302197	AR302197 Sequence
C 241	13.2	40.0	45	9	HSELH1B	X72117 H.sapiens (C 314	13	39.4	50	6	AR349554	AR349554 Sequence
C 242	13.2	40.0	45	9	HSELH2B	X72118 H.sapiens (C 315	13	39.4	50	6	AR349555	AR349555 Sequence
C 243	13.2	40.0	47	6	AR291379	AR291379 Sequence	C 316	13	39.4	50	6	AX161828	AX161828 Sequence
C 244	13	39.4	14	6	AX067858	AX067858 Sequence	C 317	13	39.4	50	6	AX322179	AX322179 Sequence
C 245	13	39.4	15	6	AR033239	AR033239 Sequence	C 318	13	39.4	50	6	BD000119	BD000119 Nucleic a
C 246	13	39.4	15	6	ARI13061	ARI13061 Sequence	C 319	13	39.4	50	6	BD004784	BD004784 Method of
C 247	13	39.4	15	6	BD206415	BD206415 Enzymatic	C 320	13	39.4	50	6	BD006778	BD006778 Method fo
C 248	13	39.4	15	6	BD206417	BD206417 Enzymatic	C 321	13	39.4	50	6	BD091995	BD091995 Potentiati
C 249	13	39.4	15	6	BD206972	BD206972 Enzymatic	C 322	13	39.4	50	6	AF057517	AF057517 Homo sapi
C 250	13	39.4	15	6	BD208267	BD208267 Enzymatic	C 323	13	39.4	50	9	AF220249	AF220249 Homo sapi
C 251	13	39.4	15	6	I57468	I57468 Sequence 5	C 324	12.8	38.8	16	6	AR285635	AR285635 Sequence
C 252	13	39.4	18	6	AR0959	AR0959 Sequence 13	C 325	12.8	38.8	16	6	AR397626	AR397626 Sequence
C 253	13	39.4	20	6	ARI67032	ARI67032 Sequence	C 326	12.8	38.8	20	6	BD196029	BD196029 Antisense
C 254	13	39.4	20	6	AR210687	AR210687 Sequence	C 327	12.8	38.8	20	6	AR382820	AR382820 Sequence
C 255	13	39.4	24	6	ARI73112	ARI73112 Sequence	C 328	12.8	38.8	21	6	E25775	E25775 Method for
C 256	13	39.4	24	6	BD139591	BD139591 Arginine	C 329	12.8	38.8	21	6	AX739982	AX739982 Sequence
C 257	13	39.4	25	6	CQ626241	CQ626241 Sequence	C 330	12.8	38.8	24	6	AE2575	AE2575 Sequence 13
C 258	13	39.4	25	6	CQ626242	CQ626242 Sequence	C 331	12.8	38.8	25	6	AX615728	AX615728 Sequence
C 259	13	39.4	25	6	CQ626243	CQ626243 Sequence	C 332	12.8	38.8	25	6	AX615729	AX615729 Sequence
C 260	13	39.4	25	6	CQ626244	CQ626244 Sequence	C 333	12.8	38.8	26	6	I46580	I46580 Sequence 55
C 261	13	39.4	25	6	CQ626246	CQ626246 Sequence	C 334	12.8	38.8	26	6	AX708898	AX708898 Sequence
C 262	13	39.4	25	6	CQ626247	CQ626247 Sequence	C 335	12.8	38.8	26	6	AX708902	AX708902 Sequence
C 263	13	39.4	25	6	CQ626248	CQ626248 Sequence	C 336	12.8	38.8	27	6	AR228696	AR228696 Sequence
C 264	13	39.4	25	6	CQ626249	CQ626249 Sequence	C 337	12.8	38.8	27	6	AR228700	AR228700 Sequence
C 265	13	39.4	25	6	E44263	E44263 Oligo-DNA s	C 338	12.8	38.8	29	6	E13337	E13337 Probe. 4/19
C 266	13	39.4	25	6	AR467304	AR467304 Sequence	C 339	12.8	38.8	30	6	BD175843	BD175843 Glutamina
C 267	13	39.4	25	6	AR467305	AR467305 Sequence	C 340	12.8	38.8	30	6	E04700	E04700 Synthetic n
C 268	13	39.4	25	6	AR467306	AR467306 Sequence	C 341	12.8	38.8	30	6	AR302472	AR302472 Sequence
C 269	13	39.4	25	6	AR467307	AR467307 Sequence	C 342	12.8	38.8	31	6	AR207931	AR207931 Sequence
C 270	13	39.4	25	6	AR467309	AR467309 Sequence	C 343	12.8	38.8	31	6	AR383217	AR383217 Sequence
C 271	13	39.4	25	6	AR467310	AR467310 Sequence	C 344	12.8	38.8	32	6	I38810	I38810 Sequence 48
C 272	13	39.4	25	6	AR467311	AR467311 Sequence	C 345	12.8	38.8	32	6	BD012896	BD012896 Gene codi
C 273	13	39.4	25	6	AR467312	AR467312 Sequence	C 346	12.8	38.8	37	6	AR112772	AR112772 Sequence
C 274	13	39.4	26	6	I83632	I83632 Sequence 6	C 347	12.8	38.8	37	6	AR374165	AR374165 Sequence
C 275	13	39.4	29	6	BD177926	BD177926 Sequence	C 348	12.8	38.8	38	6	AX260002	AX260002 Sequence
C 276	13	39.4	29	6	AR351574	AR351574 Sequence	C 349	12.8	38.8	39	6	AR103921	AR103921 Sequence
C 277	13	39.4	29	6	AX492884	AX492884 Sequence	C 350	12.8	38.8	39	6	AR401400	AR401400 Sequence
C 278	13	39.4	31	6	AR003412	AR003412 Sequence	C 351	12.8	38.8	39	6	AR474276	AR474276 Sequence
C 279	13	39.4	31	6	AR003418	AR003418 Sequence	C 352	12.8	38.8	40	6	AR043925	AR043925 Sequence
C 280	13	39.4	31	6	I21201	I21201 Sequence 47	C 353	12.8	38.8	40	6	BD000714	BD000714 Drug comp
C 281	13	39.4	31	6	I21207	I21207 Sequence 53	C 354	12.8	38.8	40	6	BD000716	BD000716 Inhibitor
C 282	13	39.4	31	6	I74468	I74468 Sequence 47	C 355	12.8	38.8	41	6	A61793	A61793 Sequence 16
C 283	13	39.4	31	6	I74474	I74474 Sequence 53	C 356	12.8	38.8	41	6	AR109121	AR109121 Sequence
C 284	13	39.4	32	6	BD211604	BD211604 Canine an	C 357	12.8	38.8	41	6	AR200776	AR200776 Sequence
C 285	13	39.4	32	6	AR241582	AR241582 Sequence	C 358	12.8	38.8	44	6	AR002174	AR002174 Sequence
C 286	13	39.4	32	6	AR254538	AR254538 Sequence	C 359	12.8	38.8	45	6	A23129	A23129 Gene fragme
C 287	13	39.4	37	6	AX930625	AX930625 Sequence	C 360	12.8	38.8	48	6	ARI79422	ARI79422 Sequence
C 288	13	39.4	38	6	BD177912	BD177912 Sequence	C 361	12.8	38.8	48	6	BD191685	BD191685 Enzymatic
C 289	13	39.4	38	6	AR286543	AR286543 Sequence	C 362	12.8	38.8	48	6	AX927790	AX927790 Sequence
C 290	13	39.4	38	6	AR286788	AR286788 Sequence	C 363	12.8	38.8	48	8	AJ718213	AJ718213 Nicotiana
C 291	13	39.4	38	6	AR351560	AR351560 Sequence	C 364	12.8	38.8	48	11	AL845045	AL845045 Arabidops
C 292	13	39.4	38	6	AR398533	AR398533 Sequence	C 365	12.6	38.2	20	6	AR272094	AR272094 Sequence
C 293	13	39.4	38	6	AR398778	AR398778 Sequence	C 366	12.6	38.2	20	6	AR489988	AR489988 Sequence
C 294	13	39.4	38	6	AX220269	AX220269 Sequence	C 367	12.6	38.2	20	6	AX175400	AX175400 Sequence
C 295	13	39.4	38	6	AX223176	AX223176 Sequence	C 368	12.6	38.2	22	6	I58643	I58643 Sequence 11
C 296	13	39.4	38	6	AX492870	AX492870 Sequence	C 369	12.6	38.2	23	6	AX172363	AX172363 Sequence
C 297	13	39.4	38	6	BD141414	BD141414 Protein d	C 370	12.6	38.2	23	6	AX183979	AX183979 Sequence
C 298	13	39.4	40	6	BD185266	BD185266 Method fo	C 371	12.6	38.2	24	6	BD233483	BD233483 Novel hum
C 299	13	39.4	40	6	CQ795377	CQ795377 Sequence	C 372	12.6	38.2	25	6	CQ626239	CQ626239 Sequence
C 300	13	39.4	40	6	EL6986	EL6986 Sense prime	C 373	12.6	38.2	25	6	CQ626240	CQ626240 Sequence
C 301	13	39.4	40	6	AX514328	AX514328 Sequence	C 374	12.6	38.2	25	6	AR467302	AR467302 Sequence
C 302	13	39.4	41	6	AX519881	AX519881 Sequence	C 375	12.6	38.2	25	6	AR467303	AR467303 Sequence
C 303	13	39.4	41	6	AR184222	AR184222 Sequence	C 376	12.6	38.2	26	6	AR373108	AR373108 Sequence
C 304	13	39.4	42	6	ARI84343	ARI84343 Sequence	C 377	12.6	38.2	26	6	AX098337	AX098337 Sequence
C 305	13	39.4	42	6	AX127931	AX127931 Sequence	C 378	12.6	38.2	27	6	AX371712	AX371712 Sequence
C 306	13	39.4	42	6	ARI184343	ARI184343 Sequence	C 379	12.6	38.2	27	10	MMBR177	MMBR177 Sequence
C 307	13	39.4	45	6	AX930620	AX930620 Sequence	C 380	12.6	38.2	28	6	AR090298	AR090298 Sequence
C 308	13	39.4	46	6	AX930620	AX930620 Sequence	C 381	12.6	38.2	28	6	BD273400	BD273400 Compositi
C 309	13	39.4	47	6	AR291704	AR291704 Sequence	C 382	12.6	38.2	28	6	AR197333	AR197333 Sequence
C 310	13	39.4	47	6	AX323099	AX323099 Sequence	C 383	12.6	38.2	28	6	AR259487	AR259487 Sequence
C 311	13	39.4	50	6	E44267	E44267 Oligo-DNA s	C 384	12.6	38.2	30	6	AX482519	AX482519 Sequence

C 385	12.6	38.2	32	6	CQ827782 Sequence	C 458	12.4	37.6	33	6	AR151927 Sequence
C 386	12.6	38.2	32	6	CQ827783 Sequence	C 459	12.4	37.6	33	6	AR226328 Sequence
C 387	12.6	38.2	34	6	AR285932 Sequence	C 460	12.4	37.6	36	4	PICAMPO
C 388	12.6	38.2	35	6	AR062177 Sequence	C 461	12.4	37.6	37	6	AX581815 Sequence
C 389	12.6	38.2	35	6	AR135155 Sequence	C 462	12.4	37.6	37	6	AX582035 Sequence
C 390	12.6	38.2	35	6	AR397922 Sequence	C 463	12.4	37.6	37	6	AX582063 Sequence
C 391	12.6	38.2	36	6	A64974 Sequence 4	C 464	12.4	37.6	38	6	CQ759371 Sequence
C 392	12.6	38.2	36	6	CQ809461 Sequence	C 465	12.4	37.6	38	6	AR286548 Sequence
C 393	12.6	38.2	36	6	AR285933 Sequence	C 466	12.4	37.6	38	6	AR286567 Sequence
C 394	12.6	38.2	36	6	AR478920 Sequence	C 467	12.4	37.6	38	6	AR286583 Sequence
C 395	12.6	38.2	37	6	AR397923 Sequence	C 468	12.4	37.6	38	6	AR286608 Sequence
C 396	12.6	38.2	37	6	AX357426 Sequence	C 469	12.4	37.6	38	6	AR286635 Sequence
C 397	12.6	38.2	37	6	AX551183 Sequence	C 470	12.4	37.6	38	6	AR286671 Sequence
C 398	12.6	38.2	37	6	AX551183 Sequence	C 471	12.4	37.6	38	6	AR286727 Sequence
C 399	12.6	38.2	37	6	AX581921 Sequence	C 472	12.4	37.6	38	6	AR286865 Sequence
C 400	12.6	38.2	37	6	AX770380 Sequence	C 473	12.4	37.6	38	6	AR286884 Sequence
C 401	12.6	38.2	37	6	AX805518 Sequence	C 474	12.4	37.6	38	6	AR287032 Sequence
C 402	12.6	38.2	38	6	CQ785742 Sequence	C 475	12.4	37.6	38	6	AR398538 Sequence
C 403	12.6	38.2	38	6	AR286920 Sequence	C 476	12.4	37.6	38	6	AR398557 Sequence
C 404	12.6	38.2	38	6	AR287036 Sequence	C 477	12.4	37.6	38	6	AR398573 Sequence
C 405	12.6	38.2	38	6	AR398910 Sequence	C 478	12.4	37.6	38	6	AR398598 Sequence
C 406	12.6	38.2	38	6	AR399026 Sequence	C 479	12.4	37.6	38	6	AR398625 Sequence
C 407	12.6	38.2	38	6	AR399092 Sequence	C 480	12.4	37.6	38	6	AR398704 Sequence
C 408	12.6	38.2	38	6	AX840442 Sequence	C 481	12.4	37.6	38	6	AR398717 Sequence
C 409	12.6	38.2	39	6	AX554035 Sequence	C 482	12.4	37.6	38	6	AR398855 Sequence
C 410	12.6	38.2	39	6	AX554036 Sequence	C 483	12.4	37.6	38	6	AR398874 Sequence
C 411	12.6	38.2	39	6	AX664363 Sequence	C 484	12.4	37.6	38	6	AR399022 Sequence
C 412	12.6	38.2	39	6	AX770241 Sequence	C 485	12.4	37.6	38	6	AX223064 Sequence
C 413	12.6	38.2	42	6	BD233647 Sequence	C 486	12.4	37.6	38	6	AX228701 Sequence
C 414	12.6	38.2	42	6	E06010 Sequence	C 487	12.4	37.6	38	6	AX228777 Sequence
C 415	12.6	38.2	42	6	E06010 A part of s	C 488	12.4	37.6	38	6	AX425251 Sequence
C 416	12.6	38.2	45	6	AR476058 Sequence	C 489	12.4	37.6	38	6	AX425379 Sequence
C 417	12.6	38.2	45	6	AX405397 Sequence	C 490	12.4	37.6	38	6	AX425391 Sequence
C 418	12.6	38.2	47	6	CQ654175 Sequence	C 491	12.4	37.6	38	6	AX665091 Sequence
C 419	12.6	38.2	47	6	CQ771101 Sequence	C 492	12.4	37.6	38	6	AX665091 Sequence
C 420	12.6	38.2	47	6	CQ779466 Sequence	C 493	12.4	37.6	41	6	AX517922 Sequence
C 421	12.6	38.2	47	6	AR291823 Sequence	C 494	12.4	37.6	41	6	AX517922 Sequence
C 422	12.6	38.2	47	6	AX357428 Sequence	C 495	12.4	37.6	42	9	HUMIGHABT
C 423	12.6	38.2	47	6	AX551185 Sequence	C 496	12.4	37.6	42	9	S66950
C 424	12.6	38.2	47	6	AX551185 Sequence	C 497	12.4	37.6	44	6	AX287943 Sequence
C 425	12.6	38.2	47	6	AX551185 Sequence	C 498	12.4	37.6	44	6	AX287943 Sequence
C 426	12.6	38.2	49	6	AX770382 Sequence	C 499	12.4	37.6	46	6	BD182388
C 427	12.6	38.2	50	6	AX772607 Sequence	C 500	12.4	37.6	46	6	BD182388
C 428	12.6	38.2	50	6	A14174	C 501	12.4	37.6	46	6	E23316
C 429	12.6	38.2	50	6	A14176	C 502	12.4	37.6	46	6	E23085
C 430	12.6	38.2	50	6	A14178	C 503	12.4	37.6	46	6	AX665090 Sequence
C 431	12.6	38.2	50	6	A14198	C 504	12.4	37.6	46	6	AX665090 Sequence
C 432	12.4	37.6	16	6	AX159306 Sequence	C 505	12.4	37.6	46	6	BD011916
C 433	12.4	37.6	16	6	AR285634 Sequence	C 506	12.4	37.6	46	6	BD011916
C 434	12.4	37.6	16	6	AR397625 Sequence	C 507	12.4	37.6	46	6	BD011972
C 435	12.4	37.6	24	6	AX288693 Sequence	C 508	12.4	37.6	46	6	BD012033
C 436	12.4	37.6	24	6	AX446885 Sequence	C 509	12.4	37.6	46	6	BD012920
C 437	12.4	37.6	26	6	BD143452 Amine oxi	C 510	12.4	37.6	46	6	BD095490
C 438	12.4	37.6	27	6	AR490873 Sequence	C 511	12.4	37.6	46	6	BD095651
C 439	12.4	37.6	27	6	AR160071 Sequence	C 512	12.4	37.6	47	6	BD140976
C 440	12.4	37.6	27	6	BD195502 Sequence	C 513	12.4	37.6	47	6	AR284770
C 441	12.4	37.6	27	6	BD217917 Sequence	C 514	12.4	37.6	47	6	AR289195
C 442	12.4	37.6	27	6	AR266434 Sequence	C 515	12.4	37.6	48	6	AR290675
C 443	12.4	37.6	27	6	AR349292 Sequence	C 516	12.4	37.6	50	6	E01067
C 444	12.4	37.6	28	6	AR451728 Sequence	C 517	12.4	37.6	50	6	BD244385
C 445	12.4	37.6	28	6	AR090964 Sequence	C 518	12.4	37.6	50	6	CQ005668
C 446	12.4	37.6	28	6	AR197999 Sequence	C 519	12.4	37.6	50	6	CQ008418
C 447	12.4	37.6	28	6	AR260153 Sequence	C 520	12.4	37.6	50	6	AX199510
C 448	12.4	37.6	30	6	AS1854 Sequence 18	C 521	12.2	37.0	17	6	AX199608
C 449	12.4	37.6	30	6	AS1858 Sequence 22	C 522	12.2	37.0	17	6	CQ621349
C 450	12.4	37.6	30	6	AS1858 Sequence 22	C 523	12.2	37.0	17	6	AR432965
C 451	12.4	37.6	32	6	I18656 Sequence 8	C 524	12.2	37.0	17	6	AR462412
C 452	12.4	37.6	32	6	AR229939 Sequence	C 525	12.2	37.0	18	6	AX676128
C 453	12.4	37.6	32	6	AX099693 Sequence	C 526	12.2	37.0	19	6	AX469884
C 454	12.4	37.6	32	6	AX367135 Sequence	C 527	12.2	37.0	20	6	AX417917
C 455	12.4	37.6	33	6	AR068945 Sequence	C 528	12.2	37.0	20	6	AX417917
C 456	12.4	37.6	33	6	AR141801 Sequence	C 529	12.2	37.0	20	6	AX417917
C 457	12.4	37.6	33	6	AR143318 Sequence	C 530	12.2	37.0	20	6	AR275387
									20	6	AR275450

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532	12.2	37.0	24	6	A62564	A62564 Sequence 2	c 605	12.2	37.0	38	6	AR125846	AR125846 Sequence
533	12.2	37.0	24	6	A62573	A62573 Sequence 11	c 606	12.2	37.0	38	6	147258	147258 Sequence 18
c 534	12.2	37.0	25	6	AX446291	AX446291 Sequence	607	12.2	37.0	38	6	BD063148	BD063148 Human G-p
c 535	12.2	37.0	24	6	A67701	A67701 Sequence 31	608	12.2	37.0	39	6	AR027114	AR027114 Sequence
536	12.2	37.0	25	6	C0629861	C0629861 Sequence	c 609	12.2	37.0	39	9	HSZ78049	Z78049 H. sapiens T
537	12.2	37.0	25	6	C0629862	C0629862 Sequence	c 610	12.2	37.0	40	6	AR053630	AR053630 Sequence
538	12.2	37.0	25	6	AR361078	AR361078 Sequence	611	12.2	37.0	40	6	AR240057	AR240057 Sequence
539	12.2	37.0	25	6	AR470924	AR470924 Sequence	c 612	12.2	37.0	40	6	AR258565	AR258565 Sequence
540	12.2	37.0	25	6	AR470925	AR470925 Sequence	c 613	12.2	37.0	40	6	AR279859	AR279859 Sequence
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c 542	12.2	37.0	25	6	AX615727	AX615727 Sequence	c 615	12.2	37.0	42	6	AX201868	AX201868 Sequence
c 543	12.2	37.0	25	6	A649745	A649745 Sequence	616	12.2	37.0	42	11	CR378503	CR378503 Arabidops
544	12.2	37.0	25	6	AX782792	AX782792 Sequence	617	12.2	37.0	45	6	AX612160	AX612160 Sequence
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547	12.2	37.0	26	6	AR259644	AR259644 Sequence	620	12.2	37.0	47	6	AR284724	AR284724 Sequence
c 548	12.2	37.0	26	6	AX115295	AX115295 Sequence	621	12.2	37.0	47	6	AR288784	AR288784 Sequence
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c 550	12.2	37.0	27	6	AR124702	AR124702 Sequence	c 623	12.2	37.0	47	6	AX378320	AX378320 Sequence
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c 552	12.2	37.0	27	6	BD267965	BD267965 Inhibitor	c 625	12.2	37.0	48	6	EL14189	EL14189 PCR primer
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c 554	12.2	37.0	27	6	BD272019	BD272019 Inhibitor	c 627	12.2	37.0	49	6	AX404131	AX404131 Sequence
c 555	12.2	37.0	27	6	BD272038	BD272038 Inhibitor	c 628	12.2	37.0	50	6	CQ002897	CQ002897 Sequence
c 556	12.2	37.0	27	6	BD274576	BD274576 Inhibitor	c 629	12.2	37.0	50	6	CQ003417	CQ003417 Sequence
c 557	12.2	37.0	27	6	BD274595	BD274595 Inhibitor	c 630	12.2	37.0	50	6	CQ004558	CQ004558 Sequence
c 558	12.2	37.0	27	6	AR181811	AR181811 Sequence	631	12.2	37.0	50	6	CQ005922	CQ005922 Sequence
c 559	12.2	37.0	27	6	AR195277	AR195277 Sequence	632	12.2	37.0	50	6	AX159730	AX159730 Sequence
c 560	12.2	37.0	27	6	AR199993	AR199993 Sequence	c 633	12.2	37.0	50	6	AX952063	AX952063 Sequence
c 561	12.2	37.0	27	6	AR201346	AR201346 Sequence	c 634	12.2	37.0	50	6	AX952657	AX952657 Sequence
c 562	12.2	37.0	27	6	AR201365	AR201365 Sequence	c 635	12	36.4	52	6	AX170909	AX170909 Sequence
c 563	12.2	37.0	27	6	AR216089	AR216089 Sequence	c 636	12	36.4	12	6	BD001050	BD001050 Method an
c 564	12.2	37.0	27	6	AR224798	AR224798 Sequence	c 637	12	36.4	12	6	BD001479	BD001479 Method an
c 565	12.2	37.0	27	6	AR317257	AR317257 Sequence	c 638	12	36.4	20	6	AR131567	AR131567 Sequence
c 566	12.2	37.0	27	6	AR337532	AR337532 Sequence	c 639	12	36.4	20	6	AR199501	AR199501 Sequence
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c 570	12.2	37.0	27	6	AR409169	AR409169 Sequence	c 643	12	36.4	20	6	AX197233	AX197233 Sequence
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c 573	12.2	37.0	28	6	AR430007	AR430007 Sequence	c 646	12	36.4	20	6	BD084985	BD084985 Target-de
c 574	12.2	37.0	28	6	AR090290	AR090290 Sequence	c 647	12	36.4	21	6	146602	146602 Sequence 58
575	12.2	37.0	29	6	BD174673	BD174673 Transcrip	c 648	12	36.4	21	6	AX298146	AX298146 Sequence
c 576	12.2	37.0	29	6	BD198147	BD198147 Method an	649	12	36.4	23	6	BD133326	BD133326 Method fo
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c 579	12.2	37.0	29	6	AR259479	AR259479 Sequence	652	12	36.4	24	6	AR179900	AR179900 Sequence
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c 582	12.2	37.0	30	6	147120	147120 Sequence 50	c 655	12	36.4	24	6	AR242171	AR242171 Sequence
583	12.2	37.0	30	6	AX417928	AX417928 Sequence	656	12	36.4	24	6	AR371877	AR371877 Sequence
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587	12.2	37.0	31	6	AR087686	AR087686 Sequence	c 660	12	36.4	24	6	BD091997	BD091997 Potentiat
588	12.2	37.0	31	6	AR094046	AR094046 Sequence	c 661	12	36.4	25	6	C0626250	C0626250 Sequence
c 589	12.2	37.0	32	6	AR308126	AR308126 Sequence	c 662	12	36.4	25	6	AR240245	AR240245 Sequence
c 590	12.2	37.0	33	6	E36464	E36464 DNA polymer	c 663	12	36.4	25	6	AR467313	AR467313 Sequence
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593	12.2	37.0	35	6	AR222012	AR222012 Sequence	666	12	36.4	25	6	AX782521	AX782521 Sequence
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598	12.2	37.0	37	6	169358	169358 Sequence 5	671	12	36.4	27	6	A09176	A09176 reverse com
599	12.2	37.0	37	6	AR205505	AR205505 Sequence	c 672	12	36.4	27	6	A09177	A09177 Nucleotide
600	12.2	37.0	37	6	AX076520	AX076520 Sequence	673	12	36.4	27	6	A09513	A09513 Mutagenic p
601	12.2	37.0	37	6	AX076522	AX076522 Sequence	c 674	12	36.4	27	6	A09514	A09514 Mutated DNA
602	12.2	37.0	37	6	AX513009	AX513009 Sequence	c 675	12	36.4	27	6	AX380913	AX380913 Sequence
603	12.2	37.0	38	6	AR034798	AR034798 Sequence	c 676	12	36.4	27	10	MMW1121	X94880 M.musculus

677	12	36.4	28	6	BD225867	BD225867 Promoter	c 750	12	36.4	39	6	CQ821263	CQ821263 Sequence
c 678	12	36.4	28	6	E48749	E48749 Process for	751	12	36.4	39	6	AR366594	AR366594 Sequence
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c 686	12	36.4	32	6	AX184038	AX184038 Sequence	c 759	12	36.4	40	6	AX538450	AX538450 Sequence
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c 689	12	36.4	33	6	AR118375	AR118375 Sequence	c 762	12	36.4	41	6	AX515859	AX515859 Sequence
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692	12	36.4	33	6	E15908	E15908 Primer. 7/1	c 765	12	36.4	41	6	BD170575	BD170575 Novel pro
c 693	12	36.4	33	6	AR302217	AR302217 Sequence	c 766	12	36.4	41	6	BD170576	BD170576 Novel pro
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c 695	12	36.4	33	6	AX813377	AX813377 Sequence	c 768	12	36.4	42	6	AR161528	AR161528 Sequence
696	12	36.4	33	6	AX813378	AX813378 Sequence	c 769	12	36.4	42	6	BD187743	BD187743 A method
c 697	12	36.4	34	6	AR285835	AR285835 Sequence	c 770	12	36.4	42	6	BD187744	BD187744 A method
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c 701	12	36.4	35	6	E09146	E09146 Synthetic D	774	12	36.4	43	6	A65369	A65369 Sequence
c 702	12	36.4	35	6	AR397826	AR397826 Sequence	775	12	36.4	45	6	AR217113	AR217113 Sequence
c 703	12	36.4	35	6	AX087984	AX087984 Sequence	776	12	36.4	47	6	AR284660	AR284660 Sequence
c 704	12	36.4	36	6	AR285836	AR285836 Sequence	777	12	36.4	48	6	A11297	A11297 Nucleotide
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707	12	36.4	37	6	AR009560	AR009560 Sequence	780	12	36.4	48	6	AX305158	AX305158 Sequence
c 708	12	36.4	37	6	CQ771098	CQ771098 Sequence	781	12	36.4	48	9	HSA224222	HSA224222 Homo sapi
709	12	36.4	37	6	CQ771099	CQ771099 Sequence	782	12	36.4	49	6	A11301	A11301 Nucleotide
c 710	12	36.4	37	6	CQ779453	CQ779453 Sequence	c 783	12	36.4	50	6	A11298	A11298 Nucleotide
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c 712	12	36.4	37	6	AR397827	AR397827 Sequence	785	12	36.4	50	6	CQ008164	CQ008164 Sequence
c 713	12	36.4	37	6	AX357425	AX357425 Sequence	c 786	12	36.4	50	6	AR443593	AR443593 Sequence
c 714	12	36.4	37	6	AX551182	AX551182 Sequence	787	12	36.4	50	9	HSHLX1A3	HSHLX1A3
c 715	12	36.4	37	6	AX551882	AX551882 Sequence	c 788	12	36.4	50	9	S85460	S85460 immunoglobu
c 716	12	36.4	37	6	AX581958	AX581958 Sequence	c 789	11.8	35.8	15	6	AR037377	AR037377 Sequence
c 717	12	36.4	37	6	AX770379	AX770379 Sequence	c 790	11.8	35.8	15	6	AR043858	AR043858 Sequence
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c 721	12	36.4	38	6	AR286616	AR286616 Sequence	c 794	11.8	35.8	15	6	I81415	I81415 Sequence
c 722	12	36.4	38	6	AR286961	AR286961 Sequence	c 795	11.8	35.8	15	6	I93806	I93806 Sequence
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c 728	12	36.4	38	6	AR366595	AR366595 Sequence	c 801	11.8	35.8	17	6	AR062073	AR062073 Sequence
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c 735	12	36.4	38	6	AX223165	AX223165 Sequence	c 808	11.8	35.8	17	6	AX265803	AX265803 Sequence
c 736	12	36.4	38	6	AX228760	AX228760 Sequence	c 809	11.8	35.8	17	6	AX265804	AX265804 Sequence
c 737	12	36.4	38	6	AX273532	AX273532 Sequence	810	11.8	35.8	17	6	AX601120	AX601120 Sequence
c 738	12	36.4	38	6	AX273912	AX273912 Sequence	811	11.8	35.8	18	6	A70960	A70960 Sequence
c 739	12	36.4	38	6	AX273918	AX273918 Sequence	c 812	11.8	35.8	19	6	CQ768632	CQ768632 Sequence
c 740	12	36.4	38	6	AX273918	AX273918 Sequence	c 813	11.8	35.8	19	6	AX250627	AX250627 Sequence
c 741	12	36.4	38	6	AX425177	AX425177 Sequence	814	11.8	35.8	19	11	HUMO453RA	D50243 A PCR prime
c 742	12	36.4	38	6	AX425312	AX425312 Sequence	815	11.8	35.8	20	6	A32034	A32034 primer DNA
c 743	12	36.4	38	6	AX425318	AX425318 Sequence	c 816	11.8	35.8	20	6	AR016183	AR016183 Sequence
c 744	12	36.4	38	6	AX425355	AX425355 Sequence	c 817	11.8	35.8	20	6	AR019181	AR019181 Sequence
c 745	12	36.4	38	6	AX425362	AX425362 Sequence	c 818	11.8	35.8	20	6	AR037376	AR037376 Sequence
c 746	12	36.4	38	6	AX425471	AX425471 Sequence	c 819	11.8	35.8	20	6	AR043857	AR043857 Sequence
c 747	12	36.4	39	6	AR156776	AR156776 Sequence	c 820	11.8	35.8	20	6	AR060259	AR060259 Sequence
c 748	12	36.4	39	6	CQ821260	CQ821260 Sequence	c 821	11.8	35.8	20	6	BD195412	BD195412 Male info
c 749	12	36.4	39	6	CQ821261	CQ821261 Sequence	822	11.8	35.8	20	6	E08714	E08714 Probe for d

C 823	11.8	35.8	20	6	I47008	I47008 Sequence 21	C 896	11.8	35.8	37	6	AX048271	AX048271 Sequence
C 824	11.8	35.8	20	6	I47656	I47656 Sequence 21	C 897	11.8	35.8	37	6	AX921633	AX921633 Sequence
C 825	11.8	35.8	20	6	I63157	I63157 Sequence 21	C 898	11.8	35.8	37	6	BD057643	BD057643 Fusion pr
C 826	11.8	35.8	20	6	I81414	I81414 Sequence 21	C 899	11.8	35.8	38	6	BD081473	BD081473 Soluble s
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C 876	11.8	35.8	31	6	AX249214	AX249214 Sequence	C 949	11.8	35.8	50	10	MMU41917	U41917 Mus musculu
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998 11.6 35.2 27 6 E41699 Process for
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ALIGNMENTS

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RESULT 1
AX802289
LOCUS AX802289 31 bp DNA linear PAT 24-NOV-2003
DEFINITION Sequence 1 from Patent WO03057910.
ACCESSION AX802289
VERSION AX802289.1 GI:38501180
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Pinal-Ober,J., Wenzig,P., Weindel,K., Bartl,K., Schoenbrunner,R.,
Malhotra,K., O'Donnell,P. and Kyger,E.
TITLE Use of silica material in an amplification reaction
JOURNAL Patent: WO 03057910-A 1 17-JUL-2003;
Roche Diagnostics GmbH (DE)
FEATURES
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Location/Qualifiers
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RESULT 2
AS2660/c
LOCUS AS2660 36 bp DNA linear PAT 12-DEC-1997

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DEFINITION Sequence 5 from Patent WO9624662.
ACCESSION AS2660
VERSION AS2660.1 GI:2851824
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Ravagnan,G., Battaglia,M., Carloni,G., Ponsetto,A. and Iacovacci,S.
TITLE PROCESS TO 'IN VITRO' PROPAGATE THE HEPATITIS C VIRUS (HCV) IN NON
LYMPHOBLASTOID ANIMAL CELL CULTURES AND PRODUCTS THEREOF
JOURNAL Patent: WO 9624662-A 5 15-AUG-1996;
CONSIGLIO NAZIONALE RICERCA (IT)
COMMENT Other publication AU 1822195 960827.
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Db 32 CGGTGTACTACCGTTCGCGAGACCACCTATG 1
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AS26291/c
LOCUS AS26291 29 bp DNA linear PAT 06-MAY-1999
DEFINITION Sequence 12 from Patent WO9746716.
ACCESSION AS26291
VERSION AS26291.1 GI:4759412
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Bosio,P., Strumia,C. and Clemenza,F.
TITLE METHOD TO DETECT HCV SPECIFIC NUCLEIC ACIDS
JOURNAL Patent: WO 9746716-A 12 11-DEC-1997;
WABCO B V (NL)
COMMENT Other publication IT RM960404 19971209.
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Db 29 TGTACTACCGTTCGCGAGACCACCTATG 1
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DEFINITION A method for determination of a nucleic acid using a control.
ACCESSION BD181364
VERSION BD181364.1 GI:30792282
KEYWORDS JP 2002335981-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 34)

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Jaeger, S.
 A method for determination of a nucleic acid using a control
 Patent: JP 2002335981-A 3 26-NOV-2002;
 F. HOFFMANN LA ROCHE AG
 OS Artificial Sequence
 PN JP 2002335981-A/3
 PD 26-NOV-2002
 PF 04-MAR-2002 JP 2002057515
 PR 02-MAR-2001 EP 01105172.9
 PI STEPHAN JAEGER
 PC C12N15/09, C12Q1/68, G01N33/50, G01N33/53, G01N33/566, G01N33/58,
 C12N15/00
 CC Description of Artificial Sequence: ST650 HCV specific probe
 sequence
 CC n represents abasic linker ((2-amino-cyclohexyl-)propan-1,3-
 diol)
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 FT N_region (15).
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 DB 1 CGGTGTACTACCGNTTCCGCGAGACCACTATGGC 34
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 AX523944
 LOCUS 34 bp DNA linear PAT 21-NOV-2002
 DEFINITION Sequence 3 from Patent EP1236804.
 ACCESSION AX523944
 VERSION AX523944.1 GI:25168875
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Jaeger, S.
 TITLE A method for determination of a nucleic acid using a control
 JOURNAL Patent: EP 1236804-A 3 04-SEP-2002;
 Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
 FEATURES source
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 DB 1 CGGTGTACTACCGNTTCCGCGAGACCACTATGGC 34
 RESULT 6
 AX524842
 LOCUS 34 bp DNA linear PAT 21-NOV-2002
 DEFINITION Sequence 3 from Patent EP1236805.

AX524842
 VERSION AX524842.1 GI:25169936
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Jaeger, S.
 TITLE A method for the determination of a nucleic acid using a control
 JOURNAL Patent: EP 1236805-A 3 04-SEP-2002;
 Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
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 Best Local Similarity 97.1%; Pred. No. 6.8e+02;
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 DB 1 CGGTGTACTACCGNTTCCGCGAGACCACTATGGC 34
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 LOCUS 41 bp DNA linear PAT 17-JAN-2003
 DEFINITION Method of detecting pathogenic microorganism.
 ACCESSION BD171248
 VERSION BD171248.1 GI:27877060
 KEYWORDS WO 02052043-A/40.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1 (bases 1 to 41)
 AUTHORS Shimada, M., Hino, F. and Kato, I.
 TITLE Method of detecting pathogenic microorganism
 JOURNAL Patent: WO 02052043-A 40 04-JUL-2002;
 TAKARA SHUZO CO LTD, MASAMITSU SHIMADA, FUMITSUGU HINO, IKUNOSHIN KATO
 COMMENT OS Artificial Sequence
 PN WO 02052043-A/40
 PD 04-JUL-2002
 PF 26-DEC-2001 WO 2001JP011422
 PR 26-DEC-2000 JP 00P 396222, 26-DEC-2000 JP 00P 396321 PR
 29-JUN-2001 JP 01P 199552, 13-SEP-2001 JP 01P 278920 PI
 MASAMITSU SHIMADA, FUMITSUGU HINO, IKUNOSHIN KATO PC
 C12Q1/68, C12N15/09
 CC Primer area to amplify a portion of HCV.
 FH Key Location/Qualifiers
 FT source 1..41
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 DB 5 CGGTGTACTACCGTTCCGCGAGACCACTATGGC 38

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DEFINITION     Method for assaying HCV gene by real time detection PCR method and
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ACCESSION      E25774.1 GI:13024962
VERSION        JP 1999103899-A/5.
KEYWORDS       unclassified
SOURCE         unclassified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 41)
AUTHORS       Michinori,O., Ryuji,K. and Aki,A.
TITLE         Method for assaying HCV gene by real time detection PCR method and
                primer and probe to be used therein
JOURNAL       Patent: JP 1999103899-A 5 20-APR-1999;
COMMENT       TOKYO MET GOV RINSHO IGAKU SOGO KENKYUSHO, SRL INC
              OS Unidentified
              PN JP 1999103899-A/5
              PD 20-APR-1999
              PF 30-SEP-1997 JP 1997283042
              PR
              PI MICHINORI OBARA, RYUJI KAWAGUCHI, AKI ABE
              PC C12Q1/70.C12N15/09.G01N21/78.G01N33/58.C12N15/00 CC
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Db 33 CGGTGTACTCACC-GTTCGCGAGACCACCTATGG 1
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DEFINITION     Sequence 4 from patent US 6638714.
ACCESSION      AR411540
VERSION        AR411540.1 GI:40163884
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 26)
AUTHORS       Linnen,J.M. and Gorman,K.M.
TITLE         Oligonucleotide primers for efficient detection of hepatitis C
                virus (HCV) and methods of use thereof
JOURNAL       Patent: US 6638714-A 4 28-OCT-2003;
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                Location/Qualifiers
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Best Local Similarity 95.5%; Pred. No. 3e+03;
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Db 1 CCGTTCGCGAGACCACCTATGGC 22
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RESULT 10
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LOCUS          BD000266          26 bp    DNA          linear          PAT 31-JAN-2002
DEFINITION     Oligonucleotide primers for efficient detection of hepatitis C
                virus (HCV) and methods of use thereof.
ACCESSION      BD000266.1 GI:18623345
VERSION        JP 2000279200-A/4.
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       synthetic sequences.
REFERENCE      1 (bases 1 to 26)
AUTHORS       Lynnen,J.M. and Gorman,K.M.
TITLE         Oligonucleotide primers for efficient detection of hepatitis C
                virus (HCV) and methods of use thereof
JOURNAL       Patent: JP 2000279200-A 4 10-OCT-2000;
COMMENT       ORTHO CLINICAL DIAGNOSTICS INC
              OS Artificial Sequence
              PN JP 2000279200-A/4
              PD 10-OCT-2000
              PF 03-FEB-2000 JP 2000032656
              PR 03-FEB-1999 US 60/118497
              PI JEFFREY M LYNEN, KEVIN M GORMAN
              PC C12Q1/68.C12N15/09/(C12N15/09.C12R1:92).C12N15/00.(C12N15/00.
              CC C12R1:92).
              FH Key Location/Qualifiers
              FT source 1..26 /organism='Artificial Sequence'.
FEATURES       source
                Location/Qualifiers
                1..26 /organism='synthetic construct'
                /mol_type='genomic DNA'
                /db_xref='taxon:32630'
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Query Match 61.8%; Score 20.4; DB 6; Length 26;
Best Local Similarity 95.5%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCGTTCGCGAGACCACCTATGGC 33
    |
Db 1 CCGTTCGCGAGACCACCTATGGC 22
    |

RESULT 11
AR094968
LOCUS          AR094968          28 bp    DNA          linear          PAT 08-SEP-2000
DEFINITION     Sequence 6 from patent US 6001990.
ACCESSION      AR094968
VERSION        AR094968.1 GI:10022389
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 28)
AUTHORS       Wands,J.R., Wakita,T. and Moradpour,D.
TITLE         Antisense inhibition of hepatitis C virus
                Patent: US 6001990-A 6 14-DEC-1999;
JOURNAL       Location/Qualifiers
FEATURES       source
                Location/Qualifiers
                1..28 /organism='unknown'
                /mol_type='unassigned DNA'
ORIGIN
Query Match 61.8%; Score 20.4; DB 6; Length 28;
Best Local Similarity 95.5%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCGTTCGCGAGACCACCTATGGC 33
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Db 4 CCGTTCGCGAGACCACCTATGGC 25
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RESULT 12
BD183050/c
LOCUS
DEFINITION Nucleic acids for grouping hepatitis C virus and method for group
ing hepatitis C virus using the same.
ACCESSION BD183050
VERSION BD183050.1 GI:31875250
KEYWORDS JP 2002345467-A/22.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 28)
AUTHORS Mukaide,M., Tsunoda,K. and Hikiji,K.
TITLE Nucleic acids for grouping hepatitis C virus and method for group
ing hepatitis C virus using the same
JOURNAL Patent: JP 2002345467-A 22 03-DEC-2002;
SRL INC
COMMENT OS Artificial Sequence
PN JP 2002345467-A/22
PD 03-DEC-2002
PF 17-APR-2001 JP 2001118810
PI MASAKAZU MUKAIDE,KOICHI TSUNODA,KAZUMASA HIKIJI PC
C12N15/09,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC Nucleic Acid
Used as signal-amplifying probe which hybridizes CC
with a
CC region in HCV 5'-UTR region
FH Key Location/Qualifiers
FT source 1..28
FT /organism='Artificial Sequence'.
FEATURES
source
1..28
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 61.8%; Score 20.4; DB 6; Length 28;
Best Local Similarity 95.5%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTATGGC 33
Db 26 CCGTTCGCGACCACTATGGC 5

RESULT 13
A70977/c
LOCUS
DEFINITION Hepatitis C virus
ACCESSION A70977
VERSION A70977.1 GI:4774962
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 36)
AUTHORS Uhlen,M. and Lundeberg,J.
TITLE THE USE OF MODULAR OLIGONUCLEOTIDES AS PROBES OR PRIMERS IN NUCLEIC
ACID BASED ASSAY
JOURNAL Patent: WO 9813522-A 31 02-APR-1998;
DZIEGLEWSKA HANNA EVA (GB)
FEATURES
source
1..36
/organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/db_xref="taxon:11103"
ORIGIN
Query Match 61.8%; Score 20.4; DB 6; Length 36;
Best Local Similarity 95.5%; Pred. No. 2.9e+03;

Qy 12 CCGTTCGCGACCACTATGGC 33
Db 27 CCGTTCGCGACCACTATGGC 6

RESULT 14
BD244766/c
LOCUS
DEFINITION Isolation method of primer extension products by modular
oligonucleotide.
ACCESSION BD244766
VERSION BD244766.1 GI:33054536
KEYWORDS JP 2002525076-A/45.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 36)
AUTHORS Lundeberg,J. and Uhlen,M.
TITLE Isolation method of primer extension products by modular
oligonucleotide.
JOURNAL Patent: JP 2002525076-A 45 13-AUG-2002;
DYNAL AS
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002525076-A/45
PD 13-AUG-2002
PF 15-SEP-1999 JP 2000570369
PR 15-SEP-1998 US 09/153242,16-SEP-1998 GB 9820185.8 PI
JOAKIM LUNDEBERG, MATHIAS UHLEN
PC C12N15/09,C12Q1/68,C12N15/00
CC Isolation method of primer extension products by modular CC
oligonucleotide
FH Key Location/Qualifiers
FT source 1..36
FT /organism='Hepatitis virus (hepatitis C FT
virus)',
FT Location/Qualifiers
1..36
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 61.8%; Score 20.4; DB 6; Length 36;
Best Local Similarity 95.5%; Pred. No. 2.9e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTATGGC 33
Db 27 CCGTTCGCGACCACTATGGC 6

RESULT 15
AR255272/c
LOCUS
DEFINITION Sequence 39 from patent US 6482592.
ACCESSION AR255272
VERSION AR255272.1 GI:27304321
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Lundeberg,J. and Uhlen,M.
TITLE Methods and kits for isolating primer extension products using
modular oligonucleotides
JOURNAL Patent: US 6482592-A 39 19-NOV-2002;
FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 61.8%; Score 20.4; DB 6; Length 36;
Best Local Similarity 95.5%; Pred. No. 2.9e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTATGGC 33
Db 27 CCGTTCGCGACCACTATGGC 6

RESULT 15
AR255272/c
LOCUS
DEFINITION Sequence 39 from patent US 6482592.
ACCESSION AR255272
VERSION AR255272.1 GI:27304321
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Lundeberg,J. and Uhlen,M.
TITLE Methods and kits for isolating primer extension products using
modular oligonucleotides
JOURNAL Patent: US 6482592-A 39 19-NOV-2002;
FEATURES
source
1..36
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 61.8%; Score 20.4; DB 6; Length 36;
Best Local Similarity 95.5%; Pred. No. 2.9e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTATGGC 33
Db 27 CCGTTCGCGACCACTATGGC 6

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ORIGIN /mol_type="unassigned DNA"

Query Match 60.6%; Score 20; DB 6; Length 38;
Best Local Similarity 96.9%; Pred. No. 4.1e+03;
Matches 31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CGGTGTACTACC-GTTCGCGAGACCCTATGG 31
|||||
Db 32 CGGTGTACTACCGGTTCCGCGAGACCCTATG 1
|||||

RESULT 20
LOCUS AR080402 30 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 3 from patent US 5968775.
ACCESSION AR080402
VERSION AR080402.1 GI:10007137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Houghton,M., Steimer,K.S. and Weiner,A.J.
TITLE Hepatitis C virus infected cell systems
JOURNAL Patent: US 5968775-A 3 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 58.8%; Score 19.4; DB 6; Length 30;
Best Local Similarity 95.2%; Pred. No. 7.3e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGAGACCCTATGG 32
|
Db 21 CGGTTCGCGAGACCCTATGG 1
|

RESULT 21
LOCUS AR118787 30 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 217 from patent US 6150087.
ACCESSION AR118787
VERSION AR118787.1 GI:14100697
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Chien,D.Y.
TITLE NANEV diagnostics and vaccines
JOURNAL Patent: US 6150087-A 217 21-NOV-2000;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 58.8%; Score 19.4; DB 6; Length 30;
Best Local Similarity 95.2%; Pred. No. 7.3e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGAGACCCTATGG 32
|
Db 21 CGGTTCGCGAGACCCTATGG 1
|

RESULT 22
LOCUS E51970 30 bp DNA linear PAT 18-JUN-2001

DEFINITION Diagnostic for NANEV.
ACCESSION E51970
VERSION E51970.1 GI:13019297
KEYWORDS JP 2000039434-A/13.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Michael,H., Quilim,C. and George,K.
TITLE Diagnostic for NANEV
JOURNAL Patent: JP 2000039434-A 13 08-FEB-2000;
COMMENT CHIRON CORP
OS Unidentified
PN JP 2000039434-A/13
PD 08-FEB-2000
PR 03-JUN-1999 JP 1999157192
PR 17-MAR-1989 US 325.338, 20-APR-1989 US 341.334, PR
18-MAY-1989 US 355.002
PI MICHAEL HOUGHTON, QUI-LIM CHOO, GEORGE KUO
PC G01N33/569, C07K14/18, G01N33/576//C12N15/09, C12P21/02, PC
(C12P21/02, C12R1:19),
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH key Location/Qualifiers
FT source 1..30
/organism='Unidentified'.
FEATURES Location/Qualifiers
source 1..30
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 58.8%; Score 19.4; DB 6; Length 30;
Best Local Similarity 95.2%; Pred. No. 7.3e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGAGACCCTATGG 32
|
Db 21 CGGTTCGCGAGACCCTATGG 1
|

RESULT 23
LOCUS I70136 30 bp DNA linear PAT 02-APR-1998
DEFINITION Sequence 3 from patent US 5679342.
ACCESSION I70136
VERSION I70136.1 GI:3006271
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Houghton,M., Steimer,K.S. and Weiner,A.J.
TITLE Hepatitis C virus infected cell systems
JOURNAL Patent: US 5679342-A 3 21-OCT-1997;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 58.8%; Score 19.4; DB 6; Length 30;
Best Local Similarity 95.2%; Pred. No. 7.3e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGAGACCCTATGG 32
|
Db 21 CGGTTCGCGAGACCCTATGG 1
|

RESULT 24

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BD004842/c
LOCUS          BD004842          30 bp    DNA          linear          PAT 31-JAN-2002
DEFINITION    Method for manufacturing amplicons, detecting method thereby.
ACCESSION     BD004842
VERSION       BD004842.1 GI:18632803
KEYWORDS      JP 2001046080-A/5.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 30)
AUTHORS       Matsuzaki,S.
TITLE         Method for manufacturing amplicons, detecting method thereby
JOURNAL       MIZUHO-MEDY CO LTD
COMMENT       OS Artificial Sequence
PN JP 2001046080-A/5
PD 20-FEB-2001
PF 15-MAR-2000 JP 2000071790
PR SEIICHIRO MATSUZAKI
PC C12N15/09,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
FH Key Location/Qualifiers
FT source 1..30
           /organism='Artificial Sequence'.
FEATURES
source      Location/Qualifiers
1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match          58.8%; Score 19.4; DB 6; Length 30;
Best Local Similarity 95.2%; Pred. No. 7.3e+03;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 12 CGTTCCGCAGACCACTATGG 32
Db 21 CGTTCCGCAGACCACTATGG 1
RESULT 25
E07367/c
LOCUS          E07367          22 bp    DNA          linear          PAT 29-SEP-1997
DEFINITION    PCR primer for gaining hepatitis C virus gene 5'noncoding region.
ACCESSION     E07367
VERSION       E07367.1 GI:2175506
KEYWORDS      JP 1994121700-A/5.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 22)
AUTHORS       Yagasaki,M. and Nunomura,K.
TITLE         METHOD FOR DETECTING HEPATITIS C VIRUS GENE
JOURNAL       Patent: JP 1994121700-A 5 06-MAY-1994;
              CHUGAI PHARMACEUT CO LTD
COMMENT       OS None
              OC Artificial sequences.
              PN JP 1994121700-A/5
              PD 06-MAY-1994
              PF 13-OCT-1992 JP 1992274273
              PI YAGASAKI MITSUO, NUNOMURA KIYOTADA
              PC C12Q1/68,C12Q1/68,C12N15/10,C12N15/51,C12Q1/70; CC
              CC topology: Linear;
              CC hypothetical: No;
              CC anti-sense: No;
              FH Key Location/Qualifiers
              FH source 1..22
              FT /organism='Artificial sequences'.
FEATURES
source      Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match          57.6%; Score 19; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TTCCGCAGACCACTATGGC 33
Db 22 TTCCGCAGACCACTATGGC 4
RESULT 27
AX250662/c
LOCUS          AX250662          24 bp    DNA          linear          PAT 05-OCT-2001
DEFINITION    Sequence 58 from Patent WO0168921.
ACCESSION     AX250662
VERSION       AX250662.1 GI:15984406
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1
AUTHORS       Koshinsky,H., Zwick,M.S. and Mccue,K.F.
TITLE         Compositions and methods for simultaneous detection of multiple
              biological entities
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match          57.6%; Score 19; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TTCCGCAGACCACTATGGC 33
Db 22 TTCCGCAGACCACTATGGC 4
RESULT 26
E07369/c
LOCUS          E07369          22 bp    DNA          linear          PAT 29-SEP-1997
DEFINITION    PCR primer for gaining hepatitis C virus gene 5'noncoding region.
ACCESSION     E07369
VERSION       E07369.1 GI:2175508
KEYWORDS      JP 1994121700-A/7.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 22)
AUTHORS       Yagasaki,M. and Nunomura,K.
TITLE         METHOD FOR DETECTING HEPATITIS C VIRUS GENE
JOURNAL       Patent: JP 1994121700-A 7 06-MAY-1994;
              CHUGAI PHARMACEUT CO LTD
COMMENT       OS None
              OC Artificial sequences.
              PN JP 1994121700-A/7
              PD 06-MAY-1994
              PF 13-OCT-1992 JP 1992274273
              PI YAGASAKI MITSUO, NUNOMURA KIYOTADA
              PC C12Q1/68,C12Q1/68,C12N15/10,C12N15/51,C12Q1/70; CC
              CC topology: Linear;
              CC hypothetical: No;
              CC anti-sense: No;
              FH Key Location/Qualifiers
              FH source 1..22
              FT /organism='Artificial sequences'.
FEATURES
source      Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match          57.6%; Score 19; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TTCCGCAGACCACTATGGC 33
Db 22 TTCCGCAGACCACTATGGC 4
RESULT 27
AX250662/c
LOCUS          AX250662          24 bp    DNA          linear          PAT 05-OCT-2001
DEFINITION    Sequence 58 from Patent WO0168921.
ACCESSION     AX250662
VERSION       AX250662.1 GI:15984406
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1
AUTHORS       Koshinsky,H., Zwick,M.S. and Mccue,K.F.
TITLE         Compositions and methods for simultaneous detection of multiple
              biological entities
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JOURNAL Patent: WO 0168921-A 58 20-SEP-2001;
FEATURES Investigator (US)
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer"

ORIGIN
Query Match 57.6%; Score 19; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCAGACCACTATGGC 33
Db 24 TTCCGCAGACCACTATGGC 6

RESULT 28
AR400912/c
LOCUS AR400912 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6623919.
ACCESSION AR400912
VERSION AR400912.1 GI:40148204
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gorman,K.M., Patterson,D.R., Linnen,J.M. and Song,K.
TITLE Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and methods of use thereof
JOURNAL Patent: US 6623919-A 1 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 57.6%; Score 19; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCAGACCACTATGGC 33
Db 25 TTCCGCAGACCACTATGGC 7

RESULT 29
AR400921/c
LOCUS AR400921 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 10 from patent US 6623919.
ACCESSION AR400921
VERSION AR400921.1 GI:40148213
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gorman,K.M., Patterson,D.R., Linnen,J.M. and Song,K.
TITLE Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and methods of use thereof
JOURNAL Patent: US 6623919-A 10 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 57.6%; Score 19; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCAGACCACTATGGC 33
Db 25 TTCCGCAGACCACTATGGC 7

JOURNAL Patent: WO 0168921-A 58 20-SEP-2001;
FEATURES Investigator (US)
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer"

ORIGIN
Query Match 57.6%; Score 19; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCAGACCACTATGGC 33
Db 24 TTCCGCAGACCACTATGGC 6

RESULT 30
AR411538/c
LOCUS AR411538 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6638714.
ACCESSION AR411538
VERSION AR411538.1 GI:40163882
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Linnen,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof
JOURNAL Patent: US 6638714-A 2 28-OCT-2003;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 57.6%; Score 19; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCAGACCACTATGGC 33
Db 25 TTCCGCAGACCACTATGGC 7

RESULT 31
AX571897/c
LOCUS AX571897 25 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 1 from Patent WO02072887.
ACCESSION AX571897
VERSION AX571897.1 GI:26004014
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Tercero,J.C., Garcia,L., Guisan,J.M., Fernandez,R. and Fuentes,M.
TITLE Immobilisation of ligands using saccharides
JOURNAL Patent: WO 02072887-A 1 19-SEP-2002;
Pharma Gen S.A. (ES)
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="A probe complementary to a Hepatitis C viral RNA sequence"

ORIGIN
Query Match 57.6%; Score 19; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCAGACCACTATGGC 33
Db 25 TTCCGCAGACCACTATGGC 7

RESULT 32
BD000246/c
Query Match 57.6%; Score 19; DB 6; Length 25;
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LOCUS BD000246 25 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and methods of use thereof.
ACCESSION BD000246
VERSION BD000246.1 GI:18623325
KEYWORDS JP 2000279198-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gorman,K.M., Paterson,D.R., Lynen,J.M. and Son,K.
TITLE Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and methods of use thereof
JOURNAL Patent: JP 2000279198-A 1 10-OCT-2000;
ORTHO CLINICAL DIAGNOSTICS INC
COMMENT PN JP 2000279198-A/1
PD 10-OCT-2000
PF 02-FEB-2000 JP 2000030237
PI 03-FEB-1999 US 60/118498
PI KEVIN M GORMAN, DAVID R PATERSON, JEFFREY M LYNEN, KEMIN SON PC
C12Q1/68, C12N15/09// (C12N15/09, C12R1:92), C12N15/00, (C12N15/00, PC
C12R1:92)
CC
FH Key Location/Qualifiers
FT source 1..25
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/mol_type="genomic DNA"
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FEATURES
source Location/Qualifiers
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Query Match 57.6%; Score 19; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TTCCGCAGACCACTATGGC 33
DB 25 TTCCGCAGACCACTATGGC 7
RESULT 33
LOCUS BD000255/c 25 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and methods of use thereof.
ACCESSION BD000255
VERSION BD000255.1 GI:18623334
KEYWORDS JP 2000279198-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gorman,K.M., Paterson,D.R., Lynen,J.M. and Son,K.
TITLE Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and methods of use thereof
JOURNAL Patent: JP 2000279198-A 10 10-OCT-2000;
ORTHO CLINICAL DIAGNOSTICS INC
COMMENT PN JP 2000279198-A/10
PD 10-OCT-2000
PF 02-FEB-2000 JP 2000030237
PI 03-FEB-1999 US 60/118498
PI KEVIN M GORMAN, DAVID R PATERSON, JEFFREY M LYNEN, KEMIN SON PC
C12Q1/68, C12N15/09// (C12N15/09, C12R1:92), C12N15/00, (C12N15/00, PC
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LOCUS BD000255/c 25 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and methods of use thereof.
ACCESSION BD000255
VERSION BD000255.1 GI:18623334
KEYWORDS JP 2000279198-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gorman,K.M., Paterson,D.R., Lynen,J.M. and Son,K.
TITLE Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and methods of use thereof
JOURNAL Patent: JP 2000279198-A 10 10-OCT-2000;
ORTHO CLINICAL DIAGNOSTICS INC
COMMENT PN JP 2000279198-A/10
PD 10-OCT-2000
PF 02-FEB-2000 JP 2000030237
PI 03-FEB-1999 US 60/118498
PI KEVIN M GORMAN, DAVID R PATERSON, JEFFREY M LYNEN, KEMIN SON PC
C12Q1/68, C12N15/09// (C12N15/09, C12R1:92), C12N15/00, (C12N15/00, PC
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LOCUS A49280 20 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 6 from Patent EP0714988.
ACCESSION A49280
VERSION A49280.1 GI:2302803
KEYWORDS .
SOURCE unidentified
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FH Key Location/Qualifiers
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DEFINITION Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.
ACCESSION BD000264
VERSION BD000264.1 GI:18623343
KEYWORDS JP 2000279200-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Lynen,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof
JOURNAL Patent: JP 2000279200-A 2 10-OCT-2000;
ORTHO CLINICAL DIAGNOSTICS INC
COMMENT OS Artificial Sequence
PN JP 2000279200-A/2
PD 10-OCT-2000
PF 03-FEB-2000 JP 2000032656
PI 03-FEB-1999 US 60/118497
PI JEFFREY M LYNEN, KEVIN M GORMAN
PC C12Q1/68, C12N15/09// (C12N15/09, C12R1:92), C12N15/00, (C12N15/00, PC
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Best Local Similarity 100.0%; Pred. No. 1.1e+04;
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DB 25 TTCCGCAGACCACTATGGC 7
RESULT 35
LOCUS A49280 20 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 6 from Patent EP0714988.
ACCESSION A49280
VERSION A49280.1 GI:2302803
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified

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unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Falkner,F.D., Haemmerle,T.D., Himmelspach,M.D., Kohl,J.D. and
Dorner,F.F.
TITLE Method for quantifying nucleic acids
JOURNAL Patent: EP 0714988-A 6 05-JUN-1996;
IMMUNO AG (AT)
COMMENT Other publication JP 8107798 960430
Other publication CA 2159044 960327
Other publication AT 401062 960625
Other publication AT 183194 951015.
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LOCUS AR301416 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 125 from patent US 6538126.
ACCESSION AR301416
VERSION AR301416.1 GI:31689200
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cho,J.M., Lee,Y.B., Park,Y.W., Lim,K.J., Choi,D.Y., So,H.S.,
Kim,C.H., Kim,S.T. and Yang,J.Y.
TITLE Hepatitis C diagnostics and vaccines
JOURNAL Patent: US 6538126-A 125 25-MAR-2003;
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RESULT 39
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DEFINITION Sequence 9 from Patent WO9918198.
ACCESSION AX004406
VERSION AX004406.1 GI:9927871
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Grandi,G. and Abrignani,S.
TITLE Hepatitis c receptor protein cd81
JOURNAL Patent: WO 9918198-A 9 15-APR-1999;
CHIRON S P A (IT); GRANDI GUIDO (IT)
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/organism="synthetic construct"
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Query Match 55.8%; Score 18.4; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Falkner,F.D., Haemmerle,T.D., Himmelspach,M.D., Kohl,J.D. and
Dorner,F.F.
TITLE Method for quantifying nucleic acids
JOURNAL Patent: EP 0714988-A 6 05-JUN-1996;
IMMUNO AG (AT)
COMMENT Other publication JP 8107798 960430
Other publication CA 2159044 960327
Other publication AT 401062 960625
Other publication AT 183194 951015.
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/organism="unidentified"
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RESULT 36
A64953
LOCUS A64953 20 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 7 from Patent WO9732040.
ACCESSION A64953
VERSION A64953.1 GI:4530922
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1
AUTHORS Stirling,D. and Ludlam,C.A.
TITLE NUCLEIC ACID SEQUENCE DETECTION
JOURNAL Patent: WO 9732040-A 7 04-SEP-1997;
ROYAL INFIRMARY OF EDINBURGH N (GB)
COMMENT Other publication AU 1889797 19970916.
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RESULT 37
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LOCUS AR020188 20 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 6 from patent US 5789153.
ACCESSION AR020188
VERSION AR020188.1 GI:3974803
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Falkner,F.-G., Haemmerle,T., Himmelspach,M., Kohl,J. and Dorner,F.
TITLE Method of quantitating nucleic acid

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OM nucleic - nucleic search, using sw model

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Title: US-10-087-631B-3

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C 5	27.4	83.0	29	2	AAV15324 Hepatitis
6	22	66.7	41	6	AAI40116 Pathogeni
C 7	21	63.6	41	2	AAI37635 HCV detec
8	20.4	61.8	26	3	AAI74622
9	20.4	61.8	28	2	AAI05216
10	20.4	61.8	28	3	AAI05216
C 11	20.4	61.8	28	10	ADCS4071
C 12	20.4	61.8	36	3	AAI29447
C 13	20	60.6	21	2	AAV35207 Hepatitis
C 14	20	60.6	22	2	AAI0497 Hepatitis
C 15	20	60.6	24	12	ADP87801
C 16	20	60.6	25	8	ABZ75892
C 17	20	60.6	25	12	ADH79952
18	20	60.6	26	12	ADP87799
19	20	60.6	32	4	AH25418 Detection
C 20	20	60.6	37	2	AAI37631 HCV detec
C 21	20	60.6	38	2	AAT12490 Labelled

C 22	19.4	58.8	30	2	AAQ21851	AaQ21851 HCV probe
C 23	19.4	58.8	30	2	AAT94722	Aat94722 Hepatitis
C 24	19.4	58.8	30	2	AAZ27492	Aaz27492 Probe for
C 25	19.4	58.8	30	3	AAA75276	Aaa75276 Probe use
C 26	19.4	58.8	30	12	ADN35930	Adn35930 HCV cDNA
C 27	19.4	58.8	31	3	AAZ99214	Aaz99214 Primer fo
C 28	19	57.6	19	10	ADD67939	Add67939 Hepatitis
C 29	19	57.6	19	10	ADF51488	Adf51488 Hepatitis
C 30	19	57.6	19	10	ADF51492	Adf51492 Hepatitis
C 31	19	57.6	19	10	ADF52184	Adf52184 Hepatitis
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C 61	18	54.5	19	10	ADF52186	Adf52186 Hepatitis
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C 76	17	51.5	17	12	ADI87279	Adi87279 HCV DNaz
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C 84	17	51.5	24	6	ABL46270	AbL46270 Hepatitis
C 85	17	51.5	27	2	AAQ64955	AaQ64955 Antisense
C 86	17	51.5	30	2	AAQ64950	AaQ64950 Antisense
C 87	17	51.5	50	3	AAA52575	Aaa52575 HCV RNA P
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c 98	16	48.5	19	10	ADFS2180	Adfs2180 Hepatitis	c 171	15	45.5	21	2	AAV15318	AAV15318 Hepatitis
c 99	16	48.5	24	2	AAV11280	AAV11280 Hepatitis	c 172	15	45.5	21	12	ADJ57847	Adj57847 Primer #1
c 100	16	48.5	24	10	ADD5637	Add5637 Oligonuc1	c 173	15	45.5	21	12	ADJ57755	Adj57755 Primer #1
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c 104	16	48.5	33	2	AAV07856	AAV07856 HCV 33.4	c 177	15	45.5	31	10	AAAL57066	AAAL57066 Flavivirus
c 105	16	48.5	33	2	AAV83084	AAV83084 Capture p	c 178	15	45.5	34	10	ADB98999	Adb98999 Xmt8 PCR
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c 107	16	48.5	39	6	ABA97126	ABA97126 Human t1c	c 180	15	45.5	37	2	AAV66472	AAV66472 Primer MO
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c 109	15.8	47.9	21	2	AAQ30154	AAQ30154 NANB hepa	c 182	15	45.5	50	3	AAA52574	AAA52574 HCV RNA p
c 110	15.8	47.9	21	2	AAQ31812	AAQ31812 Antisense	c 183	14.8	44.8	18	2	AAV15315	AAV15315 Hepatitis
c 111	15.8	47.9	21	2	AAQ31812	AAQ31812 Antisense	c 184	14.8	44.8	19	2	AAAT86456	AAAT86456 PCR prime
c 112	15.8	47.9	21	2	AAQ30783	AAQ30783 Hepatitis	c 185	14.8	44.8	19	8	AAAD51014	AAAD51014 Hepatitis
c 113	15.8	47.9	21	10	ADFS2922	Adfs2922 Hepatitis	c 186	14.8	44.8	19	10	ADFS2167	Adfs2167 Hepatitis
c 114	15.8	47.9	21	10	ADFS2979	Adfs2979 Hepatitis	c 187	14.8	44.8	19	10	ADFS1463	Adfs1463 Hepatitis
c 115	15.4	46.7	17	8	ACD56835	Accd56835 HCV DNazY	c 188	14.8	44.8	19	10	ADFS1471	Adfs1471 Hepatitis
c 116	15.4	46.7	17	12	ADI82785	Adi82785 HCV DNazY	c 189	14.8	44.8	19	10	ADFS2159	Adfs2159 Hepatitis
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c 123	15.4	46.7	23	10	ADFS2910	Adfs2910 Hepatitis	c 196	14.8	44.8	21	9	ADAI13863	Adai13863 Short int
c 124	15.4	46.7	24	2	AAV11273	AAV11273 Hepatitis	c 197	14.8	44.8	21	10	ADFS2833	Adfs2833 Hepatitis
c 125	15.4	46.7	25	8	ABV76987	ABV76987 Control p	c 198	14.8	44.8	21	10	ADFS2858	Adfs2858 Hepatitis
c 126	15.4	46.7	35	2	AAQ75822	AAQ75822 Sense pri	c 199	14.8	44.8	21	10	ADFS2840	Adfs2840 Hepatitis
c 127	15.4	46.7	34	12	ADN00279	ADN00279 RT-PCR pr	c 200	14.8	44.8	21	10	ADFS2859	Adfs2859 Hepatitis
c 128	15.2	46.1	33	2	AAV12106	AAV12106 Human B7	c 201	14.8	44.8	21	10	ADFS2866	Adfs2866 Hepatitis
c 129	15.2	46.1	38	2	AAV04401	AAV04401 Primer us	c 202	14.8	44.8	23	6	ABN79966	Abn79966 Hepatitis
c 130	15.2	46.1	38	2	AAV04403	AAV04403 Primer us	c 203	14.8	44.8	23	10	ADFS2805	Adfs2805 Hepatitis
c 131	15.2	46.1	38	2	AAV04405	AAV04405 Primer us	c 204	14.8	44.8	23	10	ADFS2807	Adfs2807 Hepatitis
c 132	15.2	46.1	38	2	AAV04344	AAV04344 Primer us	c 205	14.8	44.8	24	2	AAQ98279	AAQ98279 Hepatitis
c 133	15.2	46.1	38	2	AAV04346	AAV04346 Primer us	c 206	14.8	44.8	25	2	AAQ98277	AAQ98277 Hepatitis
c 134	15.2	46.1	38	2	AAV04407	AAV04407 Primer us	c 207	14.8	44.8	25	2	AAQ98274	AAQ98274 Hepatitis
c 135	15.2	46.1	38	5	AAFS7863	AAFS7863 Murine OP	c 208	14.8	44.8	25	2	AAV76723	AAV76723 Stacker o
c 136	15.2	46.1	38	5	AAFS7747	AAFS7747 Murine OP	c 209	14.8	44.8	25	2	AAV53936	AAV53936 Nucleotid
c 137	15.2	46.1	38	5	AAFS7745	AAFS7745 Murine OP	c 210	14.8	44.8	25	6	AAE52939	AAE52939 FEN-1 rel
c 138	15.2	46.1	38	5	AAFS7865	AAFS7865 Murine OP	c 211	14.8	44.8	28	2	AAAT05243	AAAT05243 Hepatitis
c 139	15.2	46.1	38	5	AAFS7867	AAFS7867 Murine OP	c 212	14.8	44.8	28	2	AAAT05217	AAAT05217 Hepatitis
c 140	15.2	46.1	38	5	AAFS7861	AAFS7861 Murine OP	c 213	14.8	44.8	28	3	AAZ57783	AAZ57783 Hepatitis
c 141	15.2	46.1	38	12	ADM28848	Adm28848 Mouse OP	c 214	14.8	44.8	28	3	AAZ57752	AAZ57752 Hepatitis
c 142	15.2	46.1	38	12	ADM28854	Adm28854 Mouse OP	c 215	14.8	44.8	29	2	AAV60679	AAV60679 Primer #1
c 143	15.2	46.1	38	12	ADM28716	Adm28716 Mouse OP	c 216	14.8	44.8	30	2	AAQ71841	AAQ71841 DNA probe
c 144	15.2	46.1	38	12	ADM28714	Adm28714 Mouse OP	c 217	14.8	44.8	31	8	ABZ81787	ABZ81787 HCV 5' UT
c 145	15.2	46.1	38	12	ADM28850	Adm28850 Mouse OP	c 218	14.8	44.8	32	10	ADC79170	Adc79170 Human CD8
c 146	15.2	46.1	38	12	ADM28852	Adm28852 Mouse OP	c 219	14.8	44.8	33	2	AAQ31154	AAQ31154 Probe 123
c 147	15.2	46.1	40	1	AAH81426	AAH81426 Plasmid p	c 220	14.8	44.8	33	2	AAQ46460	AAQ46460 Hepatitis
c 148	15.2	46.1	46	6	ABN72439	ABN72439 Streptoco	c 221	14.8	44.8	33	2	AAV07857	AAV07857 HCV 33.5
c 149	15	45.5	15	2	AAQ64951	AAQ64951 Antisense	c 222	14.8	44.8	33	2	AAV07857	AAV07857 HCV 33.5
c 150	15	45.5	15	2	AAQ64951	AAQ64951 Antisense	c 223	14.8	44.8	33	2	AAV83085	AAV83085 Oligonuc1
c 151	15	45.5	15	3	AAZ61838	AAZ61838 HCV 5' no	c 224	14.8	44.8	33	6	ABL46096	ABL46096 Capture p
c 152	15	45.5	15	3	AAZ62393	AAZ62393 Substrate	c 225	14.8	44.8	33	12	ADK82286	ADK82286 Control t
c 153	15	45.5	15	6	ABX01779	ABX01779 Hepatitis	c 226	14.8	44.8	33	12	ADK82286	ADK82286 Nucleic a
c 154	15	45.5	15	6	ABX01817	ABX01817 Hepatitis	c 227	14.6	44.2	40	2	AAAT31951	AAAT31951 BBP-B1X a
c 155	15	45.5	15	6	ABX03367	ABX03367 Hepatitis	c 228	14.6	44.2	30	8	ABX90079	ABX90079 S. aureus
c 156	15	45.5	15	6	ABX00224	ABX00224 Hepatitis	c 229	14.6	44.2	30	10	ADD25368	ADD25368 Oligonuc1
c 157	15	45.5	15	6	ABX01780	ABX01780 Hepatitis	c 230	14.6	44.2	33	2	AAQ66336	AAQ66336 Primer fo
c 158	15	45.5	15	6	ABX01781	ABX01781 Hepatitis	c 231	14.6	44.2	34	5	AAAD16133	AAAD16133 Human VEG
c 159	15	45.5	15	8	ACD66277	ACD66277 Anti-HCV	c 232	14.6	44.2	34	12	ADO50775	ADO50775 Human VEG
c 160	15	45.5	15	8	ACD65920	ACD65920 Anti-HCV	c 233	14.6	44.2	40	2	AAAT61664	AAAT61664 Antibody
c 161	15	45.5	15	12	ADI87519	Adi87519 Anti-HCV	c 234	14.6	44.2	41	11	ADP75582	ADP75582 Human ADA
c 162	15	45.5	15	12	ADI87706	Adi87706 Anti-HCV	c 235	14.4	43.6	17	8	ACD56838	ACD56838 HCV DNazY
c 163	15	45.5	15	12	ADP87835	ADP87835 TEX on mi	c 236	14.4	43.6	17	8	ACD65840	ACD65840 HCV minus
c 164	15	45.5	17	8	ADP56833	ADP56833 HCV DNazY	c 237	14.4	43.6	17	12	ADI82788	Adi82788 HCV DNazY
c 165	15	45.5	17	12	ADI82783	Adi82783 HCV DNazY	c 238	14.4	43.6	17	12	ADI82788	Adi82788 HCV DNazY
c 166	15	45.5	18	6	AAH40305	AAH40305 Pathogeni	c 239	14.4	43.6	18	2	AAQ52819	AAQ52819 HCV targ
c 167	15	45.5	18	6	ABN80473	Abn80473 DNA-RNA h	c 240	14.4	43.6	19	10	ADFS2163	Adfs2163 Hepatitis

C 241	14.4	43.6	19	10	ADP52164	Adf52164 Hepatitis	C 314	14	42.4	26	8	ACC43166	Acc43166 Probe use
C 242	14.4	43.6	19	10	ADP52171	Adf52171 Hepatitis	C 315	14	42.4	26	9	ACF36232	ACF36232 HCV 5' IR
C 243	14.4	43.6	19	10	ADP51468	Adf51468 Hepatitis	C 316	14	42.4	26	10	ACF36229	ACF36229 HCV 5' IR
C 244	14.4	43.6	19	10	ADP51467	Adf51467 Hepatitis	C 317	14	42.4	26	10	ACF36282	ACF36282 HCV 5' IR
C 245	14.4	43.6	19	10	ADP51475	Adf51475 Hepatitis	C 318	14	42.4	26	10	ABZ76309	ABZ76309 HCV RNA 5
C 246	14.4	43.6	22	2	AAZ25789	Aaz25789 Hepatitis	C 319	14	42.4	27	2	AAQ64949	AAQ64949 Antisense
C 247	14.4	43.6	22	2	AAZ25835	Aaz25835 Upstream	C 320	14	42.4	27	2	AAQ64949	AAQ64949 Antisense
C 248	14.4	43.6	22	3	AAAG5005	AAAG5005 Hepatitis	C 321	14	42.4	37	6	ACN31721	ACN31721 WNV minus
C 249	14.4	43.6	22	3	AAAG62977	AAAG62977 Upstream	C 322	14	42.4	37	6	ACN31721	ACN31721 WNV minus
C 250	14.4	43.6	22	3	AAAG63599	AAAG63599 PCR prime	C 323	14	42.4	37	6	ACN31718	ACN31718 WNV minus
C 251	14.4	43.6	22	4	AAAS14802	AAAS14802 Hepatitis	C 324	14	42.4	37	6	ACN30808	ACN30808 WNV minus
C 252	14.4	43.6	22	6	AAAS86271	AAAS86271 HCV gene	C 325	14	42.4	37	11	ADL75647	ADL75647 Human PTG
C 253	14.4	43.6	22	6	AAKS0239	AAKS0239 Hepatitis	C 326	14	42.4	39	2	AAAT87242	AAAT87242 IL-4 2'NH
C 254	14.4	43.6	22	9	ABX16142	ABX16142 HCV PCR p	C 327	14	42.4	42	2	AAV15321	AAV15321 Hepatitis
C 255	14.4	43.6	22	9	ABCD26344	ABCD26344 Hepatitis	C 328	14	42.4	42	2	AAAG60959	AAAG60959 Hepatitis
C 256	14.4	43.6	22	10	ADE76486	Ade76486 PCR prime	C 329	14	42.4	46	6	ABA90113	ABA90113 Oestrogen
C 257	14.4	43.6	25	2	AAQ98278	AAQ98278 Hepatitis	C 330	14	42.4	46	6	ABA901125	ABA901125 Oestrogen
C 258	14.4	43.6	25	4	AAAF58267	AAAF58267 Hepatitis	C 331	14	42.4	46	6	ABA90115	ABA90115 Oestrogen
C 259	14.4	43.6	25	9	AAI94261	AAI94261 Human mic	C 332	14	42.4	46	6	ABA90139	ABA90139 Oestrogen
C 260	14.4	43.6	26	3	AAAF74621	AAAF74621 HCV-speci	C 333	14	42.4	46	6	ABA90104	ABA90104 Oestrogen
C 261	14.4	43.6	29	3	AAAC64666	AAAC64666 Human TRA	C 334	14	42.4	46	6	ABA90137	ABA90137 Oestrogen
C 262	14.4	43.6	32	12	ADO05664	Ado05664 HCV DNA f	C 335	14	42.4	46	6	ABQ87822	ABQ87822 Human ESR
C 263	14.4	43.6	33	8	ABZ57541	ABZ57541 5-phospha	C 336	14	42.4	46	6	ABQ87848	ABQ87848 Human ESR
C 264	14.4	43.6	35	8	ACCT9269	ACCT9269 Hepatitis	C 337	14	42.4	46	6	ABQ87846	ABQ87846 Human ESR
C 265	14.4	43.6	36	4	AAAF28373	AAAF28373 Clostridi	C 338	14	42.4	46	6	ABQ87824	ABQ87824 Human ESR
C 266	14.4	43.6	36	4	AAAF28377	AAAF28377 Clostridi	C 339	14	42.4	46	6	ABQ87834	ABQ87834 Human ESR
C 267	14.4	43.6	36	4	AAAF28374	AAAF28374 Clostridi	C 340	14	42.4	46	6	ABQ87813	ABQ87813 Human ESR
C 268	14.4	43.6	36	4	AAAF28378	AAAF28378 Clostridi	C 341	14	42.4	46	6	ABX33870	ABX33870 Human ESR
C 269	14.4	43.6	41	3	AAAF26640	AAAF26640 Human HPC	C 342	14	42.4	46	8	ABX33884	ABX33884 Human ESR
C 270	14.4	43.6	45	12	ADM88395	Adm88395 Gene expr	C 343	14	42.4	46	8	ABX33849	ABX33849 Human ESR
C 271	14.4	43.6	50	6	ABZ023830	ABZ023830 Human leu	C 344	14	42.4	46	8	ABX33860	ABX33860 Human ESR
C 272	14.4	43.6	50	6	ABZ06043	ABZ06043 Human leu	C 345	14	42.4	46	8	ABX33882	ABX33882 Human ESR
C 273	14.2	43.0	21	4	AAAG1579	AAAG1579 PCR prime	C 346	14	42.4	46	8	ABX33858	ABX33858 Human ESR
C 274	14.2	43.0	25	8	ABX90046	ABX90046 S. aureus	C 347	14	42.4	47	3	AAAC81264	AAAC81264 Human/mou
C 275	14.2	43.0	25	10	ADD25342	Add25342 Oligonuc	C 348	14	42.4	49	12	ADP03533	ADP03533 PCR prime
C 276	14.2	43.0	30	2	AAAX30306	Aax30306 Streptoco	C 349	13.8	41.8	19	10	ADP51464	ADP51464 Hepatitis
C 277	14.2	43.0	33	6	ABAG05833	ABAG05833 A thalian	C 350	13.8	41.8	19	10	ADP52160	ADP52160 Hepatitis
C 278	14.2	43.0	34	12	ADN97814	Adm97814 Glucocort	C 351	13.8	41.8	20	2	AAQ58413	AAQ58413 Antisense
C 279	14.2	43.0	45	1	AAAN80951	Aan80951 Long prob	C 352	13.8	41.8	21	9	ADAI13807	ADAI13807 Short int
C 280	14.2	43.0	45	2	AAQ62683	AAQ62683 Enkephali	C 353	13.8	41.8	21	9	ADAI13814	ADAI13814 Short int
C 281	14.2	43.0	45	2	AAQ62680	AAQ62680 Enkephali	C 354	13.8	41.8	21	9	ADAI13862	ADAI13862 Short int
C 282	14.2	43.0	50	3	ADCI17102	Adci17102 Human sin	C 355	13.8	41.8	21	10	ADP52838	ADP52838 Hepatitis
C 283	14	42.4	15	6	ABX01742	ABX01742 Hepatitis	C 356	13.8	41.8	21	10	ADP52831	ADP52831 Hepatitis
C 284	14	42.4	15	8	ACD65936	ACD65936 Anti-HCV	C 357	13.8	41.8	21	10	ADP52865	ADP52865 Hepatitis
C 285	14	42.4	15	8	ACD66048	ACD66048 Anti-HCV	C 358	13.8	41.8	23	2	ABQ80471	ABQ80471 Subtilase
C 286	14	42.4	15	8	ACD66050	ACD66050 Anti-HCV	C 359	13.8	41.8	24	2	AAQ63500	AAQ63500 NANBH pr
C 287	14	42.4	15	8	ACD66276	ACD66276 Anti-HCV	C 360	13.8	41.8	25	6	ABN10993	ABN10993 Human GDM
C 288	14	42.4	15	8	ACD66272	ACD66272 Anti-HCV	C 361	13.8	41.8	25	9	ACI07693	ACI07693 Human mic
C 289	14	42.4	15	12	ADI87535	Adi87535 Anti-HCV	C 362	13.8	41.8	25	9	ACK17452	ACK17452 Human mic
C 290	14	42.4	15	12	ADI87582	Adi87582 Anti-HCV	C 363	13.8	41.8	25	9	ACK17453	ACK17453 Human mic
C 291	14	42.4	15	12	ADI87584	Adi87584 Anti-HCV	C 364	13.8	41.8	28	6	AAZ35960	AAZ35960 Corynebac
C 292	14	42.4	15	12	ADI87701	Adi87701 Anti-HCV	C 365	13.8	41.8	34	2	AAZ06813	AAZ06813 Maize elo
C 293	14	42.4	15	12	ADI87705	Adi87705 Anti-HCV	C 366	13.8	41.8	36	12	ADL24398	ADL24398 Multiple
C 294	14	42.4	17	8	ACD65837	ACD65837 HCV minus	C 367	13.8	41.8	37	2	AAQ50969	AAQ50969 Wild-type
C 295	14	42.4	17	8	ACD56839	ACD56839 HCV DNazy	C 368	13.8	41.8	39	12	ADP87792	ADP87792 HCV cDNA
C 296	14	42.4	17	12	ADI82789	Adi82789 HCV DNazy	C 369	13.8	41.8	40	2	AAZ08605	AAZ08605 Assembly
C 297	14	42.4	17	12	ADI87275	Adi87275 HCV DNazy	C 370	13.8	41.8	40	2	AAZ01615	AAZ01615 Helix-tur
C 298	14	42.4	18	12	ADP87834	ADP87834 TEX on mi	C 371	13.8	41.8	40	3	AAZ61346	AAZ61346 PCR prime
C 299	14	42.4	19	10	ADP52190	ADP52190 Hepatitis	C 372	13.8	41.8	43	6	AAAL41123	AAAL41123 pRL5CAT H
C 300	14	42.4	19	10	ADP51494	ADP51494 Hepatitis	C 373	13.8	41.8	45	6	ABK33723	ABK33723 S. pneumo
C 301	14	42.4	19	10	ADP51442	ADP51442 Hepatitis	C 374	13.8	41.8	45	6	ABK33722	ABK33722 S. pneumo
C 302	14	42.4	19	10	ADP51465	ADP51465 Hepatitis	C 375	13.8	41.8	50	4	AAAL29191	AAAL29191 Human SNP
C 303	14	42.4	19	10	ADP52161	ADP52161 Hepatitis	C 376	13.8	41.8	50	6	ABZ03836	ABZ03836 Human leu
C 304	14	42.4	19	10	ADP52138	ADP52138 Hepatitis	C 377	13.8	41.8	50	6	ABZ03337	ABZ03337 Human leu
C 305	14	42.4	20	2	AAQ75230	AAQ75230 Antisense	C 378	13.8	41.8	50	10	ADG33597	ADG33597 Human DNA
C 306	14	42.4	20	2	AAAT11283	AAAT11283 Hepatitis	C 379	13.8	41.8	50	10	ADG33416	ADG33416 Human DNA
C 307	14	42.4	25	3	AAZ60850	AAZ60850 Oligonuc	C 380	13.6	41.2	25	9	ACI64479	ACI64479 Human mic
C 308	14	42.4	25	3	AAZ60849	AAZ60849 Oligonuc	C 381	13.6	41.2	31	8	ACD43736	ACD43736 Human gen
C 309	14	42.4	25	3	AAZ60851	AAZ60851 Oligonuc	C 382	13.6	41.2	37	6	ACN31108	ACN31108 WNV minus
C 310	14	42.4	25	3	AAZ60848	AAZ60848 Oligonuc	C 383	13.6	41.2	37	11	ADL73583	ADL73583 Human PKR
C 311	14	42.4	25	9	ACK15326	ACK15326 Human mic	C 384	13.6	41.2	38	4	ABK05924	ABK05924 Human NOG
C 312	14	42.4	25	9	ACK09419	ACK09419 Human mic	C 385	13.6	41.2	38	4	ABK05855	ABK05855 Human CD2
C 313	14	42.4	26	8	ACC48584	ACC48584 Hepatitis	C 386	13.6	41.2	41	6	ABZ50544	ABZ50544 Human car

387	13.6	41.2	41.2	41	6	ABZ45285	Human car	Abz45285	Human car	13	39.4	15	3	AAZ63689	Substrate
C 388	13.6	41.2	41.2	47	3	Aaz68762	Human map	Aaz68762	Human map	13	39.4	15	3	AAZ61839	HCV 5', no
C 389	13.6	41.2	41.2	48	3	Aax36361	Primer fo	Aax36361	Primer fo	13	39.4	15	3	AAZ62394	Substrate
C 390	13.6	41.2	41.2	48	6	ABZ65550	Human TIE	ABZ65550	Human TIE	13	39.4	15	3	Aaz61837	HCV 5', no
391	13.6	41.2	41.2	50	4	Aah89609	Human gly	Aah89609	Human gly	13	39.4	15	6	ABX01782	Hepatitis
392	13.6	41.2	41.2	50	6	ABZ03706	Human leu	ABZ03706	Human leu	13	39.4	15	6	ABX03379	Hepatitis
393	13.6	41.2	41.2	50	6	ADD41458	Synthetic	ADD41458	Synthetic	13	39.4	15	6	ABX03368	Hepatitis
394	13.4	40.6	40.6	15	6	ABX01775	Hepatitis	ABX01775	Hepatitis	13	39.4	15	6	ABX00223	Hepatitis
395	13.4	40.6	40.6	15	8	ACD66255	Anti-HCV	ACD66255	Anti-HCV	13	39.4	17	8	ACD58411	Hepatitis
396	13.4	40.6	40.6	15	12	AD187684	Anti-HCV	AD187684	Anti-HCV	13	39.4	17	8	ACD58436	HCV minus
397	13.4	40.6	40.6	15	12	ADP87836	TEX on mi	ADP87836	TEX on mi	13	39.4	17	8	ACD58836	HCV minus
C 398	13.4	40.6	40.6	18	12	ADP87780	Hepatitis	ADP87780	Hepatitis	13	39.4	17	12	AD187274	HCV DNaz
C 399	13.4	40.6	40.6	19	10	ADF51479	Hepatitis	ADF51479	Hepatitis	13	39.4	17	12	AD187281	HCV DNaz
C 400	13.4	40.6	40.6	19	10	ADF52175	Hepatitis	ADF52175	Hepatitis	13	39.4	18	3	AAZ29449	Hepatitis
C 401	13.4	40.6	40.6	23	12	ADP82853	Probe use	ADP82853	Probe use	13	39.4	18	3	AAZ29449	Hepatitis
C 402	13.4	40.6	40.6	25	9	ACK00350	Human mic	ACK00350	Human mic	13	39.4	19	10	ADF51474	Hepatitis
C 403	13.4	40.6	40.6	25	9	ACI29544	Human mic	ACI29544	Human mic	13	39.4	19	10	ADF52170	Hepatitis
C 404	13.4	40.6	40.6	25	9	ACI99891	Human mic	ACI99891	Human mic	13	39.4	19	10	ADF51482	Hepatitis
C 405	13.4	40.6	40.6	26	8	ACD17036	Sample pr	ACD17036	Sample pr	13	39.4	19	10	ADF52178	Hepatitis
C 406	13.4	40.6	40.6	27	2	AAX58190	Primer fo	Aax58190	Primer fo	13	39.4	20	2	AAQ58411	Hepatitis
C 407	13.4	40.6	40.6	30	8	ACC42739	Geldanam	ACC42739	Geldanam	13	39.4	21	12	ADP03553	RT-PCR pr
C 408	13.4	40.6	40.6	30	10	AD61815	Streptomy	AD61815	Streptomy	13	39.4	24	3	AAA90945	Mutagenic
C 409	13.4	40.6	40.6	33	3	AAZ38686	DNA encod	Aaz38686	DNA encod	13	39.4	24	6	AD22588	PCR prime
C 410	13.4	40.6	40.6	33	10	ADK71260	Drug-tole	ADK71260	Drug-tole	13	39.4	24	12	ADJ51126	Human CDN
C 411	13.4	40.6	40.6	38	2	AAV31367	Trichoder	Aav31367	Trichoder	13	39.4	24	12	ADJ51126	Human CDN
C 412	13.4	40.6	40.6	39	3	AAZ95766	Hepatitis	Aaz95766	Hepatitis	13	39.4	25	3	AAA52569	Oligonuc
C 413	13.4	40.6	40.6	40	2	AAQ88332	Maize alp	Aaq88332	Maize alp	13	39.4	25	6	ABN10996	Human GDM
C 414	13.4	40.6	40.6	40	3	AAZ69959	TGF-beta-	Aaz69959	TGF-beta-	13	39.4	25	6	ABN10994	Human GDM
C 415	13.4	40.6	40.6	46	12	ADU94558	Oligonuc	ADU94558	Oligonuc	13	39.4	25	6	ABN10992	Human GDM
C 416	13.4	40.6	40.6	47	3	AAZ67556	Human map	Aaz67556	Human map	13	39.4	25	6	ABN10991	Human GDM
C 417	13.4	40.6	40.6	48	2	AAZ00287	HEV speci	Aaz00287	HEV speci	13	39.4	25	6	ABN10995	Human GDM
C 418	13.4	40.6	40.6	50	4	AAL34419	Human SNP	Aal34419	Human SNP	13	39.4	25	6	ABN10989	Human GDM
C 419	13.4	40.6	40.6	50	4	AAL34397	Human SNP	Aal34397	Human SNP	13	39.4	25	6	ABN10992	Human GDM
C 420	13.2	40.0	40.0	20	3	AAZ59852	Oligonuc	Aaz59852	Oligonuc	13	39.4	25	6	ABN10990	Human GDM
C 421	13.2	40.0	40.0	24	2	AAV65882	Stacker o	Aav65882	Stacker o	13	39.4	25	9	ACT89303	Human mic
C 422	13.2	40.0	40.0	24	9	ADMA6603	DNAP-rela	ADMA6603	DNAP-rela	13	39.4	25	9	ACK07452	Human mic
C 423	13.2	40.0	40.0	25	9	ACT131794	Human mic	ACT131794	Human mic	13	39.4	25	9	ACT18877	Human mic
C 424	13.2	40.0	40.0	25	9	ACT168851	Human mic	ACT168851	Human mic	13	39.4	25	9	ACT157751	Human mic
C 425	13.2	40.0	40.0	25	9	ACK04538	Human mic	ACK04538	Human mic	13	39.4	25	9	ACT184583	Human mic
C 426	13.2	40.0	40.0	25	9	ACT195287	Human mic	ACT195287	Human mic	13	39.4	26	2	AAQ51830	bcr mRNA
C 427	13.2	40.0	40.0	25	9	ACT169798	Human mic	ACT169798	Human mic	13	39.4	26	2	ABS70880	Hepatitis
C 428	13.2	40.0	40.0	25	9	ACT178988	Human mic	ACT178988	Human mic	13	39.4	26	2	ABS70880	Hepatitis
C 429	13.2	40.0	40.0	26	8	ABK66308	Human gen	ABK66308	Human gen	13	39.4	26	2	ABS70880	Hepatitis
C 430	13.2	40.0	40.0	29	8	ABZ81899	Primer AA	ABz81899	Primer AA	13	39.4	26	2	ABS70880	Hepatitis
C 431	13.2	40.0	40.0	31	11	ADM55506	DNazyme t	Adm55506	DNazyme t	13	39.4	26	2	ABS70880	Hepatitis
C 432	13.2	40.0	40.0	32	5	AAC86131	Llewellyn	Aac86131	Llewellyn	13	39.4	26	2	ABS70880	Hepatitis
C 433	13.2	40.0	40.0	33	5	AAC86145	Forward p	Aac86145	Forward p	13	39.4	26	2	ABS70880	Hepatitis
C 434	13.2	40.0	40.0	33	6	ABL61584	Human glu	ABL61584	Human glu	13	39.4	26	2	ABS70880	Hepatitis
C 435	13.2	40.0	40.0	33	12	ADL25807	Bacillus	ADL25807	Bacillus	13	39.4	26	2	ABS70880	Hepatitis
C 436	13.2	40.0	40.0	36	3	AAZ88354	Bispecifi	Aaz88354	Bispecifi	13	39.4	26	2	ABS70880	Hepatitis
C 437	13.2	40.0	40.0	40	9	ACD27914	E'/bacter	ACd27914	E'/bacter	13	39.4	26	2	ABS70880	Hepatitis
C 438	13.2	40.0	40.0	41	6	ABL96052	Brassica	ABL96052	Brassica	13	39.4	26	2	ABS70880	Hepatitis
C 439	13.2	40.0	40.0	41	10	AQ083785	Human mul	Aq083785	Human mul	13	39.4	26	2	ABS70880	Hepatitis
C 440	13.2	40.0	40.0	42	2	AAZ88389	Antibody	Aaz88389	Antibody	13	39.4	26	2	ABS70880	Hepatitis
C 441	13.2	40.0	40.0	45	2	AAV49402	Primer AB	Aav49402	Primer AB	13	39.4	26	2	ABS70880	Hepatitis
C 442	13.2	40.0	40.0	50	6	ABZ07910	Human leu	ABz07910	Human leu	13	39.4	26	2	ABS70880	Hepatitis
C 443	13.2	40.0	40.0	13	8	ACD65935	Anti-HCV	ACd65935	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 444	13.2	40.0	40.0	13	8	ACD66045	Anti-HCV	ACd66045	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 445	13.2	40.0	40.0	13	8	ACD66265	Anti-HCV	ACd66265	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 446	13.2	40.0	40.0	13	8	ACD66183	Anti-HCV	ACd66183	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 447	13.2	40.0	40.0	13	8	ACD66259	Anti-HCV	ACd66259	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 448	13.2	40.0	40.0	13	8	ACD66043	Anti-HCV	ACd66043	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 449	13.2	40.0	40.0	13	8	ACD65992	Anti-HCV	ACd65992	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 450	13.2	40.0	40.0	13	8	ACD66264	Anti-HCV	ACd66264	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 451	13.2	40.0	40.0	13	12	AD187577	Anti-HCV	AD187577	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 452	13.2	40.0	40.0	13	12	AD187561	Anti-HCV	AD187561	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 453	13.2	40.0	40.0	13	12	AD187688	Anti-HCV	AD187688	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 454	13.2	40.0	40.0	13	12	AD187647	Anti-HCV	AD187647	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 455	13.2	40.0	40.0	13	12	AD187534	Anti-HCV	AD187534	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 456	13.2	40.0	40.0	13	12	AD187579	Anti-HCV	AD187579	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 457	13.2	40.0	40.0	13	12	AD187694	Anti-HCV	AD187694	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 458	13.2	40.0	40.0	13	12	AD187693	Anti-HCV	AD187693	Anti-HCV	13	39.4	26	2	ABS70880	Hepatitis
C 459	13.2	40.0	40.0	15	2	AAQ99414	Hepatitis	Aaq99414	Hepatitis	13	39.4	26	2	ABS70880	Hepatitis

C 533	13	39.4	41	6	ABS60501	Human DNA	Adg93426	Human PDG
C 534	13	39.4	41	6	ABZ43742	Human aic	Adg93426	Human cel
C 535	13	39.4	41	6	ABZ49296	Human aic	Adg93426	Human cel
C 536	13	39.4	41	10	ADC46973	Synthesis	Adg93426	Human ATP
C 537	13	39.4	42	4	AH22223	Anti-A33	Adg93426	OmpA sign
C 538	13	39.4	42	5	AAH20088	Chimeric	Adg93426	OmpA sign
C 539	13	39.4	43	12	ADP96878		Adg93426	OmpA sign
C 540	13	39.4	45	4	AH46022	BCG deriv	Adg93426	LRPFLAGR
C 541	13	39.4	47	6	ABN85153	HIV-1 PR-	Adg93426	Human map
C 542	13	39.4	50	3	AAH52573	HCV RNA p	Adg93426	Human map
C 543	13	39.4	50	3	AAH89757	HCV RNA p	Adg93426	Single st
C 544	13	39.4	50	4	AAH78215	Human sil	Adg93426	Enzymatic
C 545	13	39.4	50	4	AAH90039		Adg93426	Synchroni
C 546	13	39.4	50	4	AAH92374		Adg93426	Synchroni
C 547	13	39.4	50	5	AAH23740	Oligonucle	Adg93426	Human leu
C 548	13	39.4	50	6	AAH168916	Activated	Adg93426	Human DNA
C 549	13	39.4	50	6	ABZ00962	Human leu	Adg93426	Human DNA
C 550	13	39.4	50	12	ADF94023	Microorga	Adg93426	50-mer ol
C 551	12.8	38.8	16	1	AAH50508	Sequence	Adg93426	PCR prime
C 552	12.8	38.8	16	2	AAH27082	Oligonucle	Adg93426	PCR prime
C 553	12.8	38.8	17	8	ACD65838	HCV minus	Adg93426	Human inf
C 554	12.8	38.8	17	12	ADI87276	HCV DNAY	Adg93426	Human inf
C 555	12.8	38.8	19	10	ADF51466	Hepatitis	Adg93426	Antisense
C 556	12.8	38.8	19	10	ADF52162	Hepatitis	Adg93426	Antisense
C 557	12.8	38.8	20	2	ABT80293		Adg93426	Human ELO
C 558	12.8	38.8	20	2	AAH38347	E. coli K	Adg93426	Human bcr
C 559	12.8	38.8	20	6	ABH65877	Inhibitor	Adg93426	PCR prime
C 560	12.8	38.8	21	2	AAH37636	HCV detec	Adg93426	PCR prime
C 561	12.8	38.8	21	6	ABK91422	Hepatitis	Adg93426	Human inf
C 562	12.8	38.8	21	10	ADD67944	Hepatitis	Adg93426	Human thr
C 563	12.8	38.8	21	10	ABX10616	TaqMan pr	Adg93426	Nuclear p
C 564	12.8	38.8	23	10	ADF52812	Hepatitis	Adg93426	Human GDM
C 565	12.8	38.8	24	2	AAH798072	Erwinia c	Adg93426	Human GDM
C 566	12.8	38.8	25	9	ACI114945	Human mic	Adg93426	Human GDM
C 567	12.8	38.8	25	9	ACI94260	Human mic	Adg93426	Human GDM
C 568	12.8	38.8	25	9	ACI08326	Human mic	Adg93426	Human GDM
C 569	12.8	38.8	25	9	ACI11285	Human mic	Adg93426	Human GDM
C 570	12.8	38.8	25	9	ACH61875	DNA targe	Adg93426	Human GDM
C 571	12.8	38.8	25	9	ACH58326	DNA targe	Adg93426	Human GDM
C 572	12.8	38.8	25	12	ADP13714	Renal cel	Adg93426	Human GDM
C 573	12.8	38.8	26	2	AAQ47448	Rat G pro	Adg93426	Human GDM
C 574	12.8	38.8	26	2	AAQ47440	Rat G pro	Adg93426	Human GDM
C 575	12.8	38.8	26	6	ABV99576	Human NOV	Adg93426	Human GDM
C 576	12.8	38.8	26	10	ADG32625	PCR prime	Adg93426	Human GDM
C 577	12.8	38.8	26	10	ADG32629	Human PCR	Adg93426	Human GDM
C 578	12.8	38.8	27	2	AAH89482	Human mat	Adg93426	Human GDM
C 579	12.8	38.8	27	4	AAH78705	Human pro	Adg93426	Human GDM
C 580	12.8	38.8	29	2	AAH84460	Heat choc	Adg93426	Human GDM
C 581	12.8	38.8	29	10	ADC36598	Primer of	Adg93426	Human GDM
C 582	12.8	38.8	30	2	AAQ20891	Immunosti	Adg93426	Human GDM
C 583	12.8	38.8	30	2	AAH17904	Human TPO	Adg93426	Human GDM
C 584	12.8	38.8	30	6	ABX72711	Cryptococ	Adg93426	Human GDM
C 585	12.8	38.8	31	2	AAH45810	Glucocort	Adg93426	Human GDM
C 586	12.8	38.8	31	10	AAH56124	EPO-PC ex	Adg93426	Human GDM
C 587	12.8	38.8	31	12	ADH01521	KB signal	Adg93426	Human GDM
C 588	12.8	38.8	32	4	AAH75867	PCR prime	Adg93426	Human GDM
C 589	12.8	38.8	33	12	ADH96964	Kanamycin	Adg93426	Human GDM
C 590	12.8	38.8	33	12	ADH65172	Kanamycin	Adg93426	Human GDM
C 591	12.8	38.8	33	12	ADH65882	Aminophos	Adg93426	Human GDM
C 592	12.8	38.8	37	2	AAQ49021	Multimeri	Adg93426	Human GDM
C 593	12.8	38.8	37	2	AAQ81381	Reverse p	Adg93426	Human GDM
C 594	12.8	38.8	37	3	AAH49186	Murine Ig	Adg93426	Human GDM
C 595	12.8	38.8	37	3	AAH49186	Murine Ig	Adg93426	Human GDM
C 596	12.8	38.8	37	8	ACC49424	Oligonucle	Adg93426	Human GDM
C 597	12.8	38.8	37	8	ACC49428	5' SH-X	Adg93426	Human GDM
C 598	12.8	38.8	37	8	ACC49423	5' ORI-ta	Adg93426	Human GDM
C 599	12.8	38.8	37	12	ADN62674	Reporter	Adg93426	Human GDM
C 600	12.8	38.8	37	12	ADN62673	Reporter	Adg93426	Human GDM
C 601	12.8	38.8	38	4	AAH170158	Human uro	Adg93426	Human GDM
C 602	12.8	38.8	39	2	AAQ42939	3'-5' seq	Adg93426	Human GDM
C 603	12.8	38.8	39	2	AAV07542	Human tel	Adg93426	Human GDM
C 604	12.8	38.8	39	2	AAZ08696	Human tel	Adg93426	Human GDM
C 605	12.8	38.8	40	2	AAV57697	Human PDG	Adg93426	Human GDM

c 679	12.6	38.2	37	11	ADL75588	Adl75588 Human PTG	752	12.4	37.6	24	8	ACC49080	Acc49080 Human NOV
c 680	12.6	38.2	38	12	ADK90710	Adk90710 Cloning c	753	12.4	37.6	24	8	ACC49077	Acc49077 Human NOV
c 681	12.6	38.2	39	6	ADG14579	Adg14579 Vector pM	c 754	12.4	37.6	25	9	ACI48008	ACI48008 Human mic
c 682	12.6	38.2	39	8	ABV93477	Abv93477 Bacillus	c 755	12.4	37.6	25	9	ACI84132	ACI84132 Human mic
c 683	12.6	38.2	39	8	ABV93808	Abv93808 Bacillus	c 756	12.4	37.6	25	9	ACI65258	ACI65258 Human mic
c 684	12.6	38.2	39	8	ABV93478	Abv93478 Bacillus	c 757	12.4	37.6	25	9	ACI88892	ACI88892 Human mic
c 685	12.6	38.2	39	8	ABV953807	Abv953807 Bacillus	c 758	12.4	37.6	25	9	ACI22381	ACI22381 Human mic
c 686	12.6	38.2	39	10	ADH083356	Adh083356 K. lactis	c 759	12.4	37.6	25	9	ACI50347	ACI50347 Human mic
c 687	12.6	38.2	40	3	AAZ95772	Aaz95772 Polynucle	c 760	12.4	37.6	25	9	ACI52455	ACI52455 Human mic
c 688	12.6	38.2	41	6	ABV74462	Abv74462 Human pro	c 761	12.4	37.6	25	9	ACK09418	ACK09418 Human mic
c 689	12.6	38.2	41	6	ABV74461	Abv74461 Human pro	c 762	12.4	37.6	25	9	ACI20234	ACI20234 Human mic
c 690	12.6	38.2	41	12	ADK17862	Adk17862 Cytochrom	c 763	12.4	37.6	25	9	ACI88893	ACI88893 Human mic
c 691	12.6	38.2	42	2	AAQ49175	Aaq49175 IGF-I gen	c 764	12.4	37.6	25	9	ACK15327	ACK15327 Human mic
c 692	12.6	38.2	42	3	AAZ51540	Aaz51540 PCR prime	c 765	12.4	37.6	25	9	ACI43285	ACI43285 Human mic
c 693	12.6	38.2	42	12	ADQ76051	Adq76051 TBEI in r	c 766	12.4	37.6	25	9	ACK26806	ACK26806 Human mic
c 694	12.6	38.2	45	6	ABK67757	Abk67757 Human tra	c 767	12.4	37.6	25	9	ACI65259	ACI65259 Human mic
c 695	12.6	38.2	46	6	ABA90172	Ab90172 Oestrogen	c 768	12.4	37.6	25	9	ACI36925	ACI36925 Human mic
c 696	12.6	38.2	46	6	ABA90093	Ab90093 Oestrogen	c 769	12.4	37.6	25	9	ACI03133	ACI03133 Human mic
c 697	12.6	38.2	46	6	ABA90133	Ab90133 Oestrogen	c 770	12.4	37.6	25	9	ACI60649	ACI60649 Human mic
c 698	12.6	38.2	46	6	ABA90169	Ab90169 Oestrogen	c 771	12.4	37.6	25	9	ACH58833	ACH58833 DNA targe
c 699	12.6	38.2	46	6	ABA90092	Ab90092 Oestrogen	c 772	12.4	37.6	25	9	ACH62910	ACH62910 DNA targe
c 700	12.6	38.2	46	6	ABA90110	Ab90110 Oestrogen	c 773	12.4	37.6	25	9	ACH62625	ACH62625 DNA targe
c 701	12.6	38.2	46	6	ABA90094	Ab90094 Oestrogen	c 774	12.4	37.6	26	2	AAI66491	AAI66491 RhamIso i
c 702	12.6	38.2	46	6	ABA90106	Ab90106 Oestrogen	c 775	12.4	37.6	26	2	AAI56046	AAI56046 HIV-1 Gro
c 703	12.6	38.2	46	6	ABA90170	Ab90170 Oestrogen	c 776	12.4	37.6	26	2	AAI37161	AAI37161 PCR prime
c 704	12.6	38.2	46	6	ABA90171	Ab90171 Oestrogen	c 777	12.4	37.6	26	8	ACD17029	ACD17029 Sample pr
c 705	12.6	38.2	46	6	ABA90136	Ab90136 Oestrogen	c 778	12.4	37.6	27	2	AAV47664	AAV47664 Alpha-fet
c 706	12.6	38.2	46	6	ABQ87878	Abq87878 Human ESR	c 779	12.4	37.6	27	2	AAV53646	AAV53646 Human alp
c 707	12.6	38.2	46	6	ABQ87880	Abq87880 Human ESR	c 780	12.4	37.6	27	2	AAI04761	AAI04761 Sense PCR
c 708	12.6	38.2	46	6	ABQ87881	Abq87881 Human ESR	c 781	12.4	37.6	27	3	AAA46835	AAA46835 PCR prime
c 709	12.6	38.2	46	6	ABQ87879	Abq87879 Human ESR	c 782	12.4	37.6	27	6	ABK99623	ABK99623 Adenoviru
c 710	12.6	38.2	46	6	ABQ87802	Abq87802 Human ESR	c 783	12.4	37.6	27	8	ACD07348	ACD07348 Host cell
c 711	12.6	38.2	46	6	ABQ87819	Abq87819 Human ESR	c 784	12.4	37.6	27	12	ADI36385	ADI36385 PCR prime
c 712	12.6	38.2	46	6	ABQ87842	Abq87842 Human ESR	c 785	12.4	37.6	28	6	ABK66996	ABK66996 Human gen
c 713	12.6	38.2	46	6	ABQ87801	Abq87801 Human ESR	c 786	12.4	37.6	30	2	AAI42489	AAI42489 Primer fo
c 714	12.6	38.2	46	6	ABQ87815	Abq87815 Human ESR	c 787	12.4	37.6	30	12	ADF66097	ADF66097 Mutagenic
c 715	12.6	38.2	46	6	ABQ87803	Abq87803 Human ESR	c 788	12.4	37.6	31	8	ACD65881	ACD65881 HCV DNazy
c 716	12.6	38.2	46	6	ABQ87845	Abq87845 Human ESR	c 789	12.4	37.6	31	12	ADI92043	ADI92043 HCV DNazy
c 717	12.6	38.2	46	6	ABX33914	Abx33914 Human ESR	c 790	12.4	37.6	32	4	AAF81452	AAF81452 PCR prime
c 718	12.6	38.2	46	8	ABX33855	Abx33855 Human ESR	c 791	12.4	37.6	32	6	AAI29238	AAI29238 Soybean f
c 719	12.6	38.2	46	8	ABX33915	Abx33915 Human ESR	c 792	12.4	37.6	32	10	ADC78769	ADC78769 Mouse BOR
c 720	12.6	38.2	46	8	ABX33837	Abx33837 Human ESR	c 793	12.4	37.6	33	6	ABL55300	ABL55300 Human mit
c 721	12.6	38.2	46	8	ABX33916	Abx33916 Human ESR	c 794	12.4	37.6	34	3	AAI63082	AAI63082 Cre recog
c 722	12.6	38.2	46	8	ABX33851	Abx33851 Human ESR	c 795	12.4	37.6	37	6	ABK59282	ABK59282 Human ClC
c 723	12.6	38.2	46	8	ABX33878	Abx33878 Human ESR	c 796	12.4	37.6	37	6	ABK59530	ABK59530 Human ClC
c 724	12.6	38.2	46	8	ABX33881	Abx33881 Human ESR	c 797	12.4	37.6	37	6	ABK59502	ABK59502 Human ClC
c 725	12.6	38.2	46	8	ABX33839	Abx33839 Human ESR	c 798	12.4	37.6	37	6	ACN30657	ACN30657 WNV minus
c 726	12.6	38.2	46	8	ABX33917	Abx33917 Human ESR	c 799	12.4	37.6	37	6	ACN31288	ACN31288 WNV minus
c 727	12.6	38.2	46	8	ABX33838	Abx33838 Human ESR	c 800	12.4	37.6	37	6	ACN18896	ACN18896 WNV Zinzy
c 728	12.6	38.2	47	3	AAI269202	AAI269202 Human map	c 801	12.4	37.6	37	6	ACN18941	ACN18941 WNV Zinzy
c 729	12.6	38.2	47	6	ABN71692	Abn71692 Streptoco	c 802	12.4	37.6	37	6	ACN31031	ACN31031 WNV minus
c 730	12.6	38.2	47	6	ABK23908	Abk23908 HBcAg-lys	c 803	12.4	37.6	37	6	ACN18922	ACN18922 WNV Zinzy
c 731	12.6	38.2	47	6	ABK70992	Abk70992 Molecular	c 804	12.4	37.6	37	6	ACN31185	ACN31185 WNV minus
c 732	12.6	38.2	47	6	ABK66418	Abk66418 Hepatitis	c 805	12.4	37.6	37	6	ACN31213	ACN31213 WNV minus
c 733	12.6	38.2	47	10	ADD24273	Add24273 Prion dis	c 806	12.4	37.6	37	6	ACN18880	ACN18880 WNV Zinzy
c 734	12.6	38.2	47	10	ADD15895	Add15895 K-ras tar	c 807	12.4	37.6	37	6	ACN19625	ACN19625 WNV Zinzy
c 735	12.6	38.2	47	10	ADK17284	Adk17284 Primer HB	c 808	12.4	37.6	37	6	ACN31121	ACN31121 WNV minus
c 736	12.6	38.2	47	12	ADJ67235	Adj67235 HBV core	c 809	12.4	37.6	37	6	ACN30839	ACN30839 WNV minus
c 737	12.6	38.2	47	12	ADK52241	Adk52241 Modified	c 810	12.4	37.6	37	6	ACN31156	ACN31156 WNV minus
c 738	12.6	38.2	49	3	ACN97615	Acn97615 DNA inser	c 811	12.4	37.6	37	6	ACN30765	ACN30765 WNV minus
c 739	12.6	38.2	50	4	AAI75693	Aai75693 Human sll	c 812	12.4	37.6	37	6	ACN30778	ACN30778 WNV minus
c 740	12.6	38.2	50	6	ABZ001272	Abz001272 Human leu	c 813	12.4	37.6	37	6	ACN31783	ACN31783 WNV minus
c 741	12.6	38.2	50	6	ABZ00714	Abz00714 Human leu	c 814	12.4	37.6	37	6	ACN31005	ACN31005 WNV minus
c 742	12.4	37.6	15	6	ABX01778	Abx01778 Hepatitis	c 815	12.4	37.6	37	6	ACN30633	ACN30633 WNV minus
c 743	12.4	37.6	15	6	ABX01743	Abx01743 Hepatitis	c 816	12.4	37.6	37	6	ACN31443	ACN31443 WNV minus
c 744	12.4	37.6	19	10	ADF54476	Adf54476 Hepatitis	c 817	12.4	37.6	37	8	ACA07991	ACA07991 Necrosis
c 745	12.4	37.6	19	10	ADF52172	Adf52172 Hepatitis	c 818	12.4	37.6	37	8	ACA08105	ACA08105 Necrosis
c 746	12.4	37.6	24	6	ABQ03333	Abq03333 Oligonuel	c 819	12.4	37.6	37	8	ACA08105	ACA08105 Necrosis
c 747	12.4	37.6	24	6	AB183307	Abi183307 Capture o	c 820	12.4	37.6	37	11	ADL54301	ADL54301 Human IKK
c 748	12.4	37.6	24	6	AB192573	Abi192573 Capture o	c 821	12.4	37.6	37	11	ADL75755	ADL75755 Human PTG
c 749	12.4	37.6	24	6	AB192572	Abi192572 Capture o	c 822	12.4	37.6	37	11	ADL52713	ADL52713 Human NOG
c 750	12.4	37.6	24	6	AB183306	Abi183306 Capture o	c 823	12.4	37.6	37	11	ADL75738	ADL75738 Human PTG
c 751	12.4	37.6	24	8	ABX13752	Abx13752 A. oryzae	c 824	12.4	37.6	37	11	ADL54441	ADL54441 Human IKK

C 825	12.4	37.6	37	11	ADL73586	Adl73586 Human PKR	898	12.4	37.6	50	6	ABZ04640	Abz04640 Human leu
C 826	12.4	37.6	37	11	ADL52497	Adl52497 Human NGC	899	12.4	37.6	50	6	ABZ00170	Abz00170 Human leu
C 827	12.4	37.6	37	11	ADL75649	Adl75649 Human PTG	C 900	12.4	37.6	50	8	ABZ74886	Abz74886 Human acy
C 828	12.4	37.6	38	4	AAH96935	Aah96935 Human Chk	C 901	12.4	37.6	50	10	ADG33537	Adg33537 Human DNA
C 829	12.4	37.6	38	4	AAH96859	Aah96859 Human Chk	C 902	12.4	37.6	50	10	ACD91957	Adc91957 Human col
C 830	12.4	37.6	38	4	ABK08506	Abk08506 Human CD2	C 903	12.2	37.0	17	6	ABN06097	Abn06097 Human GDM
C 831	12.4	37.6	38	6	ABK20940	Abk20940 Human ERG	C 904	12.2	37.0	17	6	ABQ99733	Abq99733 Murine Ik
C 832	12.4	37.6	38	6	ABK21080	Abk21080 Human ERG	C 905	12.2	37.0	17	11	ADL50926	Adl50926 Human PTG
C 833	12.4	37.6	38	8	ABK21068	Abk21068 Human ERG	C 906	12.2	37.0	18	6	ABQ87902	Abq87902 Enterohae
C 834	12.4	37.6	38	8	ACD53964	AcD53964 HBV zinzy	C 907	12.2	37.0	19	2	AAT40675	Aat40675 Corynebac
C 835	12.4	37.6	38	8	ACD53785	AcD53785 HBV zinzy	C 908	12.2	37.0	19	2	AAT40680	Aat40680 Corynebac
C 836	12.4	37.6	38	8	ACD53696	AcD53696 HBV zinzy	C 909	12.2	37.0	19	6	ABK51745	Abk51745 Oligonucl
C 837	12.4	37.6	38	8	ADA43202	Ada43202 Human ant	C 910	12.2	37.0	20	2	AAV60762	AAV60762 HIV-1 str
C 838	12.4	37.6	38	10	ADC64138	Adc64138 Polyhydro	C 911	12.2	37.0	20	3	AAZ91685	Aaz91685 PCR prime
C 839	12.4	37.6	38	12	ADG01903	Adg01903 Carbon bl	C 912	12.2	37.0	20	6	ABZ21433	Abz21433 Corynebac
C 840	12.4	37.6	38	12	ADK18084	Adk18084 NA05 comb	C 913	12.2	37.0	20	9	ADB68429	Adb68429 PCR prime
C 841	12.4	37.6	38	12	ADJ54036	Adj54036 Combinato	C 914	12.2	37.0	20	10	ADD06158	Add06158 Bcr-abl f
C 842	12.4	37.6	38	12	ADM62147	Adm62147 Hepatitis	C 915	12.2	37.0	20	10	ADD56725	Add56725 Human gen
C 843	12.4	37.6	38	12	ADM62284	Adm62284 Hepatitis	C 916	12.2	37.0	20	11	ADL25569	Adl25569 Shiga tox
C 844	12.4	37.6	38	12	ADM62207	Adm62207 Hepatitis	C 917	12.2	37.0	20	12	ADJ85242	Adj85242 Nucleic a
C 845	12.4	37.6	39	2	AAT87228	Aat87228 IL-4 2'NH	C 918	12.2	37.0	20	12	ADP47366	Adp47366 Intellige
C 846	12.4	37.6	39	2	AAT87229	Aat87229 IL-4 2'NH	C 919	12.2	37.0	20	12	ADP83589	Adp83589 Human Ciz
C 847	12.4	37.6	39	2	AAT87251	Aat87251 IL-4 2'NH	C 920	12.2	37.0	21	2	AAT40679	Aat40679 Corynebac
C 848	12.4	37.6	39	2	AAH91823	Aah91823 Porphorym	C 921	12.2	37.0	21	2	AAT40674	Aat40674 Corynebac
C 849	12.4	37.6	40	2	AQ38079	Aeq38079 Oligonucl	C 922	12.2	37.0	21	2	AAT40684	Aat40684 Corynebac
C 850	12.4	37.6	41	3	AAZ28988	Aaz28988 Promoter	C 923	12.2	37.0	21	2	AAT40689	Aat40689 Corynebac
C 851	12.4	37.6	41	3	AAH75683	Aah75683 Human thr	C 924	12.2	37.0	22	2	AAT40688	Aat40688 Corynebac
C 852	12.4	37.6	41	12	ADM32636	Adm32636 2'10-16	C 925	12.2	37.0	22	2	AAT40678	Aat40678 Corynebac
C 853	12.4	37.6	44	2	AAV74307	Aav74307 Streptomy	C 926	12.2	37.0	22	2	AAT40692	Aat40692 Corynebac
C 854	12.4	37.6	44	6	ADI46081	Adi46081 Single st	C 927	12.2	37.0	22	2	AAT40683	Aat40683 Corynebac
C 855	12.4	37.6	44	6	ADI46080	Adi46080 Single st	C 928	12.2	37.0	22	2	AAT40673	Aat40673 Corynebac
C 856	12.4	37.6	44	10	ABZ37321	Abz37321 URE adapt	C 929	12.2	37.0	22	6	ABK52070	Abk52070 Cytokine
C 857	12.4	37.6	46	2	AAV24262	AAV24262 Chimeric	C 930	12.2	37.0	22	12	ADNO2051	Adn02051 Escherich
C 858	12.4	37.6	46	2	AAH91870	Aah91870 Porphorym	C 931	12.2	37.0	22	12	ADNO2044	Adn02044 Escherich
C 859	12.4	37.6	46	2	AAH00106	Aax00106 Human ant	C 932	12.2	37.0	23	2	AAT40682	Aat40682 Corynebac
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C 861	12.4	37.6	46	3	AAZ69215	Aaz69215 Human L c	C 934	12.2	37.0	23	2	AAT40677	Aat40677 Corynebac
C 862	12.4	37.6	46	4	AAH69103	Aah69103 Human L c	C 935	12.2	37.0	23	2	AAT40691	Aat40691 Corynebac
C 863	12.4	37.6	46	4	AAH75080	Aah75080 Nucleotid	C 936	12.2	37.0	23	2	AAV72571	Aav72571 Thyroglob
C 864	12.4	37.6	46	4	AAH76618	Aah76618 Human Ig	C 937	12.2	37.0	23	3	AAA60648	Aaa60648 Human HNR
C 865	12.4	37.6	46	5	AAH74259	Aah74259 Nucleotid	C 938	12.2	37.0	23	2	AAT40681	Aat40681 Corynebac
C 866	12.4	37.6	46	5	AAH69159	Aaf69159 Human L c	C 939	12.2	37.0	24	2	AAT40686	Aat40686 Corynebac
C 867	12.4	37.6	46	6	ABL94795	Abi94795 Joint dis	C 940	12.2	37.0	24	2	AAT40676	Aat40676 Corynebac
C 868	12.4	37.6	46	6	ABA90126	AbA90126 Oestrogen	C 941	12.2	37.0	24	2	AAT40690	Aat40690 Corynebac
C 869	12.4	37.6	46	6	ABA90159	AbA90159 Oestrogen	C 942	12.2	37.0	24	2	AAT98070	Aat98070 Erwinia c
C 870	12.4	37.6	46	6	ABA90145	AbA90145 Oestrogen	C 943	12.2	37.0	24	2	AAT98061	Aat98061 Erwinia c
C 871	12.4	37.6	46	6	ABA90127	AbA90127 Oestrogen	C 944	12.2	37.0	24	6	ABQ09354	Abq09354 Oligonucl
C 872	12.4	37.6	46	6	ABA90132	AbA90132 Oestrogen	C 945	12.2	37.0	24	6	ABQ02739	Abq02739 Oligonucl
C 873	12.4	37.6	46	6	ABQ87854	Abq87854 Human ESR	C 946	12.2	37.0	24	6	ABQ09395	Abq09395 Oligonucl
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C 875	12.4	37.6	46	6	ABQ87841	Abq87841 Human ESR	C 948	12.2	37.0	25	3	AAC63528	Aac63528 PCR prime
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C 883	12.4	37.6	46	10	ADC64137	Adc64137 Polyhydro	C 956	12.2	37.0	25	9	ACK30659	ACK30659 Human mic
C 884	12.4	37.6	46	10	ABT31647	Abt31647 Angiogene	C 957	12.2	37.0	25	9	ACK35822	ACK35822 Human mic
C 885	12.4	37.6	46	12	ADG01902	Adg01902 Carbon bl	C 958	12.2	37.0	25	9	ACI78916	ACI78916 Human mic
C 886	12.4	37.6	46	12	ADO33816	Ado33816 Parathyro	C 959	12.2	37.0	25	9	ACI66603	ACI66603 Human mic
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C 897	12.4	37.6	50	6	ABT12663	Abt12663 Orestes s	C 970	12.2	37.0	26	2	AAV55865	AAV55865 Plaemid v

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c 977 12.2 37.0 27 2 AAX26925 Antisense
c 978 12.2 37.0 27 2 AAX19675 Cytomegal
c 979 12.2 37.0 27 3 AAZ35476 Cytomegal
c 980 12.2 37.0 27 3 AAZ54367 Primer fo
c 981 12.2 37.0 27 3 AAZ35457 Cytomegal
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ALIGNMENTS

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RESULT 1
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ID AAD43285 standard; DNA; 34 BP.
AC AAD43285;
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XX 14-NOV-2002 (first entry)
DE ST650 HCV specific probe.
XX
XX Amplification; target nucleic acid; probe; ss.
XX
XX Hepatitis C virus.
XX
XX Key Location/Qualifiers
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XX
XX 04-SEP-2002.
XX
XX 27-FEB-2002; 2002EP-00004483.
XX
XX 02-MAR-2001; 2001EP-00105172.
XX
XX (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Jaeger S;
XX
XX WPI; 2002-610695/66.
XX
XX Amplification of a target nucleic acid region using a specific control
XX sequence.
XX
XX Example 1; Fig 2; 28pp; English.
XX
XX The invention relates to a method for amplification of a target nucleic
XX acid region in a sample using a specific control sequence. The invention
XX is also directed to a method of determination of a target nucleic acid
XX using a special control nucleic acid. Nucleic acids of the invention are
XX used as a control in a reaction for amplifying target nucleic acids and
XX as a control in a hybridisation reaction for determination of target
XX nucleic acids. The present sequence is HCV (Hepatitis C virus) type I DNA
XX specific probe. This probe is used to illustrate the methods of the
XX invention. Note: This sequence is stated to be same as that shown as SEQ
XX ID NO:3 in sequence listing. However this sequence has additional C at
XX its 3' end
XX
XX Sequence 34 BP; 6 A; 13 C; 8 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 33; DB 6; Length 34;
XX Best Local Similarity 100.0%; Pred. No. 5.3e-05;
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CGGTGTTACTCACCCTCCGACAGACCACTATGCG 33
XX DB 1 CGGTGTTACTCACCCTCCGACAGACCACTATGCG 33
XX
XX
XX RESULT 2
XX AAD43737
XX ID AAD43737 standard; DNA; 34 BP.
XX
XX AC AAD43737;
XX
XX 07-AUG-2003 (revised)
XX 14-NOV-2002 (first entry)
XX
XX ST650 HCV specific probe.
XX
XX Amplification; target nucleic acid; control nucleic acid; probe; ss.
XX
XX Hepatitis C virus.
XX
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XX      04-SEP-2002.
XX
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XX
XX      02-MAR-2001; 2001EP-00105172.
XX      (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX      Jaeger S;
XX
XX      WPI; 2002-610694/66.
XX
XX      Amplification of a target nucleic acid region using control sequences.
XX
XX      Example 1; Fig 2; 29pp; English.
XX
XX      The invention relates to a method for amplification of a target nucleic
XX      acid region. The method is useful for amplification of a nucleic acid
XX      molecule using control nucleic acid sequences. The control nucleic acid
XX      sequences are at least in part parallel-complementary to the sequence of
XX      the target nucleic acid. The present sequence is ST650 HCV specific
XX      probe. Note: This sequence is stated to be same as that shown as SEQ ID
XX      NO:3 in sequence listing. However this sequence has additional C at its
XX      3' end. (Updated on 07-AUG-2003 to correct OS field.)
XX
XX      Sequence 34 BP; 6 A; 13 C; 8 G; 7 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 33; DB 6; Length 34;
XX      Best Local Similarity 100.0%; Pred. No. 5.3e-05;
XX      Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX      QY      1 CGGTGTACTACCGTTCGCGAGACCACCTATGCG 33
XX      |||||
XX      DB      1 CGGTGTACTACCGTTCGCGAGACCACCTATGCG 33
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XX      RESULT 3
XX      ACF35782
XX      ID      ACF35782 standard; DNA; 31 BP.
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XX      AC      ACF35782;
XX
XX      DT      06-NOV-2003 (first entry)
XX
XX      DE      Nucleotide sequence of a HCV-specific probe ST650p2.

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XX      Nucleic acid purification; nucleic acid amplification; cancer;
XX      sickle cell anemia; blood screening; HCV; probe; ss.
XX
XX      Hepatitis C virus.
XX
XX      Key      Location/Qualifiers
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XX      modified_base 24. .32 /*tag= b
XX      modified_base 34 /note= "FAM label incorporated between these nucleotides"
XX
XX      PN      WO2003057910-A2.
XX
XX      17-JUL-2003.
XX
XX      04-JAN-2003; 2003WO-EP0000039.
XX
XX      08-JAN-2002; 2002US-0347327P.
XX      (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX      Pinsl-Ober J, Wenzig P, Weindel K, Bartl K, Schoenbrunner R;
XX      Malhotra K, O'donnell P, Kyger E;
XX      WPI; 2003-587135/55.
XX
XX      Purification and amplification of target nucleic acid from biological
XX      sample used in diagnosis of cancer or in screening blood, involves
XX      binding target nucleic acid with unmodified silica surface, followed by
XX      amplification.
XX
XX      Example 1; Page 23; 33pp; English.
XX
XX      The invention relates to purification and amplification of target nucleic
XX      acid from biological sample. The method involves and binding target
XX      nucleic acid (TNA) in the sample with a material comprising an unmodified
XX      silica surface, separating the material from the sample and amplifying
XX      TNA in the presence of the material. The method is useful in diagnosis of
XX      certain diseases such as inherited diseases like sickle cell anemia and
XX      certain types of cancer or in screening blood for presence of target
XX      nucleic acid from virus. The method improves reaction efficiency and
XX      detection sensitivity of target nucleic acids. The present sequence
XX      represents a hepatitis C virus (HCV)-specific probe used in the method of
XX      the invention
XX
XX      Sequence 31 BP; 6 A; 11 C; 7 G; 7 T; 0 U; 0 Other;
XX
XX      Query Match      93.9%; Score 31; DB 9; Length 31;
XX      Best Local Similarity 100.0%; Pred. No. 0.00042;
XX      Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 CGGTGTACTACCGTTCGCGAGACCACCTATG 31
XX      |||||
XX      DB      1 CGGTGTACTACCGTTCGCGAGACCACCTATG 31
XX
XX      RESULT 4
XX      AAT39735/c
XX      ID      AAT39735 standard; DNA; 36 BP.
XX
XX      AC      AAT39735;
XX
XX      DT      09-APR-1997 (first entry)
XX
XX      DE      Hepatitis C virus PCR probe S1, based on nucleotides 121-157.
XX
XX      KW      Hepatitis C virus; HCV; polymerase chain reaction; amplification;
XX      replication; non-lymphoblastoid cell; monkey kidney cell;
XX      hybridisation probe; ss.

```

XX OS Synthetic.
 XX PN WO9624662-A1.
 XX PD 15-AUG-1996.
 XX PF 10-FEB-1995; 95WO-IT0000016.
 XX PR 10-FEB-1995; 95WO-IT0000016.
 XX PA (CNR) CONSIGLIO NAZ DELLE RICERCHE.
 XX PI Ravagnan G, Battaglia M, Carloni G, Ponzetto A, Iacovacci S;
 XX DR WPI; 1996-384435/38.
 XX PT Replication of hepatitis C virus in non-lymphoblastoid mammalian cells -
 XX PT useful for studies of HCV replication, prodn. of vaccines or viral
 XX PT antigens, etc.
 XX PS Disclosure; Page 8; 25pp; English.
 XX CC Hepatitis C virus can be replicated in non-lymphoblastoid mammalian cells
 CC by first incubating an HCV sample with the cells until an infecting
 CC amount of HCV has been absorbed. Infected cells are then washed and
 CC incubated under growth conditions. In an example, the presence of HCV in
 CC culture medium of monkey kidney cells inoculated with HCV-infected serum
 CC was verified by PCR amplification using two external primers (OUI and
 CC OUI2, see AAT39731 and AAT39732) and two internal primers (INI and IN2,
 CC see AAT39733 and AAT39734). The amplified products were identified by
 CC hybridisation to labelled probe S1 (see AAT39735). Small amounts of virus
 CC were shown to be released into the culture medium from secondary
 CC cultures. Control (non-inoculated) cells were negative for presence of
 CC viral genome
 XX SQ Sequence 36 BP; 9 A; 9 C; 11 G; 7 T; 0 U; 0 Other;
 Query Match 92.1%; Score 30.4; DB 2; Length 36;
 Best Local Similarity 96.9%; Pred. No. 0.00079;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CGGTGACTCACCCTCCGAGACCACTATGG 32
 Db |||||||
 32 CGGTGACTCACCCTCCGAGACCACTATGG 1
 RESULT 5
 AAV15324/c
 ID AAV15324 standard; DNA; 29 BP.
 XX AC AAV15324;
 XX DT 25-MAR-2003 (revised)
 XX DT 28-MAY-1998 (first entry)
 XX DE Hepatitis C virus probe HCV40.
 XX KW Hepatitis C virus; HCV; PCR; detection; reverse transcription; probe;
 KW enzyme immunoassay; viral RNA; ss.
 XX OS Synthetic.
 OS Hepatitis C virus.
 PN WO9746716-A1.
 XX PD 11-DEC-1997.
 XX PF 03-JUN-1997; 97WO-IT000128.
 XX PR 07-JUN-1996; 96IT-RM000404.
 XX PA (WESA) WABCO BV.

XX PI Bosio P, Strumia C, Clemenza F;
 XX DR WPI; 1998-042222/04.
 XX PT Detection of hepatitis C virus - by reverse transcription, single-step
 XX PT PCR and detection by DNA enzyme immunoassay.
 XX PS Disclosure; Page 4; 26pp; English.
 XX CC The present sequence represents a probe involved in the method of the
 CC present invention for detecting hepatitis C virus (HCV). The method
 CC comprises: (a) reverse-transcribing the viral RNA; (b) amplifying the
 CC resulting cDNA by a single polymerase chain reaction in a reaction
 CC mixture having a Mg2+/Taq polymerase ratio of about 100 nmole/enzyme unit
 CC ; and (c) detecting the amplification product by DEIA (DNA enzyme
 CC immunoassay) using an oligonucleotide probe. The sensitivity of this
 CC method is at least equal to that achievable by more complicated assays
 CC using nested PCR. (Updated on 25-MAR-2003 to correct PR field.)
 XX SQ Sequence 29 BP; 7 A; 7 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 83.0%; Score 27.4; DB 2; Length 29;
 Best Local Similarity 96.6%; Pred. No. 0.017;
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 TGTACTCACCCTCCGAGACCACTATGG 32
 Db |||||||
 29 TGTACTCACCCTCCGAGACCACTATGG 1
 RESULT 6
 AAL40116
 ID AAL40116 standard; DNA; 41 BP.
 XX AC AAL40116;
 XX DT 13-SEP-2002 (first entry)
 XX DE Pathogenic microorganism detecting PCR primer SEQ ID No 42.
 XX KW Tuberculosis; Mycobacterium; bovis; BCG; africanum; microti; canottii;
 KW monitoring therapy; pathogenic microorganism; PCR; primer; ss.
 XX OS Unidentified.
 XX PN WO200252043-A1.
 XX PD 04-JUL-2002.
 XX PF 26-DEC-2001; 2001WO-JP011422.
 XX PR 26-DEC-2000; 2000JP-00396222.
 XX PR 26-DEC-2000; 2000JP-00396321.
 XX PR 29-JUN-2001; 2001JP-00199552.
 XX PR 13-SEP-2001; 2001JP-00278920.
 XX PA (TAKI) TAKARA SHUZO CO LTD.
 XX PI Shimada M, Hino F, Kato I;
 XX DR WPI; 2002-500769/53.
 XX PT Detecting pathogenic microorganisms with oligonucleotide probes and
 XX PT primers, useful in disease diagnosis and monitoring therapy.
 XX PS Claim 57; Page 97; 106pp; Japanese.
 XX CC The invention relates to a probe containing a 410 or 20 base pair
 CC sequence, given in the specification. It is capable of detecting the
 CC tuberculosis bacterial group including Mycobacterium tuberculosis,
 CC Mycobacterium bovis BCG, Mycobacterium africanum, Mycobacterium microti
 CC and/or Mycobacterium canottii. The method is useful in disease diagnosis

CC and monitoring therapy. This polynucleotide sequence represents a PCR
CC primer relating to the detection of pathogenic microorganisms of the
CC invention
XX
SQ Sequence 41 BP; 7 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 66.7%; Score 22; DB 6; Length 41;
Best Local Similarity 97.1%; Pred. No. 4.8;
Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CGGTGTACTACACC-GTTCCGACAGACCACTATGGC 33
Db 5 CGGTGTACTACCGGTTCCGACAGACCACTATGGC 38

RESULT 7
AAAX37635/C
ID AAAX37635 standard; DNA; 41 BP.
XX
AC AAAX37635;
XX
DT 08-JUL-1999 (first entry)
XX
DE HCV detecting primer #5.
XX
KW Detection; HCV; real time; PCR; reporter; fluorescent; primer; quencher;
KW fluorescence resonance energy transfer; ss.
XX
OS Synthetic.
OS Hepatitis C virus; Virus.
XX
FN JP11103899-A.
XX
PD 20-APR-1999.
XX
PF 30-SEP-1997; 97JP-00283042.
XX
PR 30-SEP-1997; 97JP-00283042.
XX
PA (TOKR-) ZH TOKYO RINGSHO IGAKU SOGO KENKYUSHO.
PA (SRLS-) SRL KK.
XX
DR WPI; 1999-305862/26.
XX
Measurement of HCV gene using real time detecting PCR and primer and
PT probe - is highly sensitive.
XX
PS Claim 5; Page 6; 8pp; Japanese..
XX
This invention describes a method for the measurement of an HCV gene by a
CC real time detecting PCR. The invention also describes a method where a
CC reporter fluorescent colour and a quencher fluorescent colour are
CC combined to an oligonucleotide and the fluorescence of the reporter
CC fluorescent colour is controlled by fluorescence resonance energy
CC transfer. The method can measure HCV exactly with high sensitivity
XX
SQ Sequence 41 BP; 9 A; 11 C; 13 G; 8 T; 0 U; 0 Other;

Query Match 63.6%; Score 21; DB 2; Length 41;
Best Local Similarity 97.0%; Pred. No. 13;
Matches 32; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CGGTGTACTACACC-GTTCCGACAGACCACTATGG 32
Db 33 CGGTGTACTACCGGTTCCGACAGACCACTATGG 1

RESULT 8
AAA74622
ID AAA74622 standard; DNA; 26 BP.
XX
AC AAA74622;
XX

DT 08-JAN-2001 (first entry)
XX
DE HCV-specific amplification primer C133R26.
XX
KW Hepatitis C virus; HCV; HCV detection; amplification primer; ss.
XX
OS Hepatitis C virus.
XX
FN EP1026262-A2.
XX
PD 09-AUG-2000.
XX
PF 01-FEB-2000; 2000EP-00300763.
XX
PR 03-FEB-1999; 99US-0118497P.
XX
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI Linnen JM, Gorman KM;
XX
DR WPI; 2000-507254/46.
XX
DT Detecting hepatitis C virus in biological sample involves amplifying
PT reverse transcribed products of virus RNA using amplification primers
PT whose sequences correspond to 5' or 3' non-coding region of the virus
PT RNA.
XX
PS Claim 30; Page 27; 28pp; English.
XX
CC The present sequence is an amplification primer used in a method for
CC detecting hepatitis C virus (HCV) RNA in biological samples. The HCV RNA
CC is reverse transcribed to generate cDNA. This is then amplified using
CC primers, including the present sequence, corresponding to the 5' or 3'
CC non-coding region of HCV. The method is useful for the diagnosis of HCV
CC infection in patients, in testing the efficacy of anti-HCV therapeutic
CC regimes, and in screening blood for HCV-infected samples. The method
CC provides an improved single-round, reverse transcription/amplification
CC assay which detects low copy levels of HCV RNA. The primers and assay
CC system are designed to allow the co-amplification of multiple regions of
CC the HCV genome, multiple viral species, and an internal positive control
CC (IPC) RNA (or DNA). Simultaneous amplification/detection of multiple
CC regions of the HCV genome increases assay sensitivity and the co-
CC amplification of an IPC decreases the likelihood of false negative
CC results because of PCR inhibition
XX
SQ Sequence 26 BP; 4 A; 10 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 61.8%; Score 20.4; DB 3; Length 26;
Best Local Similarity 95.5%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CGGTTCGACAGACCACTATGGC 33
Db 1 CGGTTCGACAGACCACTATGGC 22

RESULT 9
AAT05216
ID AAT05216 standard; DNA; 28 BP.
XX
AC AAT05216;
XX
DT 13-JUN-1996 (first entry)
XX
DE Hepatitis C virus antisense oligonucleotide A161.
XX
KW Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;
KW translation; in vivo; ex vivo; in vitro; treatment; prevention;
KW infection; antisense; non coding; region; NCR; core region; ss.
XX
OS Synthetic.
XX
FN WO9530746-A1.

```

XX 16-NOV-1995.
XX
XX PD
XX PF 08-MAY-1995; 95WO-US005812.
XX PR 10-MAY-1994; 94US-00240382.
XX PA (GEO ) GEN HOSPITAL CORP.
XX PI Wakita T, Wands JR;
XX WPI; 1995-404113/51.
XX
XX New anti:sense hepatitis C virus oligo:nucleotide(s) - used for
XX inhibiting HCV RNA translation, for the treatment or prevention of HCV
XX infection.
XX
XX Claim 1; Page 27; 50pp; English.
XX
XX The present oligonucleotide (ON) inhibits the expression of hepatitis C
XX virus (HCV) RNA, specifically HCV type II and type III protein synthesis
XX is inhibited by 81% and 76%, respectively. The ONs of the invention
XX inhibit translation of HCV types I-V RNA in vivo, ex vivo or in vitro,
XX and can therefore be used to treat or prevent HCV infection. The
XX antisense ONs comprise 10-28 nucleotides complementary to the entire HCV
XX 5'-non-coding and part of the core region. The A or S in the ONs name
XX denotes antisense or sense, and the no. indicates the position of the 5'-
XX end of the ON. The ON was tested at 10 fold molar excess to HCV RNA
XX
XX Sequence 28 BP; 5 A; 11 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 61.8%; Score 20.4; DB 2; Length 28;
XX Best Local Similarity 95.5%; Pred. No. 24;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 12 CCGTTCGCGAGACCACTATGGC 33
DB 4 CCGTTCGCGAGACCACTATGGC 25

RESULT 10
AAZ57751
ID AAZ57751 standard; DNA; 28 BP.
AC
AC AAZ57751;
XX
XX DT 05-APR-2000 (first entry)
XX
XX Hepatitis C virus antisense inhibitor oligonucleotide A161.
XX
XX Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;
XX anti-inflammatory; translation inhibition; HCV infection; virucide.
XX
XX Hepatitis C virus.
XX
XX US6001990-A.
XX
XX 14-DEC-1999.
XX
XX 07-JUN-1995; 95US-00474700.
XX
XX 10-MAY-1994; 94US-00240382.
XX
XX (GEO ) GEN HOSPITAL CORP.
XX
XX Moradpour D, Wands JR, Wakita T;
XX
XX WPI; 2000-104900/09.
XX
XX Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating
XX Hepatitis C virus infections.
XX
XX Claim 4; Col 21; 31pp; English.

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```

XX This sequence is an antisense oligonucleotide that hybridises to
XX Hepatitis C virus (HCV) RNA, under physiological conditions. The
XX invention relates to HCV antisense oligonucleotides, and also for a
XX vector comprising a nucleotide sequence which is transcribed in an animal
XX cell to generate an antisense oligonucleotide. The oligonucleotides have
XX virucide, hepatotropic and anti-inflammatory activity, and are useful for
XX treating HCV infection by inhibiting translation of type I-V HCV RNA.
XX Hepatitis C virus is a positive strand RNA virus, and is the major
XX causative agent of post-transfusion hepatitis. Persistent HCV infection
XX can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma
XX
XX Sequence 28 BP; 5 A; 11 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 61.8%; Score 20.4; DB 3; Length 28;
XX Best Local Similarity 95.5%; Pred. No. 24;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 12 CCGTTCGCGAGACCACTATGGC 33
DB 4 CCGTTCGCGAGACCACTATGGC 25

RESULT 11
ADC54071/c
ID ADC54071 standard; DNA; 28 BP.
XX
XX AC ADC54071;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX HCV 5'UTR signal amplification probe, SEQ ID NO:22.
XX
XX HCV; hepatitis C virus; classification; interferon therapy; 5'UTR;
XX signal amplification; probe; ss.
XX
XX Hepatitis C virus.
XX
XX JP2002345467-A.
XX
XX 03-DEC-2002.
XX
XX 17-APR-2001; 2001JP-00118810.
XX
XX 23-OCT-2000; 2000JP-00322567.
XX
XX (SRLS-) SRL KK.
XX
XX WPI; 2003-460879/44.
XX
XX Probe and method for classification of hepatitis C virus (HCV) types used
XX for forecast of therapeutic effect of interferon administration.
XX
XX Disclosure; SEQ ID NO 22; 15pp; Japanese.
XX
XX The invention relates to a nucleic acid probe for the classification of
XX hepatitis C virus (HCV) into 3 genotypes. The 3 HCV genotypes are MH1Am1
XX (type 1), MH2Am1 (type 2) and MH3G3C-MH3G3C' (type 3). The probe can be
XX used to classify HCV type to enable prediction of the success or
XX otherwise of interferon therapy in a patient. Sequences ADC54068-ADC54073
XX represent HCV 5'UTR signal amplification probes. Note: The present
XX sequence is given in the sequence listing, but is not further referred to
XX in the specification.
XX
XX Sequence 28 BP; 6 A; 6 C; 11 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 61.8%; Score 20.4; DB 10; Length 28;
XX Best Local Similarity 95.5%; Pred. No. 24;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 12 CCGTTCGCGAGACCACTATGGC 33
DB 26 CCGTTCGCGAGACCACTATGGC 5

```


XX (TORU) TONEN CORP.
PA (TANA/) TANAKA E.
PA (MATS/) MATSUMOTO A.
XX
XX WPI; 1995-370481/48.
XX
XX Determination of nucleic acid copy number by competitive PCR - using
PT primers which anneal to target and to a competitor mol. of known copy
PT number.
XX
XX Disclosure; Page 6; 12pp; Japanese.
XX
XX The nucleic acid copy no. of a sample can be determined by competitive
CC PCR, using primers which anneal to the target and to a competitor mol. of
CC known copy no. . In a specific example a HCV gene was cloned using RT-PCR,
CC to give the plasmid DNA pK15 into which a 5 bp 5'-UTR deletion was
CC introduced to give pK15/D. Then a sample of HCV patient serum was
CC analysed using the claimed method, the competitor DNAs pK9 and pK11
CC (prepd. using the PCR primers AAT01493-97) and appropriate primers
XX
XX Sequence 22 BP; 5 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 60.6%; Score 20; DB 2; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 34;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 14 GTTCGGCAGACCACTATGGC 33
XX |||||
XX DB 21 GTTCGGCAGACCACTATGGC 2
XX
XX RESULT 15
XX ADP87801/C
XX ID ADP87801 standard; DNA; 24 BP.
XX AC
XX ADP87801;
XX
XX DT 09-SEP-2004 (first entry)
XX
XX DE TEX on microarray extended primer 2 #1.
XX
XX KW TEX; thermodynamic equilibrium extension of primers; primer; ss.
XX
XX OS Synthetic.
XX
XX XX US2004115643-A1.
XX
XX PN 17-JUN-2004.
XX
XX PD 12-DEC-2002; 2002US-00318416.
XX
XX PF 12-DEC-2002; 2002US-00318416.
XX
XX PR (LIZA/) LIZARDI P M.
XX (GRIB/) GRIBANOV O G.
XX
XX PA Lizardi PM, Gribanov OG;
XX
XX PI WPI; 2004-468050/44.
XX
XX DR Amplifying nucleic acid for detecting nucleic acid, by extension of one
XX or more primers using target templates having replication terminating
XX feature, dissociation of primer from templates to produce multiple
XX extended primers.
XX
XX PS Example; SEQ ID NO 34; 75pp; English.
XX
XX The invention relates to amplifying (M1) a nucleic acid, involving
XX contacting one or more extension primers (EP) and target templates (TT)
XX and incubating under conditions to promote interaction of (EP) and
XX templates, extension of (EP) using the interacting (TT), and dissociation
XX of the extended (EP) from (TT), to produce multiple extended (EP) from at

CC least one (TT), where each (TT) comprise a replication terminating
CC feature. In (M1), (EP) and target templates are incubated under
CC isothermal conditions or single set of conditions. The target templates
CC are nucleic acid sequences of interest. Each of (EP) comprises or
CC consists of a target complement portion, preferably nucleotides, where
CC the nucleotides consist of the target complement portion. Each (EP)
CC further comprises non-target complement portion. The method is known as
CC TEX (thermodynamic equilibrium extension of primers). The method is
CC useful for amplifying nucleic acid and for detecting nucleic acid
CC sequences which involves performing (M1), and detecting one or more of
CC the extended (EP). In (M1), only those sequences targeted by (EP) are
CC amplified, thus allowing specific sequences to be targeted for
CC amplification. Flexibility in the location of replication terminating
CC feature allows flexibility in targeting sequences. If a targeted sequence
CC is not present, the sequence will not be amplified. Multiple sequences
CC can be amplified in the same reaction by targeting multiple sequences
CC with (EP). Simultaneous amplification and detection is facilitated using
CC detection probes associated with a substrate. Multiplex detection can be
CC facilitate by an array of detection probes with different detection
CC probes at different locations of a substrate. The present sequence is a
CC synthetic primer sequence used to demonstrate the method of the
CC invention.
XX
XX SQ Sequence 24 BP; 6 A; 5 C; 9 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 60.6%; Score 20; DB 12; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 35;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 14 GTTCGGCAGACCACTATGGC 33
XX |||||
XX DB 24 GTTCGGCAGACCACTATGGC 5
XX
XX RESULT 16
XX ABZ75892/C
XX ID ABZ75892 standard; DNA; 25 BP.
XX AC
XX ABZ75892;
XX
XX DT 15-MAY-2003 (first entry)
XX
XX DE HCV RNA detecting primer RJD-6.
XX
XX KW HCV; hepatic disorder; envelope glycoprotein; DC-SIGN; DC-SIGNR; primer;
XX hepatoprotective; virucide; cytostatic; protein therapy; PCR; ss.
XX
XX OS Hepatitis C virus.
XX
XX PN WO2003000024-A2.
XX
XX PD 03-JAN-2003.
XX
XX PF 26-JUN-2002; 2002WO-US020875.
XX
XX PR 26-JUN-2001; 2001US-00891894.
XX
XX PA (PROG-) PROGENICS PHARM INC.
XX
XX PI Olson WC, Maddon PJ;
XX
XX DR WPI; 2003-267852/26.
XX
XX PT Treating hepatitis, cirrhosis or hepatocellular carcinoma by inhibiting
XX binding between HCV envelope glycoproteins and DC-SIGN/DC-SIGNR proteins
XX on the surface of cells.
XX
XX PS Disclosure; Page 119; 165pp; English.
XX
XX The invention relates to methods and agents for diagnosing and treating
XX Hepatitis C Virus (HCV) infections and other hepatic disorders based on
XX binding between HCV envelope glycoproteins and DC-SIGN and DC-SIGNR
XX proteins on the surface of cells. The methods may be used to identify

CC agents (antibodies, peptides and other non-peptidyl agents) that may be
CC administered to treat hepatitis, cirrhosis or hepatocellular carcinomas
CC and to diagnose these disease. The present sequence represents a primer
CC used in a hybridisation assay to detect HCV RNA
XX
SQ Sequence 25 BP; 6 A; 5 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 60.6%; Score 20; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GTTCGCAGACCACTATGGC 33
Db 25 GTTCGCAGACCACTATGGC 6
|||||

RESULT 17
ADH79952/c
ID ADH79952 standard; DNA; 25 BP.
XX
AC ADH79952;
XX
DT 22-APR-2004 (first entry)
XX
DE HCV RT-PCR primer RJD-6.
XX
KW DC-SIGN; HCV infection; liver disease; hepatocellular carcinoma;
KW hepatitis; cirrhosis; DC-SIGN; HCV envelope glycoprotein; cytostatic;
KW anti-inflammatory; hepatotropic; virucide; RT-PCR; reverse transcriptase;
KW primer; ss; RJD-6.
XX
OS Hepatitis C virus.
XX
XX
XX US2003232745-A1.
XX
XX
XX 18-DEC-2003.
XX
XX 24-DEC-2002; 2002US-00328997.
XX
XX 26-JUN-2001; 2001US-0300971P.
XX
XX (MADD/) MADDON P J.
XX (GARD/) GARDNER J P.
XX
PI Olson WC, Maddon PJ, Gardner JP;
XX
XX WPI; 2004-061306/06.
XX
XX Use of DC-SIGN and DC-SIGNR proteins for inhibiting, preventing or
XX treating HCV infection and liver disease e.g. hepatitis or cirrhosis or
XX hepatocellular carcinoma.
XX
XX Disclosure; Page 33; 55pp; English.
XX
XX The invention relates to the use of DC-SIGN and DC-SIGNR proteins for
XX inhibiting, treating or preventing HCV infection and liver diseases such
XX as hepatocellular carcinoma, hepatitis or cirrhosis. The DC-SIGN and DC-
XX SIGNR protein are useful for inhibiting HCV infection, treating HCV
XX infection or treating or preventing liver disease e.g. hepatitis,
XX cirrhosis or hepatocellular carcinoma. Antibodies to the polypeptides,
XX the polypeptides or non-peptidyl agents can be used for inhibiting
XX binding of a DC-SIGNR or DC-SIGN protein to an HCV envelope glycoprotein.
XX This sequence represents an HCV reverse transcriptase PCR (RT-PCR) primer
XX used in the scope of the invention.
XX
SQ Sequence 25 BP; 6 A; 5 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 60.6%; Score 20; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC agents (antibodies, peptides and other non-peptidyl agents) that may be
CC administered to treat hepatitis, cirrhosis or hepatocellular carcinomas
CC and to diagnose these disease. The present sequence represents a primer
CC used in a hybridisation assay to detect HCV RNA
XX
SQ Sequence 25 BP; 6 A; 5 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 60.6%; Score 20; DB 12; Length 26;
Best Local Similarity 100.0%; Pred. No. 35;

Qy 14 GTTCGCAGACCACTATGGC 33
Db 25 GTTCGCAGACCACTATGGC 6
|||||

RESULT 18
ADP87799
ID ADP87799 standard; DNA; 26 BP.
XX
AC ADP87799;
XX
DT 09-SEP-2004 (first entry)
XX
DE TEX on microarray template N2.
XX
KW TEX; thermodynamic equilibrium extension of primers; template; ss.
XX
OS Synthetic.
XX
XX US2004115643-A1.
XX
XX 17-JUN-2004.
XX
XX 12-DEC-2002; 2002US-00318416.
XX
XX 12-DEC-2002; 2002US-00318416.
XX (LIZA/) LIZARDI P M.
XX (GRIB/) GRIBANOV O G.
XX
PI Lizardi PM, Gribanov OG;
XX
XX WPI; 2004-468050/44.
XX
XX Amplifying nucleic acid for detecting nucleic acid, by extension of one
XX or more primers using target templates having replication terminating
XX feature, dissociation of primer from templates to produce multiple
XX extended primers.
XX
XX Example; SEQ ID NO 32; 75pp; English.
XX
XX The invention relates to amplifying (M1) a nucleic acid, involving
XX contacting one or more extension primers (EP) and target templates (TT)
XX and incubating under conditions to promote interaction of (EP) and
XX templates, extension of (EP) using the interacting (TT), and dissociation
XX of the extended (EP) from (TT), to produce multiple extended (EP) from at
XX least one (TT), where each (TT) comprise a replication terminating
XX feature. In (M1), (EP) and target templates are incubated under
XX isothermal conditions or single set of conditions. The target templates
XX are nucleic acid sequences of interest. Each of (EP) comprises or
XX consists of a target complement portion, preferably nucleotides, where
XX the nucleotides consist of the target complement portion. Each (EP)
XX further comprises non-target complement portion. The method is known as
XX TEX (thermodynamic equilibrium extension of primers). The method is
XX useful for amplifying nucleic acid and for detecting nucleic acid
XX sequences which involves performing (M1), and detecting one or more of
XX the extended (EP). In (M1), only those sequences targeted by (EP) are
XX amplified, thus allowing specific sequences to be targeted for
XX amplification. Flexibility in the location of replication terminating
XX feature allows flexibility in targeting sequences. If a targeted sequence
XX is not present, the sequence will not be amplified. Multiple sequences
XX can be amplified in the same reaction by targeting multiple sequences
XX with (EP). Simultaneous amplification and detection is facilitated using
XX detection probes associated with a substrate. Multiplex detection can be
XX facilitated by an array of detection probes with different detection
XX probes at different locations of a substrate. The present sequence is a
XX synthetic template sequence used to demonstrate the method of the
XX invention.
XX
SQ Sequence 26 BP; 4 A; 11 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 60.6%; Score 20; DB 12; Length 26;
Best Local Similarity 100.0%; Pred. No. 35;

```
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 GTTCGCGAGACCACTATGGC 33
DB 1 GTTCGCGAGACCACTATGGC 20

RESULT 19
AAH25418
ID AAH25418 standard; DNA; 32 BP.
XX
AC AAH25418;
XX
DT 22-AUG-2001 (first entry)
XX
DE Detection probe for a HCV DNA fragment.
XX
KW Magnetic glass particle; nucleic acid purification; probe; ss.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "derivatisation with a pentamethine-di-
FT indocarbocyanine via an alkylphosphatidyl linker"
FT 15
FT /*tag= b
FT /note= "2-(amino-cyclohexyl)-propane-1,3-diol-linker
FT derivatised with 6-carboxy-fluorescein"
FT 31
FT modified_base 1
FT /*tag= c
FT /note= "derivatised with a 3'-terminal phosphate group"
XX
PN WO200137291-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-BP011459.
XX
PR 17-NOV-1999; 99EP-00122853.
XX
PR 12-MAY-2000; 2000EP-00110165.
XX
PA (HOFF ) ROCHE DIAGNOSTICS GMEH.
XX
PI Weindel K, Riedling M, Geiger A;
XX
WPI; 2001-381247/40.
XX
PT Novel composition of magnetic glass particles for purification of DNA or
PT RNA in automated processes.
XX
PS Example 7; Page 100; 105pp; English.
XX
CC The specification describes a composition of magnetic glass particles,
CC which contain at least one magnetic object with a mean diameter between 5
CC -500 nm. The composition is useful for the purification of nucleic acids.
CC The composition can be used to process large quantities of nucleic acid
CC samples, because it does not involve the particles being centrifuged or
CC the fluids being drawn through glass fiber filters. The present sequence
CC represents a probe for a HCV DNA fragment. The DNA fragment can be
CC purified using the method of the invention
XX
SQ Sequence 32 BP; 6 A; 11 C; 7 G; 7 T; 0 U; 1 Other;

Query Match 60.8%; Score 20; DB 4; Length 32;
Best Local Similarity 96.9%; Pred. No. 36;
Matches 31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 CGGTGTACTACCG-TTCGCGAGACCACTATG 31
DB 1 CGGTGTACTACCGTTCGCGAGACCACTATG 32
```

```
RESULT 20
AAH37631/c
ID AAH37631 standard; DNA; 37 BP.
XX
AC AAH37631;
XX
DT 08-JUL-1999 (first entry)
XX
DE HCV detecting primer #1.
XX
KW Detection; HCV; real time; PCR; reporter; fluorescent; primer; quencher;
KW fluorescence resonance energy transfer; ss.
XX
OS Synthetic.
OS Hepatitis C virus; Virus.
XX
PN JP11103899-A.
XX
PD 20-APR-1999.
XX
PF 30-SEP-1997; 97JP-00283042.
XX
PR 30-SEP-1997; 97JP-00283042.
XX
PA (TOKR-) ZH TOKYO TO RINSHO IGAKU SOGO KENKYUSHO.
PA (SRLS-) SRL KK.
XX
DR WPI; 1999-305862/26.
XX
PT Measurement of HCV gene using real time detecting PCR and primer and
PT probe - is highly sensitive.
XX
PS Claim 1; Page 6; 8pp; Japanese.
XX
CC This invention describes a method for the measurement of an HCV gene by a
CC real time detecting PCR. The invention also describes a method where a
CC reporter fluorescent colour and a quencher fluorescent colour are
CC combined to an oligonucleotide and the fluorescence of the reporter
CC fluorescent colour is controlled by fluorescence resonance energy
CC transfer. The method can measure HCV exactly with high sensitivity
XX
SQ Sequence 37 BP; 6 A; 15 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 60.6%; Score 20; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 GTTCGCGAGACCACTATGGC 33
DB 37 GTTCGCGAGACCACTATGGC 18

RESULT 21
AAH12490/c
ID AAH12490 standard; DNA; 38 BP.
XX
AC AAH12490;
XX
DT 18-JUL-1996 (first entry)
XX
DE Labelled oligonucleotide probe used in fluorescence quenching method.
XX
KW Probe length; fluorescence quenching; DNA binding; detection; cleavage;
KW fluorescein; FAM; DNA intercalator; ethidium bromide; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "labelled with FAM"
FT modified_base 37
```

```

FT      /*tag= b
FT      /note= "modified thymidine with bound TAMRA"
FN      US5491063-A.
XX
XX      13-FEB-1996.
XX
XX      01-SEP-1994; 94US-00299682.
XX
XX      01-SEP-1994; 94US-00299682.
XX
XX      (HOFF ) HOFFMANN LA ROCHE INC.
XX
XX      Watson RM, Fisher ME;
XX
XX      WPI; 1996-116318/12.
XX
XX      Fluorescence quenching of labelled single-stranded oligo-nucleotide(s) -
XX      with DNA-binding cpd., esp. for detecting nucleic acid sequences.
XX
XX      Example 5; Col 18; 18pp; English.
XX
XX      AAT12490 is a ss FAM-labelled oligonucleotide probe having secondary
XX      structure (a hairpin loop, no further information given in the
XX      specification) which augments fluorescence quenching. Additionally it has
XX      a modified thymidine base to which TAMRA (a quenching agent) is bound.
XX      Formation of a hairpin structure brings the FAM and TAMRA into close
XX      proximity, thereby quenching fluorescence. The probe is used to
XX      illustrate a method for controlling the light emission of fluorescently
XX      labelled probes. The method involves the addition of a DNA-binding cpd.,
XX      to a soln of the oligonucleotide, capable of interacting with the label
XX      to modify the light emission. The DNA-binding cpd. quenches the
XX      fluorescence of the label to an extent that depends on the length of the
XX      attached oligonucleotide, i.e. quenching is greater for the full-length
XX      probe than for its cleavage fragments, so an increase in fluorescence
XX      indicates probe cleavage, indicating the presence of the target sequence
XX
XX      Sequence 38 BP; 9 A; 9 C; 12 G; 8 T; 0 U; 0 Other;
XX
XX      Query Match      60.6%; Score 20; DB 2; Length 38;
XX      Best Local Similarity 96.9%; Pred. No. 37;
XX      Matches 31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 CGGTGTACTACCGGTTCCGCAGACCACTATG 31
Db      32 CGGTGTACTACCGGTTCCGCAGACCACTATG 1

RESULT 22
AAQ21851/c
ID      AAQ21851 standard; DNA; 30 BP.
XX
XX      AAQ21851;
XX
XX      25-MAR-2003 (revised)
XX      22-JUN-1992 (first entry)
XX
XX      HCV probe Alex89.
XX
XX      HCV-1; HCV27; Alex90; JH52; ss.
XX
XX      Synthetic.
XX
XX      WO9202642-A.
XX
XX      20-FEB-1992.
XX
XX      10-AUG-1990; 90US-00566209.
XX
XX      10-AUG-1990; 90US-00566209.
XX
XX      (CHIR ) CHIRON CORP.
XX

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PI      Houghton M, Choo QL, Kuo G, Weiner AJ, Uredea MS, Irvine BD;
PI      Kolberg JA;
XX
XX      WPI; 1992-080094/10.
XX
XX      Reagents for isolating, amplifying and detecting HCV polynucleotide(s) -
XX      used to monitor spread of blood-borne non-a, non-b hepatitis virus
XX      infection and screen blood samples for virus.
XX
XX      Example 1; Page 40; 67pp; English.
XX
XX      Extracted HCV27 RNA was reverse transcribed into ss cDNA using as primer
XX      either Alex90 (AAQ21763) or JH52 (AAQ21764). Alex90 is derived from
XX      nucleotides -312 to -283 of the HCV-1 genome (positive strand). JH52 is
XX      derived from -93 to -117 (negative strand). Detection of the amplified
XX      prods. was accomplished by Southern blotting, using Alex89 as the probe.
XX      Alex89 matches nucleotide numbers -203 to -175 of HCV RNA. (Updated on 25
XX      -MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
XX      field.)
XX
XX      Sequence 30 BP; 7 A; 7 C; 10 G; 6 T; 0 U; 0 Other;
XX
XX      Query Match      58.8%; Score 19.4; DB 2; Length 30;
XX      Best Local Similarity 95.2%; Pred. No. 67;
XX      Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12 CCGTTCGCGACACCACTATGG 32
Db      21 CGGTTCGCGACACCACTATGG 1

RESULT 23
AAT94722/c
ID      AAT94722 standard; DNA; 30 BP.
XX
XX      AC      AAT94722;
XX
XX      25-MAR-2003 (revised)
XX      16-FEB-1998 (first entry)
XX
XX      Hepatitis C virus Southern blot hybridisation probe.
XX
XX      Hepatitis C virus; HCV; reverse transcription; PCR; B lymphocyte;
XX      T lymphocyte; immunoassay; vaccine; antibody; probe; ss.
XX
XX      Synthetic.
XX      Hepatitis C virus.
XX
XX      US5679342-A.
XX
XX      21-OCT-1997.
XX
XX      27-JUL-1993; 93US-00097853.
XX
XX      18-NOV-1987; 87US-00122714.
XX      30-DEC-1987; 87US-00139886.
XX      26-FEB-1988; 88US-00161072.
XX      06-MAY-1988; 88US-00191263.
XX      26-OCT-1988; 88US-00263584.
XX      14-NOV-1988; 88US-00271450.
XX      17-MAR-1989; 89US-00325338.
XX      20-APR-1989; 89US-00341334.
XX      21-APR-1989; 89US-00353896.
XX      18-MAY-1989; 89US-00355002.
XX      18-MAY-1989; 89US-00355961.
XX      25-AUG-1989; 89US-00398667.
XX      21-DEC-1989; 89US-00456637.
XX      08-NOV-1990; 90US-00611365.
XX
XX      (CHIR ) CHIRON CORP.
XX
XX      Weiner AJ, Steimer KS, Houghton M;
XX

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```
DR WPI; 1997-525681/48.
XX
PT Cell line comprising B or T lymphocytes infected with HCV - for
PT production of HCV proteins for use in immunoassays, vaccines and drug
PT screening.
XX
XX Disclosure; Col 27; 22pp; English.
XX
CC A novel cell line has been developed which is infected with hepatitis C
CC virus (HCV). The cells in the cell line are B or T lymphocytes and are
CC capable of replicating HCV. The present sequence represents an
CC oligonucleotide probe used in the detection of HCV RNA by strand specific
CC RT-PCR. The cell line may be used for producing HCV proteins for use in
CC immunoassays for anti-HCV antibodies; for producing HCV protein-
CC containing fractions for use in vaccines; and for drug screening to
CC develop antiviral agents for treating hepatitis C. (Updated on 25-MAR-
CC 2003 to correct PF field.)
XX
SQ Sequence 30 BP; 7 A; 7 C; 10 G; 6 T; 0 U; 0 Other;
Query Match 58.8%; Score 19.4; DB 2; Length 30;
Best Local Similarity 95.2%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCGTTCGCGAGACCACTATGG 32
Db 21 CCGTTCGCGAGACCACTATGG 1
RESULT 24
AAZ27492/c
ID AAZ27492 standard; DNA; 30 BP.
XX
AC AAZ27492;
XX
DT 27-AUG-2003 (revised)
DT 20-MAR-2003 (revised)
DT 13-DEC-1999 (first entry)
XX
DE Probe for HCV RNA.
XX
KW Probe; HCV; detection; diagnosis; HCV infection; therapy;
KW antiviral agent; viral replication; ss.
XX
OS Hepatitis C virus.
XX
PN US5968775-A.
XX
PD 19-OCT-1999.
XX
PF 10-MAY-1995; 95US-00438435.
XX
PR 18-NOV-1987; 87US-00122714.
PR 30-DEC-1987; 87US-00139886.
PR 26-FEB-1988; 88US-00161072.
PR 06-MAY-1988; 88US-00191263.
PR 26-OCT-1988; 88US-00263584.
PR 14-NOV-1988; 88US-00271450.
PR 18-NOV-1988; 88WO-US004125.
PR 17-MAR-1989; 89US-00325338.
PR 20-APR-1989; 89US-00341334.
PR 21-APR-1989; 89US-00353896.
PR 18-MAY-1989; 89US-00355002.
PR 18-MAY-1989; 89US-00355961.
PR 25-AUG-1989; 89US-00398667.
PR 21-DEC-1989; 89US-00456637.
PR 08-NOV-1990; 90US-00611965.
PR 27-JUL-1993; 93US-00097853.
XX
XX (CHIR ) CHIRON CORP.
PA
XX
XX Weiner AJ, Steimer KS, Houghton M;
XX
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```
DR WPI; 1999-590406/50.
XX
PT Use of extracorporeal cell systems infected with hepatitis C virus in the
PT detection of an anti-HCV antibody.
XX
XX Example; Col 27; 21pp; English.
XX
CC This sequence represents a probe for hepatitis c virus (HCV) RNA. The
CC invention relates to a method of preparing a composition for the
CC detection of an anti-HCV antibody comprises: (a) purifying or partially
CC purifying HCV virus particles or polypeptides from a cell line infected
CC with HCV, where the cells in the cell line are B lymphocytes or T
CC lymphocytes, and are capable of replicating HCV; and (b) fixing the
CC particles or polypeptides to a solid phase. The method is useful in the
CC diagnosis, treatment and prevention of HCV infection. The HCV infected
CC cell systems can also be used screening programs to develop antiviral
CC agents for treating HCV. The antiviral agents identified this way may
CC block infection of the cell systems or may prevent viral replication in
CC infected cells. (Updated on 20-MAR-2003 to correct PR field.) (Updated on
CC 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 30 BP; 7 A; 7 C; 10 G; 6 T; 0 U; 0 Other;
Query Match 58.8%; Score 19.4; DB 2; Length 30;
Best Local Similarity 95.2%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCGTTCGCGAGACCACTATGG 32
Db 21 CCGTTCGCGAGACCACTATGG 1
RESULT 25
AAA75276/c
ID AAA75276 standard; DNA; 30 BP.
XX
AC AAA75276;
XX
DT 15-JAN-2001 (first entry)
XX
DE Probe used to isolate HCV cDNA clone 18g.
XX
KW Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
KW viral infectivity; viral replication; probe; ss.
XX
OS Hepatitis C virus.
XX
PN EP1034785-A2.
XX
PD 13-SEP-2000.
XX
PF 16-MAR-1990; 2000EP-00109602.
XX
PR 17-MAR-1989; 89US-00325338.
PR 20-APR-1989; 89US-00341334.
PR 18-MAY-1989; 89US-00355002.
PR 16-MAR-1990; 90EP-00302866.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Houghton M, Choo Q, Kuo G;
PI
XX WPI; 2000-566891/53.
XX
PT Novel composition comprising a hepatitis C virus antisense polynucleotide
PT which is complementary to or corresponds to a sense strand of the virus
PT genome, and selectively hybridizes to it.
XX
XX Example; Page 25; 75pp; English.
PS
XX
CC The specification describes a pharmaceutical composition which comprises
CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
CC characterized by a positive stranded RNA genome which has 40% homology at
```


CC the polypeptide level to a HCV polypeptide. The antisense polynucleotide
 CC binds to cellular polynucleotides which enhance and/or are required for
 CC viral infectivity, replicative ability or chronicity. The antisense
 CC polynucleotides may also be designed to bind with high specificity, to be
 CC of increased stability, to be stable and to have low toxicity. The
 CC composition also comprises an agent which causes viral RNA to be
 CC inactive. The composition is used for preventing HCV replication in a
 CC system. The present sequence represents a probe which was used to isolate
 CC a novel HCV cDNA sequence

XX SQ Sequence 30 BP; 7 A; 7 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 58.8%; Score 19.4; DB 3; Length 30;
 Best Local Similarity 95.2%; Pred. No. 67;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACACCACTATGG 32
 Db 21 CCGTTCGCGACCACTATGG 1

RESULT 26
 ADN35930/c
 ID ADN35930 standard; DNA; 30 BP.

XX AC ADN35930;

XX DT 17-JUN-2004 (first entry)

XX DE HCV cDNA clone 189 probe.

XX KW Antiviral; Vaccine; hepatitis C virus infection; HCV infection; probe;
 XX ss.

XX OS Hepatitis C virus.

XX FN EPI394255-A2.

XX PD 03-MAR-2004.

XX PF 16-MAR-1990; 2003EP-00016585.

XX PR 17-MAR-1989; 89US-00325338.

XX PR 20-APR-1989; 89US-00341334.

XX PR 18-MAY-1989; 89US-00355002.

XX PR 16-MAR-1990; 90EP-00302866.

XX PA (CHIR) CHIRON CORP.

XX PI Houghton M, Choo Q, Kuo G;

XX DR WPI; 2004-193149/19.

XX PT Novel purified hepatitis C virus polypeptide comprising epitope encoded
 XX by hepatitis C virus cDNA, useful as vaccine for treating hepatitis C
 XX virus.

XX PS Example 1; Page 26; 79pp; English.

XX CC The present invention relates to hepatitis C virus (HCV) proteins and
 XX cDNA sequences. The sequences are useful in immunoassays for detecting
 XX antibodies directed against HCV antigen; preparing host cells transformed
 XX with a recombinant polynucleotide; screening antiviral agents and
 XX determining the effect of antiviral agent in inhibiting viral replication
 XX in cell culture system; and developing vaccine for treating HCV
 XX infection. The present sequence was used to isolate a HCV cDNA clone of
 XX the invention.

XX SQ Sequence 30 BP; 7 A; 7 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 58.8%; Score 19.4; DB 12; Length 30;
 Best Local Similarity 95.2%; Pred. No. 67;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTATGG 32
 Db 21 CCGTTCGCGACCACTATGG 1

RESULT 27

AAZ99214/c

ID AAZ99214 standard; DNA; 31 BP.

XX AC AAZ99214;

XX DT 19-JUN-2000 (first entry)

XX DE Primer for primer-specific and mispair extension analysis of HCV.

XX KW Primer-specific and mispair extension assay; PSMEA;

XX KW genotype determination; HCV; gene variation; PCR primer; ss.

XX OS Hepatitis C virus.

XX FN WO200009745-A1.

XX PD 24-FEB-2000.

XX PF 09-AUG-1999; 99WO-CA000733.

XX PR 13-AUG-1998; 98CA-02245039.

XX PA (CABL-) CANADIAN BLOOD SERVICES.

XX PA (HEMA-) HEMA-QUEBEC.

XX PI Hu Y;

XX DR WPI; 2000-224367/19.

XX PT Primer-specific and mispair extension assay for identifying gene
 XX variations, comprises specific primer amplification of unknown nucleic
 XX acid sequences of patients using incomplete dNTP sets.

XX PS Disclosure; Page 13; 65pp; English.

XX CC AAZ99212-26 represent PCR primers used in a primer-specific and mispair
 XX extension assay (PSMEA) for genotype determination of Hepatitis C virus
 XX (HCV). The method comprises extending an unknown nucleic acid sequence
 XX (from a patient) using a primer specific for particular genotype and
 XX incomplete set of dNTPs under suitable conditions followed by
 XX characterizing and comparing the extension products with known nucleic
 XX acid sequences of various genotypes. The present primers are used for
 XX detecting nucleotide variations in the 5' untranslated region of the HCV
 XX genome. PSMEA is capable of accurately detecting heterozygotes and
 XX nucleotide mutations in a nucleic acid sequence. The PSMEA is useful for
 XX identifying gene variations such as in different genotypes or subtypes of
 XX a given genotype, especially Hepatitis C virus genotypes and subtypes

XX SQ Sequence 31 BP; 7 A; 8 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 58.8%; Score 19.4; DB 3; Length 31;

Best Local Similarity 95.2%; Pred. No. 67;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTATGG 32
 Db 21 CCGTTCGCGACCACTATGG 1

RESULT 28

ADD67939

ID ADD67939 standard; DNA; 19 BP.

XX AC ADD67939;

XX DT 15-JAN-2004 (first entry)

```
XX Hepatitis C virus RT-PCR primer seq id 11.
DE
XX
XX antiviral; hepatitis C virus; HCV; viral replication inhibitor;
KW replication competent HCV; 3' non-translated region;
KW reverse transcriptase PCR; RT-PCR; primer; ss; lightcycler RT-PCR.
XX
XX Hepatitis C virus.
OS
XX US2003125541-A1.
PN
XX 03-JUL-2003.
PD
XX
XX 27-SEP-2002; 2002US-00259275.
PF
XX
XX 23-DEC-1999; 99US-0171909P.
PR
XX 23-DEC-2000; 2000US-00747419.
PR
XX 27-SEP-2001; 2001US-0325236P.
PR
XX 13-NOV-2001; 2001US-0338123P.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX Lemon SM, Yi M;
PI
XX
XX WPI; 2003-811006/76.
DR
XX
XX Identifying a compound that inhibits replication of a hepatitis C virus
PT (HCV) RNA comprises contacting a cell comprising a replication competent
PT HCV RNA containing a heterologous polynucleotide encoding a
PT transactivator, with a compound.
XX
XX Example 6; SEQ ID NO 11; 95pp; English.
PS
XX
XX The invention describes a method of identifying a compound that inhibits
CC replication of a hepatitis C virus (HCV) RNA. The method comprises
CC contacting a cell comprising a replication competent HCV RNA containing a
CC heterologous polynucleotide having a first coding sequence encoding a
CC transactivator, with a compound. The method is useful for identifying a
CC compound that inhibits replication of HCV RNA. The kit is useful for
CC detecting replication competent HCV RNA. This sequence represents a
CC primer used to isolate DNA encoding HCV in order to detect the production
CC of the viral RNA in cell lines.
XX
XX Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 57.6%; Score 19; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 GTTCCGACAGACCACTATGG 32
DB 1 GTTCCGACAGACCACTATGG 19
RESULT 29
ADF51488/c
ID ADF51488 standard; RNA; 19 BP.
XX
XX ADF51488;
AC
XX
XX 12-FEB-2004 (first entry)
DT
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID78.
XX short interfering nucleic acid; siNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX
XX Hepatitis C virus.
OS
XX WO2003070750-A2.
PN
XX
```

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PD 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
PF
XX
XX 20-FEB-2002; 2002US-0358580P.
PR
XX 11-MAR-2002; 2002US-0363124P.
PR
XX 26-MAR-2002; 2002WO-US009187.
PR
XX 06-JUN-2002; 2002US-0386782P.
PR
XX 05-AUG-2002; 2002US-0401104P.
PR
XX 29-AUG-2002; 2002US-0406784P.
PR
XX 05-SEP-2002; 2002US-0408378P.
PR
XX 09-SEP-2002; 2002US-0409293P.
PR
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
PA
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
PI
XX WPI; 2003-689778/65.
DR
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
XX Example 3; SEQ ID NO 78; 183pp; English.
PS
XX
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains.
XX
XX Sequence 19 BP; 4 A; 4 C; 7 G; 0 T; 4 U; 0 Other;
SQ
Query Match 57.6%; Score 19; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TTCCGACAGACCACTATGGC 33
DB 19 TTCCGACAGACCACTATGGC 1
RESULT 30
ADF51492/c
ID ADF51492 standard; RNA; 19 BP.
XX
XX ADF51492;
AC
XX
XX 12-FEB-2004 (first entry)
DT
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID82.
XX short interfering nucleic acid; siNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX
XX Hepatitis C virus.
OS
XX
```

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PN WO2003070750-A2.
XX
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
XX Example 3; SEQ ID NO 82; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure; hepatocellular cancer
XX and cirrhosis), and also for drug screening, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains.
XX
XX Sequence 19 BP; 4 A; 5 C; 6 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 57.6%; Score 19; DB 10; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 95;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 14 GTTCGCGACACCTATGCG 32
XX |||||
XX Db 19 GTTCGCGACACCTATGCG 1
XX
XX RESULT 31
XX ADF52184
XX ID ADF52184 standard; RNA; 19 BP.
XX
XX AC ADF52184;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Hepatitis C virus siNA antisense strand SeqID774.
XX
XX short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.
XX
OS Hepatitis C virus.
XX
XX WO2003070750-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
XX Example 3; SEQ ID NO 774; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure; hepatocellular cancer
XX and cirrhosis), and also for drug screening, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains.
XX
XX Sequence 19 BP; 4 A; 7 C; 4 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 57.6%; Score 19; DB 10; Length 19;
XX Best Local Similarity 78.9%; Pred. No. 95;
XX Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 15 TTCCGCGACACCTATGCG 33
XX :|||||:|||||:|||||
XX Db 1 UUCCGCGACACCAUUGGC 19
XX
XX RESULT 32
XX ADF52188
XX ID ADF52188 standard; RNA; 19 BP.
XX
XX AC ADF52188;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Hepatitis C virus siNA antisense strand SeqID778.
XX
XX short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.

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KW hepatocellular cancer; cirrhosis; ss.
 OS Hepatitis C virus.
 XX WO2003070750-A2.
 PN 28-AUG-2003.
 XX 20-FEB-2003; 2003WO-US005043.
 PF 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002WO-US009187.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 05-AUG-2002; 2002US-0401104P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 PA Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
 PI WPI; 2003-689778/65.
 DR New double-stranded short interfering nucleic acid comprises sugar-
 modified pyrimidine bases useful for treating infection with hepatitis C
 virus.
 XX Example 3; SEQ ID NO 778; 183pp; English.
 XX This invention relates to novel double-stranded short interfering nucleic
 acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
 one strand is an antisense strand (ASS) that is complementary to (part
 of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
 ASS, and where most of the pyrimidine nucleotides comprise a sugar
 modification. The invention may allow development of compounds with
 virucide, antiinflammatory, hepatotropic or cytostatic activities by
 modulation (inhibition) of expression or activity of HCV RNA, by RNA
 interference. The siNA's of the invention may be used to inhibit
 replication of HCV in cells, tissue explants or organisms, for treating
 HCV infection and its consequences (liver failure; hepatocellular cancer
 and cirrhosis), and also for drug screening, diagnosis, target
 identification and validation, genetic engineering, pharmacogenomics,
 studying gene function and gene mapping (for example of single-nucleotide
 polymorphisms). The chemical modification improves stability, activity,
 cellular uptake and/or binding affinity. The siNA can be directed to
 conserved regions of HCV genes, so are active against many different
 CC strains.
 XX Sequence 19 BP; 4 A; 6 C; 5 G; 0 T; 4 U; 0 Other;
 SQ
 Query Match 57.6%; Score 19; DB 10; Length 19;
 Best Local Similarity 78.9%; Pred. No. 95;
 Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 OY 14 GTTCGCGACACCATGCG 32
 |:::|||||:::|
 DB 1 GUUCCGCGACACCATGCG 19
 |:::|||||:::|
 RESULT 33
 ABX10611
 ID ABX10611 standard; DNA; 19 BP.
 XX
 AC ABX10611;
 XX
 DT 11-APR-2003 (first entry)
 XX
 DE Light Cycler reverse PCR primer used to detect Viral RNA.
 XX PCR; primer; ss; replication competent; hepatitis C virus; HCV;
 KW

KW 3' non-translated RNA; 3'NTR; chronic viral hepatitis; hepatic fibrosis;
 KW cirrhosis; hepatocellular carcinoma; secretory alkaline phosphatase;
 SEAP.
 XX Hepatitis c virus.
 OS US2002155582-A1.
 PN 24-OCT-2002.
 XX 23-DEC-2000; 2000US-00747419.
 PF 23-DEC-1999; 99US-0171909P.
 PR (LEMO/) LEMON S M.
 PA (YIMW/) YI M.
 PR Lemon SM, Yi M;
 PI WPI; 2003-182640/18.
 DR Novel replication competent hepatitis C virus for producing infectious
 viral particles and as antigen for detecting hepatitis C virus
 antibodies, comprises hepatitis C virus genome and heterologous
 polynucleotide.
 XX Example 6; Page 16; 37pp; English.
 XX The invention discloses a replication competent hepatitis C virus (HCV)
 comprising a HCV virus genome and a heterologous polynucleotide, where
 the HCV genome comprises a 3' non-translated RNA and the heterologous
 polynucleotide is present in the 3' non-translated RNA. HCV is a cause of
 chronic viral hepatitis, hepatic fibrosis, cirrhosis and/or the
 development of hepatocellular carcinoma. A cell comprising the HCV is
 useful for selecting or detecting a replication competent HCV, for
 identifying a compound that inhibits replication of HCV, for producing
 infectious viral particles which are useful as a source of virus
 particles for various assays, including evaluating methods for
 inactivating particles, excluding particles from serum, identifying a
 neutralising compound and as an antigen for use in detecting anti-HCV
 antibodies in an animal. The cell comprising the HCV is also useful for
 identifying a variant HCV. An HCV particle is useful as an antigen, as a
 positive-control in assays that test for the presence of anti-HCV
 antibodies, to produce antibodies to detect the presence of viral
 particles in biological samples (e.g. blood products and cell-free blood
 products) and as a source of viral antigen to measure the presence and
 amount of antibody present in an animal. The sequence presented is the
 Light Cycler reverse PCR primer which was used to detect viral RNA in Huh
 CC -secretory alkaline phosphatase (SEAP)-010 cell lines
 XX Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 57.6%; Score 19; DB 10; Length 19;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 14 GTTCGCGACACCATGCG 32
 |:::|||||:::|
 DB 1 GTTCGCGACACCATGCG 19
 |:::|||||:::|
 RESULT 34
 AAQ65023
 ID AAQ65023 standard; DNA; 20 BP.
 XX
 AC AAQ65023;
 XX
 DT 21-DEC-1994 (first entry)
 XX
 DE Antisense oligonucleotide SMS21 complementary to HCV genome.
 XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
 KW inhibition; viral protein precursor; ss.

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XX OS Synthetic.
XX FH
XX FT Key Location/Qualifiers
XX FT misc_feature 1..20
XX FT /tag= a
XX FT /note= "phosphorothioate linkages between these
XX FT nucleotides"
XX PN CA2104649-A.
XX PD 26-FEB-1994.
XX XX 23-AUG-1993; 93CA-02104649.
XX XX 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX XX (SEKI/) SEKI M.
XX PI Seki M, Honda Y, Yamada E;
XX WPI; 1994-151836/19.
XX DR
XX XX
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX PT genome - are useful as antiviral agents.
XX PS Example 3; Page 112; 262pp; English.
XX CC This oligonucleotide is an example of an antisense compound designed to
XX CC hybridise to a hepatitis C virus sequence. Such antisense
XX CC oligonucleotides are useful for inhibiting translation of HCV genes
XX XX
XX SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 57.6%; Score 19; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCGCGAGACCACTATGG 32
Db 2 GTTCGCGAGACCACTATGG 20

RESULT 35
AAZ88590/c
ID AAZ88590 standard; DNA; 20 BP.
XX AC AAZ88590;
XX DT 04-MAY-2000 (first entry)
XX DE Hepatitis C genome PCR primer 3.
XX KW Detection; serum; plasma; probe; infection; PCR primer; ss.
XX OS Hepatitis C virus.
XX PN DE19832050-A1.
XX PD 27-JAN-2000.
XX PF 16-JUL-1998; 98DE-01032050.
XX PR 16-JUL-1998; 98DE-01032050.
XX XX (BIOT ) BIOTEST PHARMA GMBH.
XX PI Jochum C;
XX DR WPI; 2000-148478/14.
XX PT Detection of Hepatitis C and B viral genomes in serum or plasma using

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PT specific oligonucleotide primers and probes.
XX Claim 1c; Page 2; 7pp; German.
XX CC This invention describes a novel method to detect Hepatitis C (HCV)
XX CC and/or Hepatitis B (HBV) viral genomes in a serum or plasma sample using
XX CC specific primers and probes. The method and oligonucleotide primers and
XX CC probes are useful for the specific detection of Hepatitis C and/or
XX CC Hepatitis B viral sequences in plasma and serum samples. This may be
XX CC useful for preventing Hepatitis B and/or C infection in patients through
XX CC contaminated blood and/or serum products. The method is able to detect
XX CC all reference samples of HBV subtypes AD and AY and HCV subtypes 1 - 5
XX CC with 100% accuracy. AAZ88588-288591 represent PCR primers used to detect
XX CC HCV virus in a sample
XX SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 57.6%; Score 19; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCGCGAGACCACTATGG 32
Db 19 GTTCGCGAGACCACTATGG 1

RESULT 36
AAQ67619/c
ID AAQ67619 standard; DNA; 22 BP.
XX AC AAQ67619;
XX DT 31-JAN-1995 (first entry)
XX DE Primer for amplifying hepatitis C virus 5' non-coding region.
XX KW Hepatitis C virus; HCV; testing; detection; probe; linker;
XX KW non-coding region; acridinium N-hydroxy succinimide; ss.
XX OS Synthetic.
XX PN JP06121700-A.
XX PD 06-MAY-1994.
XX PF 13-OCT-1992; 92JP-00274273.
XX PR 13-OCT-1992; 92JP-00274273.
XX PA (CHUS ) CHUGAI PHARM CO LTD.
XX DR WPI; 1994-185929/23.
XX PT Method of detecting Hepatitis C virus - using a labelled DNA probe.
XX PS Disclosure; Page 2; 13pp; Japanese.
XX CC 7 Primers (AAQ67617-20, AAQ67622-24) were used to amplify regions of the
XX CC hepatitis C virus 5' non-coding (5'NC) region. A probe (See AAQ67615, 5',
XX CC AAQ67616) which is specific for a conserved base sequence within the 5',
XX CC non-coding (5'NC) region of hepatitis C virus (HCV) gene was then used to
XX CC detect amplification products. The probe was labelled using an acridinium
XX CC N-hydroxy succinimide ester which is attached to the probe via a linker
XX XX
XX SQ Sequence 22 BP; 6 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 57.6%; Score 19; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCGAGACCACTATGGC 33
Db 22 TTCCGCGAGACCACTATGGC 4

```

Forward PCR primer used to amplify a 5' noncoding region of HCV.

HCV; HIV; viral detection; PCR primer; ss.

Hepatitis C virus.

CA2296044-A1.

03-AUG-2000.

01-FEB-2000; 2000CA-02296044.

03-FEB-1999; 99US-0118498P.

(ORTH) ORTHO CLINICAL DIAGNOSTICS INC.

Linnen JM, Song K, Patterson DR, Gorman KM;

WPI; 2000-594741/57.

New methods for the simultaneous detection of hepatitis C virus and human immunodeficiency virus in biological samples from humans.

Claim 1; Page 21; 45pp; English.

The specification describes a method for co-detecting Hepatitis C Virus (HCV) RNA and human immunodeficiency virus (HIV) RNA in a biological sample. The method uses HCV and HIV specific reverse transcription primers, either separately or in combination. The reverse transcribed products are then amplified using primers specific for the 5' noncoding region of HCV and/or HIV. The presence of specific products indicates the presence of the appropriate RNA in the sample. The method is used for the simultaneous detection of the presence of HCV RNA and HIV RNA in a sample. PCR primers AAA96551-52 are used to the amplify 5' noncoding region of HCV

Sequence 25 BP; 6 A; 4 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 57.6%; Score 19; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCAGACCACTATGGC 33
|||||
Db 25 TTCCGCAGACCACTATGGC 7

RESULT 39
AAA96560/c
ID ID AAA96560 standard; DNA; 25 BP.
XX AAA96560;
XX AC
XX CC
DT DT (first entry)
DE DE Forward PCR primer used to amplify a HCV fragment.
XX HCV; HIV; viral detection; PCR primer; ss.
XX Hepatitis C virus.
OS OS
XX CA2296044-A1.
PN PN
XX 03-AUG-2000.
PD PD
XX 01-FEB-2000; 2000CA-02296044.
PF PF
XX 03-FEB-1999; 99US-0118498P.
PR PR
XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
PA PA
PI Linnen JM, Song K, Patterson DR, Gorman KM;

XX WPI; 2000-594741/57.
XX New methods for the simultaneous detection of hepatitis C virus and human
PT immunodeficiency virus in biological samples from humans.
XX Claim 16; Page 27; 45pp; English.
XX The specification describes a method for co-detecting Hepatitis C Virus
CC (HCV) RNA and human immunodeficiency virus (HIV) RNA in a biological
CC sample. The method uses HCV and HIV specific reverse transcription
CC primers, either separately or in combination. The reverse transcribed
CC products are then amplified using primers specific for the 5' noncoding
CC region of HCV and/or HIV. The presence of specific products indicates the
CC presence of the appropriate RNA in the sample. The method is used for the
CC simultaneous detection of the presence of HCV RNA and HIV RNA in a
CC sample. PCR primers AAA96560-61 are used to the amplify a fragment of HCV
XX Sequence 25 BP; 6 A; 4 C; 11 G; 4 T; 0 U; 0 Other;
SQ
Query Match 57.6%; Score 19; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 TTCCGCAGACCACTATGGC 33
Db 25 TTCCGCAGACCACTATGGC 7
RESULT 40
AAA74620/c
ID AAA74620 standard; DNA; 25 BP.
XX
AC AAA74620;
XX
DT 08-JAN-2001 (first entry)
XX
DE HCV-specific amplification primer C131P25.
XX
KW Hepatitis C virus; HCV; HCV detection; amplification primer; ss.
XX
OS Hepatitis C virus.
XX
FN EP1026262-A2.
XX
PD 09-AUG-2000.
XX
PF 01-FEB-2000; 2000EP-00300763.
XX
PR 03-FEB-1999; 99US-0118497P.
XX
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI Linnen JM, Gorman KM;
XX
DR WPI; 2000-507254/46.
XX
PT Detecting hepatitis C virus in biological sample involves amplifying
PT reverse transcribed products of virus RNA using amplification primers
PT whose sequences correspond to 5' or 3' non-coding region of the virus
PT RNA.
XX
PS Claim 30; Page 27; 28pp; English.
XX
CC The present sequence is an amplification primer used in a method for
CC detecting hepatitis C virus (HCV) RNA in biological samples. The HCV RNA
CC is reverse transcribed to generate cDNA. This is then amplified using
CC primers, including the present sequence, corresponding to the 5' or 3'
CC non-coding region of HCV. The method is useful for the diagnosis of HCV
CC infection in patients, in testing the efficacy of anti-HCV therapeutic
CC regimes, and in screening blood for HCV-infected samples. The method
CC provides an improved single-round, reverse transcription/amplification
CC assay which detects low copy levels of HCV RNA. The primers and assay

CC system are designed to allow the co-amplification of multiple regions of
CC the HCV genome, multiple viral species, and an internal positive control
CC (IPC) RNA (or DNA). Simultaneous amplification/detection of multiple
CC regions of the HCV genome increases assay sensitivity and the co-
CC amplification of an IPC decreases the likelihood of false negative
CC results because of PCR inhibition
XX
SQ Sequence 25 BP; 6 A; 4 C; 11 G; 4 T; 0 U; 0 Other;
Query Match 57.6%; Score 19; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 TTCCGCAGACCACTATGGC 33
Db 25 TTCCGCAGACCACTATGGC 7
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Job time : 201.112 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 38.191 Seconds
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Title: US-10-087-631B-3
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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.4	61.8	26	4	US-09-493-353-4
2	20.4	61.8	28	3	US-08-474-700B-6
3	20.4	61.8	28	5	PCT-US95-05812-6
4	20.4	61.8	36	4	US-09-153-242-39
5	20	60.6	38	1	US-08-299-682-9
6	20	60.6	38	1	US-08-299-682-10
7	19.4	58.8	30	1	US-08-097-853-2
8	19.4	58.8	30	2	US-08-438-435-3
9	19.4	58.8	30	3	US-08-444-818-217
10	19	57.6	25	4	US-09-494-332A-13
11	19	57.6	25	4	US-09-494-332A-10
12	19	57.6	25	4	US-09-493-353-2
13	18.4	55.8	20	1	US-08-533-820A-6
14	18.4	55.8	20	4	US-08-150-204E-125
15	18.4	55.8	26	1	US-08-299-682-11
16	18.4	55.8	26	1	US-08-240-547-23
17	17.4	52.7	20	3	US-08-397-220B-50
18	17.4	52.7	20	3	US-08-650-093C-50
19	16	48.5	16	3	US-08-954-210-9
20	16	48.5	16	4	US-09-431-419A-9
21	16	48.5	16	4	US-09-474-432B-24
22	16	48.5	16	4	US-09-476-387-24
23	16	48.5	33	1	US-08-438-639-46
24	16	48.5	33	1	US-08-813-338A-46
25	16	48.5	33	2	US-08-470-124-79
26	16	48.5	33	3	US-08-441-971-122
27	16	48.5	33	3	US-08-221-653-122

28	16	48.5	33	3	US-08-442-144A-122	Sequence 122, App
29	16	48.5	33	3	US-08-441-970-122	Sequence 122, App
30	16	48.5	33	3	US-08-435-568A-28	Sequence 28, Appl
31	16	48.5	33	3	US-08-417-551-5	Sequence 5, Appli
32	16	48.5	33	3	US-08-316-385-5	Sequence 5, Appli
33	15.4	46.7	18	3	US-09-034-205-52	Sequence 52, Appl
34	15.4	46.7	18	3	US-09-677-218B-52	Sequence 52, Appl
35	15.4	46.7	18	3	US-09-677-192-52	Sequence 52, Appl
36	15.4	46.7	18	4	US-09-402-618B-52	Sequence 52, Appl
37	15.4	46.7	37	6	5166057-36	Patent No. 5166057
38	15.4	46.7	33	2	US-08-316-439A-21	Sequence 21, Appl
39	15.2	46.1	33	3	US-09-039-982A-54	Sequence 54, Appl
40	15.2	46.1	33	3	US-09-039-762A-54	Sequence 54, Appl
41	15.2	46.1	33	3	US-09-194-285-46	Sequence 46, Appl
42	15.2	46.1	33	3	US-09-042-492D-54	Sequence 54, Appl
43	15.2	46.1	33	4	US-08-913-612A-60	Sequence 60, Appl
44	15.2	46.1	38	3	US-08-974-022-31	Sequence 31, Appl
45	15.2	46.1	38	3	US-08-974-022-33	Sequence 33, Appl
46	15.2	46.1	38	3	US-08-795-445A-31	Sequence 31, Appl
47	15.2	46.1	38	3	US-08-795-445A-33	Sequence 33, Appl
48	15.2	46.1	38	3	US-08-795-447A-31	Sequence 31, Appl
49	15.2	46.1	38	3	US-08-795-447A-33	Sequence 33, Appl
50	15.2	46.1	38	3	US-08-974-186-31	Sequence 31, Appl
51	15.2	46.1	38	3	US-08-974-186-33	Sequence 33, Appl
52	15.2	46.1	38	3	US-08-795-446B-31	Sequence 31, Appl
53	15.2	46.1	38	3	US-08-795-446B-33	Sequence 33, Appl
54	15.2	46.1	38	3	US-08-706-945D-26	Sequence 26, Appl
55	15.2	46.1	38	3	US-08-706-945D-28	Sequence 28, Appl
56	15.2	46.1	38	4	US-08-577-788C-31	Sequence 31, Appl
57	15.2	46.1	38	4	US-08-577-788C-33	Sequence 33, Appl
58	15	45.5	15	1	US-08-182-968A-4	Sequence 4, Appli
59	15	45.5	15	2	US-08-774-306A-4	Sequence 4, Appli
60	15	45.5	15	3	US-09-064-156A-4	Sequence 4, Appli
61	15	45.5	26	4	US-10-029-907-19	Sequence 19, Appl
62	15	45.5	27	1	US-08-688-649-11	Sequence 11, Appl
63	14.8	44.8	21	3	US-08-397-220B-13	Sequence 13, Appl
64	14.8	44.8	21	3	US-08-650-093C-13	Sequence 13, Appl
65	14.8	44.8	21	4	US-08-823-895A-13	Sequence 13, Appl
66	14.8	44.8	25	1	US-08-361-442-4	Sequence 4, Appli
67	14.8	44.8	25	2	US-08-823-516-121	Sequence 121, App
68	14.8	44.8	25	3	US-08-759-038-96	Sequence 96, Appl
69	14.8	44.8	25	4	US-08-758-314-96	Sequence 96, Appl
70	14.8	44.8	25	4	US-09-684-938-96	Sequence 96, Appl
71	14.8	44.8	25	4	US-09-308-825A-96	Sequence 96, Appl
72	14.8	44.8	26	1	US-08-379-078-664	Sequence 664, App
73	14.8	44.8	28	3	US-08-474-700B-7	Sequence 7, Appli
74	14.8	44.8	28	3	US-08-474-700B-33	Sequence 33, Appl
75	14.8	44.8	28	5	PCT-US95-05812-7	Sequence 7, Appli
76	14.8	44.8	28	5	PCT-US95-05812-33	Sequence 33, Appl
77	14.8	44.8	30	5	PCT-US93-00928-3	Sequence 3, Appli
78	14.8	44.8	33	1	US-08-438-639-47	Sequence 47, Appl
79	14.8	44.8	33	1	US-07-813-338A-47	Sequence 47, Appl
80	14.8	44.8	33	2	US-08-470-124-80	Sequence 80, Appl
81	14.8	44.8	33	2	US-08-441-971-123	Sequence 123, App
82	14.8	44.8	33	3	US-08-221-653-123	Sequence 123, App
83	14.8	44.8	33	3	US-09-034-205-63	Sequence 63, Appl
84	14.8	44.8	33	3	US-08-442-144A-123	Sequence 123, App
85	14.8	44.8	33	3	US-08-441-970-123	Sequence 123, App
86	14.8	44.8	33	3	US-09-677-218B-63	Sequence 63, Appl
87	14.8	44.8	33	3	US-09-677-192-63	Sequence 63, Appl
88	14.8	44.8	33	4	US-09-402-618B-63	Sequence 63, Appl
89	14.8	44.8	46	1	US-08-347-029-12	Sequence 12, Appl
90	14.8	44.8	46	5	PCT-US95-14932-12	Sequence 12, Appl
91	14.4	43.6	22	3	US-08-938-033-1	Sequence 1, Appli
92	14.4	43.6	22	4	US-09-311-487-1	Sequence 1, Appli
93	14.4	43.6	26	4	US-08-493-353-3	Sequence 3, Appli
94	14.4	43.6	41	3	US-08-813-507-79	Sequence 79, Appl
95	14.4	43.6	41	3	US-09-464-453-79	Sequence 79, Appl
96	14.2	43.0	30	4	US-09-151-409-9	Sequence 9, Appli
97	14.2	43.0	36	5	PCT-US91-02942-71	Sequence 71, Appl
98	14	42.4	26	4	US-10-353-589-3	Sequence 3, Appli
99	14	42.4	37	4	US-09-770-158-1	Sequence 1, Appli
100	14	42.4	38	4	US-09-474-432B-1107	Sequence 1107, Ap

c 101	14	42.4	38	4	US-09-476-387-1106	Sequence 1106, Ap	174	12.8	38.8	31	3	US-08-653-648A-39	Sequence 39, Appl
c 102	14	42.4	47	4	US-09-561-490E-27	Sequence 27, Appl	175	12.8	38.8	31	4	US-09-564-418-34	Sequence 34, Appl
c 103	13.8	41.8	20	3	US-08-397-220B-51	Sequence 51, Appl	c 176	12.8	38.8	32	1	US-07-882-838E-48	Sequence 48, Appl
c 104	13.8	41.8	20	3	US-08-650-093C-51	Sequence 51, Appl	c 177	12.8	38.8	37	3	US-08-479-744A-33	Sequence 33, Appl
c 105	13.8	41.8	25	4	US-08-866-108A-10985	Sequence 10985, A	c 178	12.8	38.8	37	3	US-08-280-757B-33	Sequence 33, Appl
c 106	13.8	41.8	34	3	US-09-257-584-30	Sequence 30, Appl	c 179	12.8	38.8	37	4	US-09-425-762-33	Sequence 33, Appl
c 107	13.8	41.8	37	5	US-08-341-560B-14	Sequence 14, Appl	c 180	12.8	38.8	39	3	US-09-018-545-5	Sequence 11, Appl
c 108	13.8	41.8	37	5	PCT-US93-03895-14	Sequence 14, Appl	c 181	12.8	38.8	39	4	US-09-940-173A-11	Sequence 11, Appl
c 109	13.8	41.8	40	3	US-09-485-737B-74	Sequence 74, Appl	c 182	12.8	38.8	39	4	US-09-730-893-11	Sequence 11, Appl
c 110	13.6	41.2	47	4	US-09-641-638-708	Sequence 708, App	c 183	12.8	38.8	40	1	US-08-258-283-1	Sequence 1, Appl
c 111	13.6	41.2	47	4	US-10-170-097-708	Sequence 708, App	c 184	12.8	38.8	40	5	PCT-US92-10359-1	Sequence 1, Appl
c 112	13.6	41.2	48	4	US-09-136-801-29	Sequence 29, Appl	c 185	12.8	38.8	41	3	US-08-813-507-80	Sequence 80, Appl
c 113	13.6	41.2	48	4	US-09-202-088A-29	Sequence 29, Appl	c 186	12.8	38.8	41	3	US-09-464-453-80	Sequence 80, Appl
c 114	13.4	40.6	27	3	US-09-149-922-46	Sequence 46, Appl	c 187	12.8	38.8	44	1	US-08-259-148A-28	Sequence 28, Appl
c 115	13.4	40.6	33	4	US-09-311-784A-104	Sequence 104, App	c 188	12.8	38.8	44	2	US-07-876-941A-44	Sequence 44, Appl
c 116	13.4	40.6	40	3	US-09-275-850-154	Sequence 154, App	c 189	12.8	38.8	48	3	US-08-849-567A-98	Sequence 98, Appl
c 117	13.4	40.6	47	4	US-09-422-978-1903	Sequence 1903, Ap	c 190	12.6	38.2	20	4	US-09-688-313A-164	Sequence 164, App
c 118	13.2	40.0	24	4	US-09-940-244-121	Sequence 121, App	c 191	12.6	38.2	20	4	US-09-953-318-111	Sequence 111, App
c 119	13.2	40.0	26	3	US-08-859-998-396	Sequence 396, App	c 192	12.6	38.2	22	1	US-08-152-621-11	Sequence 11, App
c 120	13.2	40.0	26	3	US-09-225-928-396	Sequence 396, App	c 193	12.6	38.2	22	5	PCT-US92-05035-11	Sequence 11, Appl
c 121	13.2	40.0	26	4	US-09-225-201B-396	Sequence 396, App	c 194	12.6	38.2	25	4	US-09-866-108A-10979	Sequence 10979, A
c 122	13.2	40.0	45	3	US-09-232-478-26	Sequence 26, Appl	c 195	12.6	38.2	25	4	US-09-866-108A-10980	Sequence 10980, A
c 123	13.2	40.0	45	4	US-09-785-055-26	Sequence 26, Appl	c 196	12.6	38.2	26	4	US-09-396-154-56	Sequence 56, Appl
c 124	13.2	40.0	47	4	US-09-422-978-3114	Sequence 3114, Ap	c 197	12.6	38.2	27	3	US-09-447-356-10	Sequence 10, Appl
c 125	13	39.4	15	1	US-08-182-968A-5	Sequence 5, Appl	c 198	12.6	38.2	28	2	US-08-859-998-418	Sequence 418, App
c 126	13	39.4	15	2	US-08-774-306A-5	Sequence 5, Appl	c 199	12.6	38.2	28	3	US-09-225-928-418	Sequence 418, App
c 127	13	39.4	15	3	US-09-064-156A-5	Sequence 5, Appl	c 200	12.6	38.2	28	4	US-09-225-201B-418	Sequence 418, App
c 128	13	39.4	20	3	US-08-397-220B-49	Sequence 49, Appl	c 201	12.6	38.2	29	4	US-09-304-232-329	Sequence 329, App
c 129	13	39.4	20	3	US-08-650-093C-49	Sequence 49, Appl	c 202	12.6	38.2	29	4	US-09-304-232-856	Sequence 856, App
c 130	13	39.4	24	3	US-09-521-668B-15	Sequence 15, Appl	c 203	12.6	38.2	29	4	US-09-474-432B-304	Sequence 304, App
c 131	13	39.4	25	4	US-09-866-108A-10981	Sequence 10981, A	c 204	12.6	38.2	35	2	US-07-829-461A-14	Sequence 14, Appl
c 132	13	39.4	25	4	US-09-866-108A-10982	Sequence 10982, A	c 205	12.6	38.2	35	3	US-09-197-649-15	Sequence 15, Appl
c 133	13	39.4	25	4	US-09-866-108A-10983	Sequence 10983, A	c 206	12.6	38.2	35	4	US-09-476-387-303	Sequence 303, App
c 134	13	39.4	25	4	US-09-866-108A-10984	Sequence 10984, A	c 207	12.6	38.2	36	4	US-09-474-432B-305	Sequence 305, App
c 135	13	39.4	25	4	US-09-866-108A-10986	Sequence 10986, A	c 208	12.6	38.2	36	4	US-09-125-491C-6	Sequence 6, Appl
c 136	13	39.4	25	4	US-09-866-108A-10987	Sequence 10987, A	c 209	12.6	38.2	37	4	US-09-476-387-304	Sequence 304, App
c 137	13	39.4	25	4	US-09-866-108A-10988	Sequence 10988, A	c 210	12.6	38.2	38	4	US-09-474-432B-1292	Sequence 1292, Ap
c 138	13	39.4	25	4	US-09-866-108A-10989	Sequence 10989, A	c 211	12.6	38.2	38	4	US-09-474-432B-1408	Sequence 1408, Ap
c 139	13	39.4	26	1	US-08-363-233B-6	Sequence 6, Appl	c 212	12.6	38.2	38	4	US-09-474-432B-1474	Sequence 1474, Ap
c 140	13	39.4	29	4	US-09-770-158-16	Sequence 16, Appl	c 213	12.6	38.2	38	4	US-09-476-387-1291	Sequence 1291, Ap
c 141	13	39.4	31	1	US-08-049-264C-47	Sequence 47, Appl	c 214	12.6	38.2	38	4	US-09-476-387-1407	Sequence 1407, Ap
c 142	13	39.4	31	1	US-08-049-264C-53	Sequence 53, Appl	c 215	12.6	38.2	38	4	US-09-476-387-1473	Sequence 1473, Ap
c 143	13	39.4	31	1	US-08-476-562-47	Sequence 47, Appl	c 216	12.6	38.2	42	4	US-09-388-089B-14	Sequence 14, Appl
c 144	13	39.4	31	1	US-08-476-562-53	Sequence 53, Appl	c 217	12.6	38.2	42	5	PCT-US93-02457-4	Sequence 4, Appl
c 145	13	39.4	31	1	US-08-479-723A-47	Sequence 47, Appl	c 218	12.6	38.2	42	5	PCT-US93-11458-5	Sequence 5, Appl
c 146	13	39.4	31	1	US-08-479-723A-53	Sequence 53, Appl	c 219	12.6	38.2	47	4	US-09-422-978-3558	Sequence 3558, Ap
c 147	13	39.4	31	5	PCT-US94-04310-47	Sequence 47, Appl	c 220	12.4	37.6	16	4	US-09-474-432B-6	Sequence 6, Appl
c 148	13	39.4	31	5	PCT-US94-04310-53	Sequence 53, Appl	c 221	12.4	37.6	16	4	US-09-476-387B-6	Sequence 6, Appl
c 149	13	39.4	32	4	US-09-322-409-138	Sequence 138, App	c 222	12.4	37.6	26	2	US-08-912-129A-19	Sequence 19, Appl
c 150	13	39.4	32	4	US-09-451-527-138	Sequence 915, App	c 223	12.4	37.6	26	4	US-08-547-602-1	Sequence 1, Appl
c 151	13	39.4	38	4	US-09-474-432B-915	Sequence 915, App	c 224	12.4	37.6	27	3	US-09-033-428-11	Sequence 11, Appl
c 152	13	39.4	38	4	US-09-474-432B-1160	Sequence 1160, Ap	c 225	12.4	37.6	27	4	US-09-033-556-24	Sequence 24, Appl
c 153	13	39.4	38	4	US-09-770-158-2	Sequence 2, Appl	c 226	12.4	37.6	27	4	US-09-474-699-17	Sequence 17, Appl
c 154	13	39.4	38	4	US-09-476-387-914	Sequence 914, App	c 227	12.4	37.6	27	4	US-09-898-883-11	Sequence 11, Appl
c 155	13	39.4	38	4	US-09-476-387-1159	Sequence 1159, Ap	c 228	12.4	37.6	27	4	US-09-151-376-49	Sequence 49, Appl
c 156	13	39.4	42	3	US-09-425-638A-6	Sequence 6, Appl	c 229	12.4	37.6	28	2	US-08-859-998-1084	Sequence 1084, Ap
c 157	13	39.4	42	3	US-09-543-004-6	Sequence 6, Appl	c 230	12.4	37.6	28	3	US-09-225-928-1084	Sequence 1084, Ap
c 158	13	39.4	47	4	US-09-422-978-3439	Sequence 3439, Ap	c 231	12.4	37.6	28	4	US-09-225-201B-1084	Sequence 1084, Ap
c 159	13	39.4	50	4	US-09-576-537-2	Sequence 2, Appl	c 232	12.4	37.6	30	2	US-08-860-882A-22	Sequence 22, Appl
c 160	13	39.4	50	4	US-09-519-859A-2	Sequence 2, Appl	c 233	12.4	37.6	30	4	US-09-011-769A-18	Sequence 18, Appl
c 161	13	39.4	50	4	US-09-519-859A-3	Sequence 3, Appl	c 234	12.4	37.6	32	1	US-08-055-390-8	Sequence 8, Appl
c 162	12.8	38.8	16	1	US-07-639-684A-4	Sequence 4, Appl	c 235	12.4	37.6	32	4	US-09-665-189A-49	Sequence 49, Appl
c 163	12.8	38.8	16	4	US-09-474-432B-7	Sequence 7, Appl	c 236	12.4	37.6	33	2	US-08-734-591A-105	Sequence 105, App
c 164	12.8	38.8	16	4	US-09-476-387-7	Sequence 7, Appl	c 237	12.4	37.6	33	3	US-08-470-335-105	Sequence 105, App
c 165	12.8	38.8	16	4	US-09-112-580-60	Sequence 60, Appl	c 238	12.4	37.6	33	3	US-08-734-664A-105	Sequence 105, App
c 166	12.8	38.8	26	1	US-08-379-078-559	Sequence 559, App	c 239	12.4	37.6	33	4	US-08-470-339-105	Sequence 105, App
c 167	12.8	38.8	26	3	US-07-974-409C-182	Sequence 182, App	c 240	12.4	37.6	38	4	US-08-467-602-105	Sequence 920, App
c 168	12.8	38.8	26	3	US-07-974-409C-228	Sequence 228, App	c 241	12.4	37.6	38	4	US-09-474-432B-920	Sequence 920, App
c 169	12.8	38.8	26	5	PCT-US93-00977-182	Sequence 182, App	c 242	12.4	37.6	38	4	US-09-474-432B-939	Sequence 939, App
c 170	12.8	38.8	26	5	PCT-US93-00977-228	Sequence 228, App	c 243	12.4	37.6	38	4	US-09-474-432B-955	Sequence 955, App
c 171	12.8	38.8	27	4	US-08-832-488-6	Sequence 6, Appl	c 244	12.4	37.6	38	4	US-09-474-432B-980	Sequence 980, App
c 172	12.8	38.8	27	4	US-08-832-488-10	Sequence 10, Appl	c 245	12.4	37.6	38	4	US-09-474-432B-1007	Sequence 1007, Ap
c 173	12.8	38.8	30	4	US-09-946-678-19	Sequence 19, Appl	c 246	12.4	37.6	38	4	US-09-474-432B-1086	Sequence 1086, Ap

C 247	12.4	37.6	38	4	US-09-474-432B-1099	Sequence 1099, Appl	320	12.2	37.0	36	4	US-09-403-422-8	Sequence 8, Appli
C 248	12.4	37.6	38	4	US-09-474-432B-1237	Sequence 1237, Ap	321	12.2	37.0	37	1	US-08-423-691-5	Sequence 5, Appli
C 249	12.4	37.6	38	4	US-09-474-432B-1256	Sequence 1256, Ap	322	12.2	37.0	37	3	US-08-867-260-5	Sequence 5, Appli
C 250	12.4	37.6	38	4	US-09-474-432B-1404	Sequence 1404, Ap	323	12.2	37.0	38	1	US-08-706-945D-38	Sequence 38, Appl
C 251	12.4	37.6	38	4	US-09-476-387-919	Sequence 919, App	C 324	12.2	37.0	37	1	US-08-384-708A-188	Sequence 188, App
C 252	12.4	37.6	38	4	US-09-476-387-938	Sequence 938, App	C 325	12.2	37.0	38	2	US-08-465-976A-6	Sequence 6, Appli
C 253	12.4	37.6	38	4	US-09-476-387-954	Sequence 954, App	C 326	12.2	37.0	38	2	US-08-982-412-6	Sequence 6, Appli
C 254	12.4	37.6	38	4	US-09-476-387-979	Sequence 979, App	C 327	12.2	37.0	38	3	US-08-687-421-188	Sequence 188, App
C 255	12.4	37.6	38	4	US-09-476-387-1006	Sequence 1006, Ap	C 328	12.2	37.0	38	4	US-08-442-423-188	Sequence 188, App
C 256	12.4	37.6	38	4	US-09-476-387-1085	Sequence 1085, Ap	C 329	12.2	37.0	39	2	US-08-343-923-14	Sequence 14, Appl
C 257	12.4	37.6	38	4	US-09-476-387-1098	Sequence 1098, Ap	C 330	12.2	37.0	40	2	US-08-425-684-54	Sequence 54, Appl
C 258	12.4	37.6	38	4	US-09-476-387-1236	Sequence 1236, Ap	C 331	12.2	37.0	40	2	US-08-675-502-54	Sequence 54, Appl
C 259	12.4	37.6	38	4	US-09-476-387-1255	Sequence 1255, Ap	C 332	12.2	37.0	40	4	US-08-675-502-54	Sequence 54, Appl
C 260	12.4	37.6	38	4	US-09-476-387-1403	Sequence 1403, Ap	C 333	12.2	37.0	40	4	US-09-538-702-1192	Sequence 1192, Ap
C 261	12.4	37.6	41	4	US-09-674-677-33	Sequence 33, Appl	C 334	12.2	37.0	40	4	US-09-245-802-54	Sequence 54, Appl
C 262	12.4	37.6	47	4	US-09-671-317-822	Sequence 822, App	C 335	12.2	37.0	47	2	US-08-811-492-126	Sequence 126, App
C 263	12.4	37.6	47	4	US-09-422-978-930	Sequence 930, App	C 336	12.2	37.0	47	4	US-09-671-317-776	Sequence 776, App
C 264	12.4	37.6	47	4	US-09-422-978-2410	Sequence 2410, Ap	C 337	12.2	37.0	47	4	US-09-422-978-519	Sequence 519, App
C 265	12.2	37.0	17	3	US-08-946-138-27	Sequence 27, Appl	C 338	12.2	37.0	47	4	US-09-422-978-3353	Sequence 3353, Ap
C 266	12.2	37.0	17	4	US-09-907-795-2	Sequence 2, Appli	C 339	12.2	37.0	48	3	US-08-675-566-102	Sequence 102, App
C 267	12.2	37.0	17	4	US-09-865-108A-6089	Sequence 6089, Ap	C 340	12	36.4	20	3	US-09-020-846-34	Sequence 34, Appl
C 268	12.2	37.0	20	4	US-09-319-588C-21	Sequence 21, Appl	C 341	12	36.4	20	3	US-09-034-205-60	Sequence 60, Appl
C 269	12.2	37.0	20	4	US-09-319-588C-88	Sequence 88, Appl	C 342	12	36.4	20	3	US-09-677-218B-60	Sequence 60, Appl
C 270	12.2	37.0	22	3	US-09-339-622-8	Sequence 8, Appli	C 343	12	36.4	20	3	US-09-677-192-60	Sequence 60, Appl
C 271	12.2	37.0	23	3	US-08-840-551-2	Sequence 2, Appli	C 344	12	36.4	20	4	US-08-944-410-9	Sequence 9, Appli
C 272	12.2	37.0	25	4	US-09-395-448-18	Sequence 18, Appl	C 345	12	36.4	20	4	US-09-402-618B-60	Sequence 60, Appl
C 273	12.2	37.0	25	4	US-09-865-108A-14601	Sequence 14601, A	C 346	12	36.4	21	1	US-08-379-078-581	Sequence 581, App
C 274	12.2	37.0	25	4	US-09-866-108A-14602	Sequence 14602, A	C 347	12	36.4	21	5	US-07-974-409C-204	Sequence 204, App
C 275	12.2	37.0	25	4	US-09-925-796-18	Sequence 18, Appl	C 348	12	36.4	25	4	PCT-US93-00977-204	Sequence 204, App
C 276	12.2	37.0	25	4	US-09-941-450-18	Sequence 18, Appl	C 349	12	36.4	24	3	US-09-302-812-18	Sequence 18, Appl
C 277	12.2	37.0	26	3	US-08-859-998-575	Sequence 575, App	C 350	12	36.4	24	3	US-09-511-507-18	Sequence 18, Appl
C 278	12.2	37.0	26	3	US-09-225-928-575	Sequence 575, App	C 351	12	36.4	24	4	US-09-651-374A-10	Sequence 10, Appl
C 279	12.2	37.0	26	4	US-09-225-928-575	Sequence 575, App	C 352	12	36.4	25	4	US-09-641-259B-33	Sequence 33, Appl
C 280	12.2	37.0	27	3	US-09-332-769-8	Sequence 8, Appli	C 353	12	36.4	25	4	US-09-866-108A-10990	Sequence 10990, A
C 281	12.2	37.0	27	3	US-09-257-584-14	Sequence 14, Appl	C 354	12	36.4	27	4	US-09-254-180C-61	Sequence 61, Appl
C 282	12.2	37.0	27	3	US-09-456-153-8	Sequence 8, Appli	C 355	12	36.4	27	4	US-09-254-180C-106	Sequence 106, App
C 283	12.2	37.0	27	3	US-09-456-153-8	Sequence 8, Appli	C 356	12	36.4	29	2	US-08-889-909A-14	Sequence 14, Appl
C 284	12.2	37.0	27	3	US-09-426-533-8	Sequence 8, Appli	C 357	12	36.4	29	3	US-09-156-163A-14	Sequence 14, Appl
C 285	12.2	37.0	27	3	US-09-609-205-9	Sequence 9, Appli	C 358	12	36.4	29	4	US-09-304-232-748	Sequence 748, App
C 286	12.2	37.0	27	3	US-09-516-945-8	Sequence 8, Appli	C 359	12	36.4	29	4	US-09-982-308B-14	Sequence 14, Appl
C 287	12.2	37.0	27	3	US-09-757-218-9	Sequence 9, Appli	C 360	12	36.4	30	1	US-08-186-229-30	Sequence 30, Appl
C 288	12.2	37.0	27	3	US-09-516-757-8	Sequence 8, Appli	C 361	12	36.4	30	2	US-08-470-124-30	Sequence 30, Appl
C 289	12.2	37.0	27	3	US-09-516-750-8	Sequence 8, Appli	C 362	12	36.4	32	4	US-09-586-216C-9	Sequence 9, Appli
C 290	12.2	37.0	27	3	US-09-342-577-9	Sequence 9, Appli	C 363	12	36.4	33	3	US-09-232-071-18	Sequence 18, Appl
C 291	12.2	37.0	27	3	US-09-516-756-8	Sequence 8, Appli	C 364	12	36.4	33	3	US-09-292-071-19	Sequence 19, Appl
C 292	12.2	37.0	27	3	US-09-828-051A-9	Sequence 9, Appli	C 365	12	36.4	33	3	US-09-292-069A-18	Sequence 18, Appl
C 293	12.2	37.0	27	3	US-09-463-917-8	Sequence 8, Appli	C 366	12	36.4	33	3	US-09-292-069A-19	Sequence 19, Appl
C 294	12.2	37.0	27	4	US-09-347-673-9	Sequence 9, Appli	C 367	12	36.4	33	3	US-09-418-721-18	Sequence 18, Appl
C 295	12.2	37.0	27	4	US-09-757-213-9	Sequence 9, Appli	C 368	12	36.4	33	3	US-09-418-721-19	Sequence 19, Appl
C 296	12.2	37.0	27	4	US-09-656-653-8	Sequence 8, Appli	C 369	12	36.4	33	3	US-09-155-107-42	Sequence 42, Appl
C 297	12.2	37.0	27	4	US-09-757-251-9	Sequence 9, Appli	C 370	12	36.4	33	4	US-09-767-013-18	Sequence 18, Appl
C 298	12.2	37.0	27	4	US-09-828-259A-9	Sequence 9, Appli	C 371	12	36.4	33	4	US-09-767-013-19	Sequence 19, Appl
C 299	12.2	37.0	27	4	US-09-719-878-9	Sequence 9, Appli	C 372	12	36.4	33	4	US-09-292-072-18	Sequence 18, Appl
C 300	12.2	37.0	27	4	US-09-757-217A-9	Sequence 9, Appli	C 373	12	36.4	33	4	US-09-292-072-19	Sequence 19, Appl
C 301	12.2	37.0	27	4	US-09-828-325A-9	Sequence 9, Appli	C 374	12	36.4	34	4	US-09-474-432B-207	Sequence 207, App
C 302	12.2	37.0	27	4	US-09-756-248-8	Sequence 8, Appli	C 375	12	36.4	35	2	US-08-889-909A-11	Sequence 11, Appl
C 303	12.2	37.0	28	3	US-09-341-955-2	Sequence 2, Appli	C 376	12	36.4	35	3	US-09-156-163A-11	Sequence 11, Appl
C 304	12.2	37.0	28	4	US-09-779-881-2	Sequence 2, Appli	C 377	12	36.4	35	4	US-09-982-308B-11	Sequence 11, Appl
C 305	12.2	37.0	29	2	US-08-859-998-410	Sequence 410, App	C 378	12	36.4	35	4	US-09-476-387-207	Sequence 207, App
C 306	12.2	37.0	29	3	US-09-225-928-410	Sequence 410, App	C 379	12	36.4	36	4	US-09-474-432B-208	Sequence 208, App
C 307	12.2	37.0	29	4	US-09-225-201B-410	Sequence 410, App	C 380	12	36.4	37	1	US-08-244-378A-25	Sequence 25, Appl
C 308	12.2	37.0	30	1	US-08-384-708A-50	Sequence 50, Appl	C 381	12	36.4	37	4	US-09-476-387-208	Sequence 208, App
C 309	12.2	37.0	30	3	US-08-687-421-50	Sequence 50, Appl	C 382	12	36.4	38	3	US-09-476-387-208	Sequence 8, Appli
C 310	12.2	37.0	30	4	US-08-442-423-50	Sequence 50, Appl	C 383	12	36.4	38	3	US-09-609-154-8	Sequence 8, Appli
C 311	12.2	37.0	31	2	US-08-484-933B-54	Sequence 54, Appl	C 384	12	36.4	38	4	US-09-474-432B-937	Sequence 937, App
C 312	12.2	37.0	31	2	US-08-484-158B-54	Sequence 54, Appl	C 385	12	36.4	38	4	US-09-474-432B-988	Sequence 988, App
C 313	12.2	37.0	31	2	US-08-484-596A-54	Sequence 54, Appl	C 386	12	36.4	38	4	US-09-474-432B-1333	Sequence 1333, Ap
C 314	12.2	37.0	31	2	US-08-480-150A-54	Sequence 54, Appl	C 387	12	36.4	38	4	US-09-474-432B-1362	Sequence 1362, Ap
C 315	12.2	37.0	31	3	US-08-458-731-54	Sequence 54, Appl	C 388	12	36.4	38	4	US-09-371-772B-11262	Sequence 11262, A
C 316	12.2	37.0	31	3	US-08-149-223A-54	Sequence 54, Appl	C 389	12	36.4	38	4	US-09-371-772B-11420	Sequence 11420, A
C 317	12.2	37.0	32	4	US-09-837-644-4	Sequence 4, Appli	C 390	12	36.4	38	4	US-09-371-772B-11559	Sequence 11559, A
C 318	12.2	37.0	34	3	US-08-706-945D-36	Sequence 36, Appl	C 391	12	36.4	38	4	US-09-371-772B-13652	Sequence 13652, A
C 319	12.2	37.0	35	4	US-09-491-522-13	Sequence 13, Appl	C 392	12	36.4	38	4	US-09-476-387-936	Sequence 936, App

C 393	12	36.4	38	4	US-09-476-387-987	Sequence 987, App	466	11.8	35.8	35	3	US-09-199-149-21	Sequence 21, Appl
C 394	12	36.4	38	4	US-09-476-387-1332	Sequence 1332, App	C 467	11.8	35.8	37	4	US-09-813-781-19	Sequence 19, Appl
C 395	12	36.4	38	4	US-09-476-387-1361	Sequence 1361, App	468	11.8	35.8	37	4	US-09-842-164A-19	Sequence 19, Appl
C 396	12	36.4	39	3	US-09-476-299-7	Sequence 7, Appl	469	11.8	35.8	37	5	PCT-US93-08067-11	Sequence 11, Appl
C 397	12	36.4	39	3	US-09-609-154-7	Sequence 7, Appl	C 470	11.8	35.8	38	4	US-09-968-255-15	Sequence 15, Appl
C 398	12	36.4	40	1	US-08-049-264C-31	Sequence 31, Appl	471	11.8	35.8	38	4	US-07-623-611-15	Sequence 15, Appl
C 399	12	36.4	40	1	US-08-476-562-31	Sequence 31, Appl	C 472	11.8	35.8	39	5	PCT-US91-09108-15	Sequence 15, Appl
C 400	12	36.4	40	1	US-08-479-723A-31	Sequence 31, Appl	473	11.8	35.8	41	4	US-08-962-281-24	Sequence 24, Appl
C 401	12	36.4	40	2	US-08-425-684-13	Sequence 13, Appl	474	11.8	35.8	41	4	US-08-962-281-26	Sequence 26, Appl
C 402	12	36.4	40	2	US-08-675-502-13	Sequence 13, Appl	475	11.8	35.8	41	4	US-08-962-281-28	Sequence 28, Appl
C 403	12	36.4	40	4	US-09-245-803-13	Sequence 13, Appl	C 476	11.8	35.8	41	4	US-08-962-281-36	Sequence 36, Appl
C 404	12	36.4	40	5	PCT-US94-04310-31	Sequence 31, Appl	C 477	11.8	35.8	42	3	US-09-146-319-3	Sequence 3, Appl
C 405	12	36.4	42	3	US-09-306-405-28	Sequence 28, Appl	C 478	11.8	35.8	42	3	US-09-175-973-3	Sequence 3, Appl
C 406	12	36.4	45	4	US-09-518-914-18	Sequence 18, Appl	479	11.8	35.8	42	3	US-09-425-638A-5	Sequence 5, Appl
C 407	12	36.4	47	4	US-09-671-317-712	Sequence 712, App	480	11.8	35.8	42	3	US-09-543-004-5	Sequence 5, Appl
C 408	12	36.4	48	4	US-10-165-857-4	Sequence 4, Appl	C 481	11.8	35.8	46	3	US-07-920-222-42	Sequence 42, Appl
C 409	12	36.4	50	4	US-09-443-199C-4	Sequence 4, Appl	C 482	11.8	35.8	47	1	US-07-726-576B-25	Sequence 25, Appl
C 410	12	36.4	50	5	PCT-US93-01901-26	Sequence 26, Appl	C 483	11.8	35.8	47	1	US-09-641-638-1069	Sequence 1069, Ap
C 411	11.8	35.8	15	1	US-08-502-185-22	Sequence 22, Appl	484	11.8	35.8	47	4	US-09-538-709-127	Sequence 127, App
C 412	11.8	35.8	15	1	US-08-398-945-22	Sequence 22, Appl	485	11.8	35.8	47	4	US-09-538-709-1294	Sequence 831, App
C 413	11.8	35.8	15	1	US-08-501-779-22	Sequence 22, Appl	C 486	11.8	35.8	47	4	US-09-671-317-831	Sequence 831, App
C 414	11.8	35.8	15	1	US-08-501-713-22	Sequence 22, Appl	C 487	11.8	35.8	47	4	US-09-422-978-1323	Sequence 1323, Ap
C 415	11.8	35.8	15	1	US-08-378-860-22	Sequence 22, Appl	C 488	11.8	35.8	47	4	US-09-422-978-1414	Sequence 1414, Ap
C 416	11.8	35.8	15	1	US-08-501-626-22	Sequence 22, Appl	C 489	11.8	35.8	47	4	US-09-422-978-1414	Sequence 2548, Ap
C 417	11.8	35.8	15	1	US-08-501-356-22	Sequence 22, Appl	C 490	11.8	35.8	47	4	US-10-170-097-1069	Sequence 1069, Ap
C 418	11.8	35.8	16	2	US-08-292-620A-1617	Sequence 1617, Ap	C 491	11.8	35.8	48	1	US-08-399-412A-104	Sequence 104, App
C 419	11.8	35.8	16	3	US-09-071-845-1617	Sequence 1617, Ap	C 492	11.8	35.8	48	2	US-08-615-961-13	Sequence 13, Appl
C 420	11.8	35.8	17	2	US-08-757-653-152	Sequence 152, App	493	11.8	35.8	48	3	US-09-485-737B-23	Sequence 23, Appl
C 421	11.8	35.8	17	3	US-08-520-948-152	Sequence 152, App	494	11.8	35.8	50	1	US-08-207-901-90	Sequence 90, Appl
C 422	11.8	35.8	17	4	US-09-655-378A-152	Sequence 152, App	495	11.6	35.2	18	2	US-09-156-424-25	Sequence 25, Appl
C 423	11.8	35.8	17	4	US-09-866-108A-6087	Sequence 6087, Ap	496	11.6	35.2	18	4	US-09-387-341-39	Sequence 39, Appl
C 424	11.8	35.8	17	4	US-09-866-108A-6088	Sequence 6088, Ap	497	11.6	35.2	19	4	US-09-387-341-7	Sequence 7, Appl
C 425	11.8	35.8	20	1	US-08-502-185-21	Sequence 21, Appl	C 499	11.6	35.2	20	3	US-09-392-580-25	Sequence 25, Appl
C 426	11.8	35.8	20	1	US-08-398-945-21	Sequence 21, Appl	500	11.6	35.2	20	4	US-09-780-173A-26	Sequence 26, Appl
C 427	11.8	35.8	20	1	US-08-501-779-21	Sequence 21, Appl	C 501	11.6	35.2	20	4	US-08-894-454-60	Sequence 60, Appl
C 428	11.8	35.8	20	1	US-08-501-713-21	Sequence 21, Appl	502	11.6	35.2	21	3	US-09-153-947-5	Sequence 5, Appl
C 429	11.8	35.8	20	1	US-08-378-860-21	Sequence 21, Appl	503	11.6	35.2	21	4	US-09-657-472-1611	Sequence 1611, Ap
C 430	11.8	35.8	20	1	US-08-531-556-71	Sequence 71, Appl	504	11.6	35.2	22	1	US-08-283-203-13	Sequence 13, Appl
C 431	11.8	35.8	20	1	US-08-472-416-71	Sequence 71, Appl	505	11.6	35.2	22	3	US-09-475-316A-102	Sequence 102, App
C 432	11.8	35.8	20	1	US-08-501-626-21	Sequence 21, Appl	506	11.6	35.2	22	4	US-09-704-640-102	Sequence 102, App
C 433	11.8	35.8	20	1	US-08-501-356-21	Sequence 21, Appl	C 507	11.6	35.2	23	4	US-09-527-030G-155	Sequence 155, App
C 434	11.8	35.8	20	2	US-08-753-979A-25	Sequence 25, Appl	508	11.6	35.2	23	4	US-09-928-385B-15	Sequence 15, Appl
C 435	11.8	35.8	20	3	US-09-296-280-36	Sequence 36, Appl	509	11.6	35.2	23	4	US-09-379-888B-19	Sequence 19, Appl
C 436	11.8	35.8	20	3	US-09-686-179A-11	Sequence 11, Appl	C 510	11.6	35.2	24	1	US-08-758-626-10	Sequence 10, Appl
C 437	11.8	35.8	20	4	US-09-198-452A-5638	Sequence 5638, Ap	511	11.6	35.2	24	1	US-08-912-976-19	Sequence 19, Appl
C 438	11.8	35.8	20	4	US-09-509-595-36	Sequence 36, Appl	512	11.6	35.2	24	2	US-08-632-575B-56	Sequence 56, Appl
C 439	11.8	35.8	20	4	US-09-981-621-11	Sequence 11, Appl	513	11.6	35.2	24	4	US-09-199-542B-56	Sequence 56, Appl
C 440	11.8	35.8	22	4	US-09-528-348-5	Sequence 5, Appl	514	11.6	35.2	24	4	US-09-514-907A-4	Sequence 4, Appl
C 441	11.8	35.8	24	3	US-08-891-292A-90	Sequence 90, Appl	515	11.6	35.2	24	4	US-09-896-994-4	Sequence 4, Appl
C 442	11.8	35.8	24	4	US-09-927-737C-90	Sequence 90, Appl	C 516	11.6	35.2	24	5	PCT-US94-07684-10	Sequence 10, Appl
C 443	11.8	35.8	25	1	US-08-502-185-23	Sequence 23, Appl	517	11.6	35.2	25	4	US-09-866-108A-10978	Sequence 10978, A
C 444	11.8	35.8	25	1	US-08-398-945-23	Sequence 23, Appl	C 518	11.6	35.2	26	5	PCT-US92-04426-2	Sequence 2, Appl
C 445	11.8	35.8	25	1	US-08-501-779-23	Sequence 23, Appl	519	11.6	35.2	27	5	US-08-758-626-31	Sequence 31, Appl
C 446	11.8	35.8	25	1	US-08-501-713-23	Sequence 23, Appl	C 520	11.6	35.2	27	5	PCT-US94-07684-31	Sequence 31, Appl
C 447	11.8	35.8	25	1	US-08-378-860-23	Sequence 23, Appl	521	11.6	35.2	28	3	US-08-933-358-14	Sequence 14, Appl
C 448	11.8	35.8	25	1	US-08-501-626-23	Sequence 23, Appl	C 522	11.6	35.2	29	1	US-07-642-734C-8	Sequence 8, Appl
C 449	11.8	35.8	25	3	US-08-501-356-23	Sequence 23, Appl	523	11.6	35.2	29	3	US-08-439-009A-8	Sequence 8, Appl
C 450	11.8	35.8	25	3	US-09-103-577A-10	Sequence 10, Appl	C 524	11.6	35.2	29	3	US-08-613-298-2	Sequence 2, Appl
C 451	11.8	35.8	26	1	US-08-460-344-17	Sequence 17, Appl	525	11.6	35.2	29	4	US-09-810-506-4	Sequence 4, Appl
C 452	11.8	35.8	26	1	US-08-133-598A-17	Sequence 17, Appl	C 526	11.6	35.2	29	4	US-09-810-506-4	Sequence 2, Appl
C 453	11.8	35.8	26	1	US-08-886-999-17	Sequence 17, Appl	527	11.6	35.2	29	5	PCT-US95-04971-2	Sequence 2, Appl
C 454	11.8	35.8	26	5	PCT-US93-05085-17	Sequence 47, Appl	C 528	11.6	35.2	30	1	US-07-854-596B-21	Sequence 21, Appl
C 455	11.8	35.8	28	3	US-08-839-624-35	Sequence 35, Appl	529	11.6	35.2	30	2	US-08-676-378-1	Sequence 1, Appl
C 456	11.8	35.8	28	3	US-09-150-812-35	Sequence 35, Appl	C 530	11.6	35.2	30	3	US-08-899-595-10	Sequence 10, Appl
C 457	11.8	35.8	28	3	US-08-721-684C-5	Sequence 5, Appl	531	11.6	35.2	31	3	US-09-248-588-20	Sequence 20, Appl
C 458	11.8	35.8	29	2	US-09-005-970-5	Sequence 5, Appl	C 532	11.6	35.2	31	3	US-09-651-656-54	Sequence 54, Appl
C 459	11.8	35.8	29	3	US-09-407-715-5	Sequence 5, Appl	533	11.6	35.2	31	5	US-09-650-855-54	Sequence 54, Appl
C 460	11.8	35.8	29	3	US-08-578-649-6	Sequence 6, Appl	C 534	11.6	35.2	31	5	PCT-US94-04208-9	Sequence 9, Appl
C 461	11.8	35.8	31	1	US-08-050-319B-13	Sequence 13, Appl	535	11.6	35.2	31	5	PCT-US94-04208-10	Sequence 10, Appl
C 462	11.8	35.8	33	1	US-08-465-982-13	Sequence 13, Appl	C 536	11.6	35.2	32	4	US-09-410-935B-12	Sequence 12, Appl
C 463	11.8	35.8	33	2	US-09-617-548-10	Sequence 10, Appl	537	11.6	35.2	32	4	US-09-784-403A-12	Sequence 12, Appl
C 464	11.8	35.8	34	4	US-08-361-337-49	Sequence 49, Appl	C 538	11.6	35.2	33	1	US-08-051-935A-27	Sequence 27, Appl

C 539	11.6	35.2	33	3	US-08-840-062-11	Sequence 11, Appl	612	11.4	34.5	24	5	PCT-US95-16766-16	Sequence 16, Appl
C 540	11.6	35.2	33	4	US-09-302-765-2	Sequence 2, Appl	C 613	11.4	34.5	25	2	US-08-743-637B-124	Sequence 124, App
C 541	11.6	35.2	34	4	US-09-474-432B-270	Sequence 270, App	C 614	11.4	34.5	25	2	US-08-743-637B-270	Sequence 270, App
C 542	11.6	35.2	34	5	PCT-US93-00031-2	Sequence 2, Appl	C 615	11.4	34.5	25	3	US-08-526-840B-124	Sequence 124, App
C 543	11.6	35.2	35	1	US-08-464-531-62	Sequence 62, Appl	C 616	11.4	34.5	25	3	US-09-306-595C-41	Sequence 41, Appl
C 544	11.6	35.2	35	2	US-08-461-598-62	Sequence 62, Appl	C 617	11.4	34.5	25	4	US-09-925-388-41	Sequence 41, Appl
C 545	11.6	35.2	35	3	US-08-322-137-62	Sequence 62, Appl	C 618	11.4	34.5	25	4	US-08-866-108A-14597	Sequence 14597, A
C 546	11.6	35.2	35	3	US-08-936-632B-18	Sequence 18, Appl	C 619	11.4	34.5	25	4	US-08-866-108A-14598	Sequence 14598, A
C 547	11.6	35.2	35	3	US-08-582-333A-70	Sequence 70, Appl	C 620	11.4	34.5	25	4	US-08-866-108A-14599	Sequence 14599, A
C 548	11.6	35.2	35	4	US-09-476-387-269	Sequence 269, App	C 621	11.4	34.5	25	4	US-08-866-108A-14600	Sequence 14600, A
C 549	11.6	35.2	36	2	US-08-782-760-1	Sequence 1, Appl	C 622	11.4	34.5	26	1	US-08-464-202-5	Sequence 5, Appl
C 550	11.6	35.2	36	4	US-09-940-244-404	Sequence 404, App	C 623	11.4	34.5	26	1	US-08-484-434C-5	Sequence 5, Appl
C 551	11.6	35.2	36	5	PCT-US96-00995-1	Sequence 1, Appl	C 624	11.4	34.5	26	2	US-09-384-361-5	Sequence 5, Appl
C 552	11.6	35.2	37	3	US-08-435-568A-29	Sequence 29, Appl	C 625	11.4	34.5	27	4	US-09-758-282B-137	Sequence 137, App
C 553	11.6	35.2	37	3	US-08-822-516-9	Sequence 9, Appl	C 626	11.4	34.5	27	4	US-09-577-304A-137	Sequence 137, App
C 554	11.6	35.2	37	3	US-09-131-684-9	Sequence 9, Appl	C 627	11.4	34.5	28	1	US-09-331-793-39	Sequence 39, Appl
C 555	11.6	35.2	38	1	US-08-418-859-37	Sequence 37, Appl	C 628	11.4	34.5	29	1	US-08-307-444A-20	Sequence 20, Appl
C 556	11.6	35.2	38	2	US-08-643-181-37	Sequence 37, Appl	C 629	11.4	34.5	29	1	US-08-587-389-20	Sequence 20, Appl
C 557	11.6	35.2	38	4	US-09-474-432B-1090	Sequence 1090, Ap	C 630	11.4	34.5	29	3	US-09-403-066A-6	Sequence 6, Appl
C 558	11.6	35.2	38	4	US-09-474-432B-1121	Sequence 1121, Ap	C 631	11.4	34.5	29	4	US-09-470-276-43	Sequence 43, Appl
C 559	11.6	35.2	38	4	US-09-474-432B-1224	Sequence 1224, Ap	C 632	11.4	34.5	30	3	US-08-444-818-180	Sequence 180, App
C 560	11.6	35.2	38	4	US-09-474-432B-1316	Sequence 1316, Ap	C 633	11.4	34.5	30	4	US-09-733-042-41	Sequence 41, Appl
C 561	11.6	35.2	38	4	US-09-474-432B-1345	Sequence 1345, Ap	C 634	11.4	34.5	30	4	US-09-747-391-274	Sequence 274, App
C 562	11.6	35.2	38	4	US-09-371-772B-12294	Sequence 12294, A	C 635	11.4	34.5	30	5	PCT-US95-14418-16	Sequence 16, Appl
C 563	11.6	35.2	38	4	US-09-476-387-1089	Sequence 1089, Ap	C 636	11.4	34.5	30	5	PCT-US95-15327-16	Sequence 16, Appl
C 564	11.6	35.2	38	4	US-09-476-387-1120	Sequence 1120, Ap	C 637	11.4	34.5	30	5	PCT-US95-15327-17	Sequence 17, Appl
C 565	11.6	35.2	38	4	US-09-476-387-1223	Sequence 1223, Ap	C 638	11.4	34.5	31	2	US-08-961-749-5	Sequence 5, Appl
C 566	11.6	35.2	38	4	US-09-476-387-1315	Sequence 1315, Ap	C 639	11.4	34.5	31	2	US-08-164-664-2	Sequence 2, Appl
C 567	11.6	35.2	38	4	US-09-476-387-1344	Sequence 1344, Ap	C 640	11.4	34.5	31	3	US-09-569-601A-8	Sequence 8, Appl
C 568	11.6	35.2	40	2	US-08-031-538-15	Sequence 15, Appl	C 641	11.4	34.5	32	4	US-08-538-875-71	Sequence 71, Appl
C 569	11.6	35.2	40	2	US-08-031-538-16	Sequence 16, Appl	C 642	11.4	34.5	33	1	US-08-469-526A-105	Sequence 105, App
C 570	11.6	35.2	40	6	5519127-27	Patent No. 5519127	C 643	11.4	34.5	33	1	US-08-951-822-8	Sequence 8, Appl
C 571	11.6	35.2	41	3	US-09-142-355B-3	Sequence 3, Appl	C 644	11.4	34.5	33	2	US-09-368-951-8	Sequence 8, Appl
C 572	11.6	35.2	41	4	US-09-699-931-3	Sequence 3, Appl	C 645	11.4	34.5	33	3	US-09-368-951-8	Sequence 8, Appl
C 573	11.6	35.2	45	2	US-08-814-806-26	Sequence 26, Appl	C 646	11.4	34.5	33	4	US-09-229-947-8	Sequence 8, Appl
C 574	11.6	35.2	45	3	US-09-217-228-4	Sequence 4, Appl	C 647	11.4	34.5	33	4	US-08-829-931-3	Sequence 3, Appl
C 575	11.6	35.2	45	3	US-09-410-935B-17	Sequence 17, Appl	C 648	11.4	34.5	34	2	US-08-569-150A-20	Sequence 20, Appl
C 576	11.6	35.2	45	4	US-09-293-854-26	Sequence 26, Appl	C 649	11.4	34.5	35	2	US-08-537-402-2	Sequence 2, Appl
C 577	11.6	35.2	45	4	US-09-784-403A-17	Sequence 17, Appl	C 650	11.4	34.5	35	3	US-09-014-416-12	Sequence 12, Appl
C 578	11.6	35.2	47	1	US-07-990-303A-1	Sequence 1, Appl	C 651	11.4	34.5	35	5	PCT-US96-06224-5	Sequence 5, Appl
C 579	11.6	35.2	47	1	US-08-196-103A-1	Sequence 1, Appl	C 652	11.4	34.5	35	1	US-08-154-916-7	Sequence 7, Appl
C 580	11.6	35.2	47	1	US-08-357-396-1	Sequence 1, Appl	C 653	11.4	34.5	36	1	US-08-455-860-6	Sequence 6, Appl
C 581	11.6	35.2	47	1	US-08-386-141-1	Sequence 1, Appl	C 654	11.4	34.5	36	1	US-08-383-749-6	Sequence 6, Appl
C 582	11.6	35.2	47	2	US-08-659-567-16	Sequence 16, Appl	C 655	11.4	34.5	36	2	US-08-600-908A-8	Sequence 8, Appl
C 583	11.6	35.2	47	4	US-09-422-978-345	Sequence 345, App	C 656	11.4	34.5	36	3	US-08-683-838A-8	Sequence 8, Appl
C 584	11.6	35.2	47	4	US-09-422-978-1841	Sequence 1841, Ap	C 657	11.4	34.5	36	3	US-09-182-859-11	Sequence 11, Appl
C 585	11.6	35.2	47	4	US-09-422-978-3780	Sequence 3780, Ap	C 658	11.4	34.5	36	4	US-09-537-168-10	Sequence 10, Appl
C 586	11.6	35.2	47	4	US-09-408-926-33	Sequence 33, Appl	C 659	11.4	34.5	36	4	US-09-672-459-11	Sequence 11, Appl
C 587	11.6	35.2	49	3	US-09-109-063-28	Sequence 28, Appl	C 660	11.4	34.5	36	4	US-09-636-252A-8	Sequence 8, Appl
C 588	11.6	35.2	49	3	US-09-109-063-29	Sequence 29, Appl	C 661	11.4	34.5	36	4	US-09-169-205D-18	Sequence 18, App
C 589	11.6	35.2	49	4	US-09-448-310-28	Sequence 28, Appl	C 662	11.4	34.5	36	4	US-09-474-432B-200	Sequence 200, App
C 590	11.6	35.2	49	4	US-09-448-310-29	Sequence 29, Appl	C 663	11.4	34.5	36	4	US-09-474-432B-219	Sequence 219, App
C 591	11.6	35.2	50	3	US-09-390-867A-12	Sequence 12, Appl	C 664	11.4	34.5	36	4	US-09-474-432B-249	Sequence 249, App
C 592	11.6	35.2	50	3	US-09-548-260-12	Sequence 12, Appl	C 665	11.4	34.5	36	4	US-09-474-432B-255	Sequence 255, App
C 593	11.4	34.5	21	2	US-08-832-449A-2	Sequence 2, Appl	C 666	11.4	34.5	36	4	US-10-186-042-11	Sequence 11, Appl
C 594	11.4	34.5	21	4	US-09-447-103A-11	Sequence 11, Appl	C 667	11.4	34.5	37	1	US-08-709-912-47	Sequence 47, Appl
C 595	11.4	34.5	22	1	US-08-400-580A-7	Sequence 7, Appl	C 668	11.4	34.5	37	2	US-09-047-370-47	Sequence 47, Appl
C 596	11.4	34.5	22	2	US-08-068-729-2	Sequence 2, Appl	C 669	11.4	34.5	37	4	US-09-477-135A-150	Sequence 150, App
C 597	11.4	34.5	22	3	US-09-255-671-2	Sequence 2, Appl	C 670	11.4	34.5	37	4	US-09-476-387-200	Sequence 200, App
C 598	11.4	34.5	22	4	US-09-393-366-2	Sequence 2, Appl	C 671	11.4	34.5	37	4	US-09-476-387-219	Sequence 219, App
C 599	11.4	34.5	22	4	US-09-371-615A-4	Sequence 4, Appl	C 672	11.4	34.5	37	4	US-09-476-387-248	Sequence 248, App
C 600	11.4	34.5	22	4	US-09-589-560B-80	Sequence 80, Appl	C 673	11.4	34.5	37	4	US-09-476-387-254	Sequence 254, App
C 601	11.4	34.5	23	5	PCT-US94-05085A-16	Sequence 16, Appl	C 674	11.4	34.5	38	3	US-08-811-463-10	Sequence 10, Appl
C 602	11.4	34.5	23	5	PCT-US94-05085-16	Sequence 16, Appl	C 675	11.4	34.5	38	4	US-09-474-432B-908	Sequence 908, App
C 603	11.4	34.5	24	1	US-08-360-096-7	Sequence 7, Appl	C 676	11.4	34.5	38	4	US-09-474-432B-1134	Sequence 1134, Ap
C 604	11.4	34.5	24	1	US-08-538-875-35	Sequence 35, Appl	C 677	11.4	34.5	38	4	US-09-474-432B-1152	Sequence 1152, Ap
C 605	11.4	34.5	24	2	US-08-812-003-6	Sequence 6, Appl	C 678	11.4	34.5	38	4	US-09-474-432B-1168	Sequence 1168, Ap
C 606	11.4	34.5	24	2	US-08-899-371-18	Sequence 18, Appl	C 679	11.4	34.5	38	4	US-09-474-432B-1265	Sequence 1265, Ap
C 607	11.4	34.5	24	2	US-08-859-998-754	Sequence 754, App	C 680	11.4	34.5	38	4	US-09-474-432B-1416	Sequence 1416, Ap
C 608	11.4	34.5	24	3	US-08-576-202-16	Sequence 16, Appl	C 681	11.4	34.5	38	4	US-09-371-772B-7971	Sequence 7971, Ap
C 609	11.4	34.5	24	3	US-09-225-928-754	Sequence 754, App	C 682	11.4	34.5	38	4	US-09-371-772B-7980	Sequence 7980, Ap
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C 611	11.4	34.5	24	4	US-09-225-201B-754	Sequence 754, App	C 684	11.4	34.5	38	4	US-09-371-772B-10896	Sequence 10896, A

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c 686	11.4	34.5	38	4	US-09-476-387-907	Sequence 907, App		759	11.2	33.9	19	4	US-09-696-791-1089	Sequence 1089, Ap
c 687	11.4	34.5	38	4	US-09-476-387-1133	Sequence 1133, Ap		760	11.2	33.9	19	4	US-09-696-791-1090	Sequence 1090, Ap
c 688	11.4	34.5	38	4	US-09-476-387-1151	Sequence 1151, Ap		c 761	11.2	33.9	20	3	US-09-047-347-50	Sequence 50, Appl
c 689	11.4	34.5	38	4	US-09-476-387-1167	Sequence 1167, Ap		c 762	11.2	33.9	20	4	US-09-033-336-40	Sequence 40, Appl
c 690	11.4	34.5	38	4	US-09-476-387-1264	Sequence 1264, Ap		c 763	11.2	33.9	20	4	US-09-935-316B-4	Sequence 4, Appl
c 691	11.4	34.5	38	4	US-09-476-387-1415	Sequence 1415, Ap		c 764	11.2	33.9	20	4	US-09-917-963-85	Sequence 85, Appl
c 692	11.4	34.5	40	1	US-08-066-961-34	Sequence 34, Appl		c 765	11.2	33.9	21	2	US-08-403-888A-91	Sequence 91, Appl
c 693	11.4	34.5	40	1	US-08-191-866D-88	Sequence 88, Appl		c 766	11.2	33.9	22	3	US-08-619-542B-74	Sequence 74, Appl
c 694	11.4	34.5	40	1	US-08-480-640A-140	Sequence 140, Appl		c 767	11.2	33.9	22	3	US-09-468-872-13	Sequence 13, Appl
c 695	11.4	34.5	40	3	US-08-235-802-140	Sequence 140, App		c 768	11.2	33.9	22	4	US-08-669-656A-10	Sequence 10, Appl
c 696	11.4	34.5	40	3	US-08-686-968C-67	Sequence 67, Appl		c 769	11.2	33.9	22	4	US-09-079-723-118	Sequence 118, App
c 697	11.4	34.5	40	3	US-08-488-237A-140	Sequence 140, App		c 770	11.2	33.9	23	1	US-08-301-722A-7	Sequence 7, Appl
c 698	11.4	34.5	40	3	US-08-375-992A-140	Sequence 140, App		c 771	11.2	33.9	23	3	US-09-139-617-4	Sequence 4, Appl
c 699	11.4	34.5	40	4	US-08-897-956A-27	Sequence 27, Appl		c 772	11.2	33.9	23	4	US-09-561-741A-4	Sequence 4, Appl
c 700	11.4	34.5	40	4	US-08-472-679H-140	Sequence 140, App		c 773	11.2	33.9	23	4	US-09-558-795-4	Sequence 7, Appl
c 701	11.4	34.5	41	1	US-07-623-611-14	Sequence 14, Appl		c 774	11.2	33.9	23	4	US-09-674-826B-7	Sequence 7, Appl
c 702	11.4	34.5	41	5	PCT-US91-09108-14	Sequence 14, Appl		c 775	11.2	33.9	23	4	US-09-587-945-25	Sequence 25, Appl
c 703	11.4	34.5	42	3	US-09-275-850-218	Sequence 218, App		c 776	11.2	33.9	24	1	US-08-758-626-9	Sequence 9, Appl
c 704	11.4	34.5	42	4	US-09-787-465-6	Sequence 6, Appl		c 777	11.2	33.9	24	1	US-08-912-976-18	Sequence 18, Appl
c 705	11.4	34.5	43	1	US-08-384-708A-183	Sequence 183, App		c 778	11.2	33.9	24	5	PCT-US94-0768A-9	Sequence 9, Appl
c 706	11.4	34.5	43	3	US-08-732-708C-22	Sequence 22, Appl		c 779	11.2	33.9	25	3	US-08-840-316-8	Sequence 8, Appl
c 707	11.4	34.5	43	3	US-08-687-421-183	Sequence 183, App		c 780	11.2	33.9	25	3	US-08-809-523-8	Sequence 8, Appl
c 708	11.4	34.5	43	4	US-08-442-423-183	Sequence 183, App		c 781	11.2	33.9	25	3	US-08-471-971-8	Sequence 8, Appl
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836	11.2	33.9	34	3	US-08-469-318-170	Sequence 170, App	909	11.2	33.9	50	4	US-08-706-054A-7	Sequence 7, Appli
837	11.2	33.9	34	3	US-08-468-609A-170	Sequence 170, App	c 910	11.2	33.9	50	4	US-09-313-299-7	Sequence 7, Appli
838	11.2	33.9	34	3	US-08-471-045-51	Sequence 51, Appl	c 911	11.2	33.9	50	4	US-08-956-171E-5135	Sequence 5135, Ap
c 839	11.2	33.9	34	3	US-08-469-712A-51	Sequence 51, Appl	c 912	11.2	33.9	50	4	US-08-781-986A-5135	Sequence 5135, Ap
c 840	11.2	33.9	34	3	US-08-974-549A-482	Sequence 482, App	c 913	11.2	33.9	50	4	US-09-034-205-12	Sequence 12, Appl
841	11.2	33.9	34	3	US-08-875-533-23	Sequence 23, Appl	c 914	11	33.3	11	3	US-08-934-097A-12	Sequence 12, Appl
842	11.2	33.9	34	3	US-08-446-871-51	Sequence 51, Appl	c 915	11	33.3	11	3	US-08-851-588-12	Sequence 12, Appl
843	11.2	33.9	34	3	US-08-446-872A-170	Sequence 170, App	c 916	11	33.3	11	3	US-09-677-218B-12	Sequence 12, Appl
844	11.2	33.9	34	3	US-08-468-910-51	Sequence 51, Appl	c 917	11	33.3	11	3	US-09-677-192-12	Sequence 12, Appl
845	11.2	33.9	34	4	US-08-761-907-51	Sequence 51, Appl	c 918	11	33.3	11	4	US-09-402-618B-12	Sequence 12, Appl
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c 847	11.2	33.9	34	4	US-08-912-951-249	Sequence 249, App	c 920	11	33.3	11	4	US-09-676-768-12	Sequence 12, Appl
c 848	11.2	33.9	34	4	US-09-402-181B-482	Sequence 482, App	c 921	11	33.3	15	3	US-09-034-205-62	Sequence 62, Appl
c 849	11.2	33.9	34	4	US-09-721-456-482	Sequence 482, App	c 922	11	33.3	15	3	US-09-677-218B-62	Sequence 62, Appl
c 850	11.2	33.9	34	5	PCT-US95-01185-170	Sequence 170, App	c 923	11	33.3	15	3	US-09-677-192-62	Sequence 62, Appl
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c 854	11.2	33.9	36	1	US-08-309-512-59	Sequence 59, Appl	c 927	11	33.3	19	3	US-08-488-208A-80	Sequence 80, Appl
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c 857	11.2	33.9	36	2	US-08-482-293A-29	Sequence 29, Appl	c 930	11	33.3	19	4	US-08-438-421A-80	Sequence 80, Appl
c 858	11.2	33.9	36	3	US-08-943-363-29	Sequence 29, Appl	c 931	11	33.3	19	4	US-08-488-225A-80	Sequence 80, Appl

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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05812-6

Query Match 61.8%; Score 20.4; DB 5; Length 28;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTATGGC 33
Db 4 CCGTTCGCGACCACTATGGC 25

RESULT 4
US-09-153-242-39/c
Sequence 39, Application US/09153242
Patent No. 6482592
GENERAL INFORMATION:
APPLICANT: Lundberg, Joakim
APPLICANT: Uhlen, Mathias
TITLE OF INVENTION: MODULAR PROBES II
CURRENT APPLICATION NUMBER: US/09/153,242
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LENGTH: 36
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ORGANISM: Hepatitis C virus
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Query Match 61.8%; Score 20.4; DB 4; Length 36;
Best Local Similarity 95.5%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 27 CCGTTCGCGACCACTATGGC 6

RESULT 5
US-08-299-682-9/c
Sequence 9, Application US/08299682
Patent No. 5491063
GENERAL INFORMATION:
APPLICANT: Fisher, Mary Ellen
APPLICANT: Watson, Robert Malcom
TITLE OF INVENTION: Methods for In-Solution Quenching of
Fluorescently Labeled Oligonucleotide Probes
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,682
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2977
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-299-682-9

Query Match 60.6%; Score 20; DB 1; Length 38;
Best Local Similarity 96.9%; Pred. No. 3.6;
Matches 31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CGGTGTACTACC-GTTCGCGACCACTATG 31
Db 32 CGGTGTACTACC-GTTCGCGACCACTATG 1

RESULT 6
US-08-299-682-10/C
Sequence 10, Application US/08299682
Patent No. 5491063
GENERAL INFORMATION:
APPLICANT: Fisher, Mary Ellen
APPLICANT: Watson, Robert Malcom
TITLE OF INVENTION: Methods for In-Solution Quenching of
Fluorescently Labeled Oligonucleotide Probes
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,682
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2977
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-299-682-10

Query Match 60.6%; Score 20; DB 1; Length 38;
Best Local Similarity 96.9%; Pred. No. 3.6;
Matches 31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGGTGTACTCACC-GTTCGCGACCACTATG 31
|||||
DB 32 CGGTGTACTCACC-GTTCGCGACCACTATG 1

RESULT 7

US-08-097-853-3/c
; Sequence 3, Application US/08097853
; Patent No. 5679342
; GENERAL INFORMATION:
; APPLICANT: HAN, JANG H.
; APPLICANT: YOO, BYONG J.
; APPLICANT: SUH, BYUNG S.
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTED CELL SYSTEMS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,853
; FILING DATE: 19930727
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDMAN, KENNETH M.
; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 0088.003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; TELEX: n/a

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-097-853-3

Query Match 58.8%; Score 19.4; DB 1; Length 30;
Best Local Similarity 95.2%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CGGTTCGCGACCACTATGG 32
|||||
DB 21 CGGTTCGCGACCACTATGG 1

US-08-097-853-3
; Sequence 3, Application US/08438435
; Patent No. 5968775
; GENERAL INFORMATION:
; APPLICANT: HAN, JANG H.
; APPLICANT: YOO, BYONG J.
; APPLICANT: SUH, BYUNG S.
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTED CELL SYSTEMS
; NUMBER OF SEQUENCES: 3

QY 12 CGGTTCGCGACCACTATGG 32
|||||
DB 21 CGGTTCGCGACCACTATGG 1

RESULT 8

US-08-438-435-3/c
; Sequence 3, Application US/08438435
; Patent No. 5968775
; GENERAL INFORMATION:
; APPLICANT: HAN, JANG H.
; APPLICANT: YOO, BYONG J.
; APPLICANT: SUH, BYUNG S.
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTED CELL SYSTEMS
; NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION
STREET: 4560 Horton Street, R-440
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,435
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,853
; FILING DATE: 27-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDMAN, KENNETH M.
; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 0088.003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; TELEX: n/a

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-438-435-3

Query Match 58.8%; Score 19.4; DB 2; Length 30;
Best Local Similarity 95.2%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CGGTTCGCGACCACTATGG 32
|||||
DB 21 CGGTTCGCGACCACTATGG 1

US-08-438-435-3

Query Match 58.8%; Score 19.4; DB 2; Length 30;
Best Local Similarity 95.2%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CGGTTCGCGACCACTATGG 32
|||||
DB 21 CGGTTCGCGACCACTATGG 1

RESULT 9

US-08-444-818-217/c
; Sequence 217, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995

US-08-444-818-217/c
; Sequence 217, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995

ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic polynucleotide
DESCRIPTION: probe used for isolation of clone 18g."
US-08-444-818-217

Query Match 58.8%; Score 19.4; DB 3; Length 30;
Best Local Similarity 95.2%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTATGG 32
Db 21 CCGTTCGCGACCACTATGG 1

RESULT 10
US-09-494-332A-1/c
Sequence 1, Application US/09494332A
Patent No. 6623919
GENERAL INFORMATION:
APPLICANT: GORMAN, Kevin
APPLICANT: PATTERSON, David
APPLICANT: LINNEN, Jeffrey
APPLICANT: SONG, Reming
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT MULTIPLEX DETECTION OF HEPATITIS C VIRUS (HCV) AND HUMAN IMMUNODEFICIENCY VIRUS (HIV) AND METHODS OF USE
FILE REFERENCE: 2049/1E285-US1
CURRENT APPLICATION NUMBER: US/09/494,332A
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/118,498
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer
US-09-494-332A-1

Query Match 57.6%; Score 19; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCGACCACTATGGC 33
Db 25 TTCCGCGACCACTATGGC 7

RESULT 11
US-09-494-332A-10/c
Sequence 10, Application US/09494332A
Patent No. 6623919
GENERAL INFORMATION:
APPLICANT: GORMAN, Kevin
APPLICANT: PATTERSON, David
APPLICANT: LINNEN, Jeffrey
APPLICANT: SONG, Reming
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT MULTIPLEX DETECTION OF HEPATITIS C VIRUS (HCV) AND HUMAN IMMUNODEFICIENCY VIRUS (HIV) AND METHODS OF USE

FILE REFERENCE: 2049/1E285-US1
CURRENT APPLICATION NUMBER: US/09/494,332A
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/118,498
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer
US-09-494-332A-10

Query Match 57.6%; Score 19; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCGACCACTATGGC 33
Db 25 TTCCGCGACCACTATGGC 7

RESULT 12
US-09-493-353-2/c
Sequence 2, Application US/09493353
Patent No. 6638714
GENERAL INFORMATION:
APPLICANT: Johnson & Johnson
APPLICANT: LINNEN, J.M.
APPLICANT: GORMAN, K.M.
TITLE OF INVENTION: DETECTION OF HEPATITIS C VIRUS (HCV) AND METHODS OF USE
FILE REFERENCE: 2094/1E286-US1
CURRENT APPLICATION NUMBER: US/09/493,353
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/118,497
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer
US-09-493-353-2

Query Match 57.6%; Score 19; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCGACCACTATGGC 33
Db 25 TTCCGCGACCACTATGGC 7

RESULT 13
US-08-533-820A-6
Sequence 6, Application US/08533820A
Patent No. 5789153
GENERAL INFORMATION:
APPLICANT: FALKNER, Falko-Guenther
APPLICANT: HAEMMERLE, Thomas
APPLICANT: HIMMELSPACH, Michele
APPLICANT: KOHL, Johann
APPLICANT: DORNER, Friedrich
TITLE OF INVENTION: A METHOD OF QUANTITATING NUCLEIC ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,820A
FILING DATE: 26-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 1831/94
FILING DATE: 26-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 2245/94
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40433/140/SOPA
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-533-820A-6

Query Match 55.8%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGGTTCCGCGACCACTATG 31
DB 1 CGGTTCCGCGACCACTATG 20

RESULT 14
US-08-150-204E-125/c
Sequence 125, Application US/08150204E
Patent No. 6538126
GENERAL INFORMATION:
APPLICANT: CHO, Joong Myung
LEE, Yong Beom
PARK, Young Woo
LIM, Kook Jin
CHOI, Deog Young
SO, Hong Seob
KIM, Chun Hyung
KIM, Sung Taek
YANG, Jae Young
TITLE OF INVENTION: HEPATITIS C DIAGNOSTICS AND VACCINES
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: YANG, Jae Young
STREET: 386-1, Doryong-dong, Yuseong-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-340
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
COMPUTER: IBM PC/pentium
OPERATING SYSTEM: Windows
SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/150,204E
FILING DATE: 20-Apr-1994
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 91-9510
FILING DATE: 10-JUN-1991
APPLICATION NUMBER: KR 91-13601
FILING DATE: 6-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Shahan Islam, Esq.
REGISTRATION NUMBER: 321,507
REFERENCE/DOCKET NUMBER: 2695/FLK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 940-8564
TELEFAX: (212) 940-8776
INFORMATION FOR SEQ ID NO: 125
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: primer A
SEQUENCE DESCRIPTION: SEQ ID NO: 125
US-08-150-204E-125

Query Match 55.8%; Score 18.4; DB 4; Length 20;
Best Local Similarity 95.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGGTTCCGCGACCACTATG 31
DB 20 CGGTTCCGCGACCACTATG 1

RESULT 15
US-08-299-682-11/c
Sequence 11, Application US/08299682
Patent No. 5491063
GENERAL INFORMATION:
APPLICANT: Fisher, Mary Ellen
APPLICANT: Watson, Robert Malcom
TITLE OF INVENTION: Methods for In-Solution Quenching of
TITLE OF INVENTION: Fluorescently Labeled Oligonucleotide Probes
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,682
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-299-682-11

Query Match      55.8%; Score 18.4; DB 1; Length 26;
Best Local Similarity 95.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12  CCGTTCCGCAGACCCTATG 31
Db      20  CCGTTCCGCAGACCCTATG 1

RESULT 16
US-08-240-547-43/c
; Sequence 43, Application US/08240547
; Patent No. 5527869
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2977
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-240-547-43

Query Match      55.8%; Score 18.4; DB 1; Length 26;
Best Local Similarity 95.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12  CCGTTCCGCAGACCCTATG 31
Db      20  CCGTTCCGCAGACCCTATG 1

RESULT 17
US-08-397-220B-50
; Sequence 50, Application US/08397220B
; Patent No. 6284458
```

```
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: Compositions And Methods For Treatment
;       Of Hepatitis C Virus-Associated Diseases
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,220B
; FILING DATE: 09-Mar-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/01293
; FILING DATE: 10-Sep-93
; APPLICATION NUMBER: JP 5-87195
; FILING DATE: 14-Apr-93
; APPLICATION NUMBER: 07/945,289
; FILING DATE: 10-Sep-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-08-397-220B-50

Query Match      52.7%; Score 17.4; DB 3; Length 20;
Best Local Similarity 94.7%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12  CCGTTCCGCAGACCCTAT 30
Db      2  CCGTTCCGCAGACCCTAT 20

RESULT 18
US-08-650-093C-50
; Sequence 50, Application US/08650093C
; Patent No. 6391542
; GENERAL INFORMATION:
; APPLICANT: Kevin P. Anderson et al.
; TITLE OF INVENTION: Compositions And Methods For Treatment Of
;       Hepatitis C Virus-Associated Diseases
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LICATA & TYRRELL P.C.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM Compatible
```

OPERATING SYSTEM: Windows 95
SOFTWARE: WORDPERFECT 6.1 for Windows
CURRENT APPLICATION DATA: US/08/650,093C
APPLICATION NUMBER: US/08/650,093C
FILING DATE: 17-May-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/452,841
FILING DATE: May 30, 1995
APPLICATION NUMBER: 08/397,220
FILING DATE: March 9, 1995
APPLICATION NUMBER: 07/945,289
FILING DATE: September 10, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-08-650-093C-50

Query Match 52.7%; Score 17.4; DB 3; Length 20;
Best Local Similarity 94.7%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCGTTCGCGAGACCACCTAT 30
|||||
DB 2 CCGTTCGCGAGACCACCTAT 20

RESULT 19
US-08-954-210-9/c
; Sequence 9, Application US/08954210
; Patent No. 6043077
; GENERAL INFORMATION:
; APPLICANT: Barber, Jack R.
; APPLICANT: Welch, Peter J.
; APPLICANT: Tritz, Richard
; APPLICANT: Yei, Soonpin
; APPLICANT: Yu, Mang
; TITLE OF INVENTION: HEPATITIS C VIRUS RIBOZYMES
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,210
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480124.403C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-954-210-9

Query Match 48.5%; Score 16; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCCGCGAGACCACCTA 29
|||||
DB 16 GTTCCGCGAGACCACCTA 1

RESULT 20
US-09-431-419A-9/c
; Sequence 9, Application US/09431419A
; Patent No. 6458567
; GENERAL INFORMATION:
; APPLICANT: Barber, Jack R.
; APPLICANT: Welch, Peter J.
; APPLICANT: Tritz, Richard
; APPLICANT: Yei, Soonpin
; APPLICANT: Yu, Mang
; TITLE OF INVENTION: HEPATITIS C VIRUS RIBOZYMES
; FILE REFERENCE: 480124.403C3
; CURRENT APPLICATION NUMBER: US/09/431,419A
; CURRENT FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Hepatitis C Virus
US-09-431-419A-9

Query Match 48.5%; Score 16; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCCGCGAGACCACCTA 29
|||||
DB 16 GTTCCGCGAGACCACCTA 1

RESULT 21
US-09-474-432B-24/c
; Sequence 24, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Svedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511

; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-09-474-432B-24

Query Match 48.5%; Score 16; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCAGACCACTAT 30
| | | | | | | | | | | | | | | | | |
Db 16 TTCCGCAGACCACTAT 1

RESULT 22

US-09-476-387-24/c
; Sequence 24, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpetsky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Svedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
; FILE REFERENCE: MBH00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476.387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hepatitis C Virus
US-09-476-387-24

Query Match 48.5%; Score 16; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCAGACCACTAT 30
| | | | | | | | | | | | | | | | | |
Db 16 TTCCGCAGACCACTAT 1

RESULT 23

US-08-438-639-46
; Sequence 46, Application US/08438639
; Patent No. 5712383
; GENERAL INFORMATION:
; APPLICANT: Sheridan, Patrick
; APPLICANT: Chang, Chu-An
; APPLICANT: Running, Joyce
; APPLICANT: Urdea, Michael S.
; TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID

; TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION - R440
; STREET: P.O. Box 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,639
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,338
; FILING DATE: 23-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Kenneth, M.
; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 0232.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-438-639-46

Query Match 48.5%; Score 16; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 CGCAGACCACTATGCC 33
| | | | | | | | | | | | | | | | | |
Db 1 CGCAGACCACTATGCC 16

RESULT 24

US-07-813-338A-46
; Sequence 46, Application US/07813338A
; Patent No. 5747244
; GENERAL INFORMATION:
; APPLICANT: Sheridan, Patrick
; APPLICANT: Chang, Chu-An
; APPLICANT: Running, Joyce
; APPLICANT: Urdea, Michael S.
; TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION - R440
; STREET: P.O. Box 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/813,338A
; FILING DATE: 23-DEC-1991

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Kenneth, M.
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 0232.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2719
TELEFAX: (510) 655-3542
TELEX: N/A
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-813-338A-46

Query Match 48.5%; Score 16; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACTATGGC 33
DB 1 CGCAGACCACTATGGC 16

RESULT 25
US-08-470-124-79
Sequence 79, Application US/08470124
Patent No. 5849481
GENERAL INFORMATION:
APPLICANT: Urdea, Michael S.
APPLICANT: Horn, Thomas
APPLICANT: Chang, Chu-An
APPLICANT: Warner, Brian
APPLICANT: Fultz, Timothy J.
TITLE OF INVENTION: LARGE COMB-TYPE BRANCHED
POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Forster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,588
FILING DATE: 23 December 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clotti, Thomas E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20104.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-124-79

Query Match 48.5%; Score 16; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACTATGGC 33
DB 1 CGCAGACCACTATGGC 16

RESULT 25
US-08-470-124-79
Sequence 79, Application US/08470124
Patent No. 5849481
GENERAL INFORMATION:
APPLICANT: Urdea, Michael S.
APPLICANT: Horn, Thomas
APPLICANT: Chang, Chu-An
APPLICANT: Warner, Brian
APPLICANT: Fultz, Timothy J.
TITLE OF INVENTION: LARGE COMB-TYPE BRANCHED
POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Forster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,588
FILING DATE: 23 December 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clotti, Thomas E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20104.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-124-79

Query Match 48.5%; Score 16; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACTATGGC 33
DB 1 CGCAGACCACTATGGC 16

RESULT 25
US-08-441-971-122
Sequence 122, Application US/08441971
Patent No. 6071693
GENERAL INFORMATION:
APPLICANT: Tai-An Cha
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,971
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,653
FILING DATE:
APPLICATION NUMBER: US/07/881,528
FILING DATE:
APPLICATION NUMBER: 07/697,326
FILING DATE: 8 May 1991
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J.
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: C0772/7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 720-3500
TELEFAX: (617) 720-2441
TELEX: EZEKIEL
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-441-971-122

Query Match 48.5%; Score 16; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACTATGGC 33
DB 1 CGCAGACCACTATGGC 16

RESULT 27
US-08-221-653-122
Sequence 122, Application US/08221653
Patent No. 6190864
GENERAL INFORMATION:

APPLICANT: Tai-An Cha
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: US/08/221,653
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/881,528
FILING DATE: 8 May 1991
APPLICATION NUMBER: 07/697,326
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J.
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: C0772/7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 720-3500
TELEFAX: (617) 720-2441
TELEX: EZEKIEL
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-221-653-122

Query Match 48.5%; Score 16; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACCTATGCG 33
DB 1 CGCAGACCACCTATGCG 16

RESULT 28
US-08-442-144A-122
Sequence 122, Application US/08442144A
Patent No. 6214583
GENERAL INFORMATION:
APPLICANT: Tai-An Cha
APPLICANT: Eileen Beall
APPLICANT: Bruce Irvine
APPLICANT: Janice Kolberg
APPLICANT: Michael S. Urdea
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 Inch

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,144A
FILING DATE: MAY 16, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/221,653
FILING DATE: APRIL 1, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Doreen Yatko Trujillo
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CHIR-0121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
TELEX:
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 Nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: DNA
US-08-442-144A-122

Query Match 48.5%; Score 16; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACCTATGCG 33
DB 1 CGCAGACCACCTATGCG 16

RESULT 29
US-08-441-970-122
Sequence 122, Application US/08441970
Patent No. 6297370
GENERAL INFORMATION:
APPLICANT: Tai-An Cha
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,970
FILING DATE: 16-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/881,528
FILING DATE: 08-MAY-1992
APPLICATION NUMBER: 07/697,326
FILING DATE: 8 May 1991
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J.
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: C0772/7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 720-3500
TELEFAX: (617) 720-2441

```

; TELEX: EZEKIEL
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-441-970-122

Query Match      48.5%; Score 16; DB 3; Length 33;
Best Local Similarity 100.0%; Pred.No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   18 CGCAGACCACTATGGC 33
    |||
DB   1 CGCAGACCATTGCG 16

RESULT 30
US-08-435-568A-28
; Sequence 28, Application US/08435568A
; Patent No. 6143298
; GENERAL INFORMATION:
; APPLICANT: Greve, Jeffrey M.
; APPLICANT: McClelland, Alan
; APPLICANT: Davis, Gary
; TITLE OF INVENTION: Soluble Truncated Forms of ICAM-1
; FILE REFERENCE: MCI 208.4C2D2
; CURRENT APPLICATION NUMBER: US/08/435.568A
; CURRENT FILING DATE: 1995-05-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-435-568A-28

Query Match      48.5%; Score 16; DB 3; Length 39;
Best Local Similarity 79.2%; Pred.No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY   6 TACTCACCGTTCGCAGACCACTA 29
    |||
DB   11 TCCTCACCGTTCTGGAGTCCAGTA 34

RESULT 31
US-08-417-551-5
; Sequence 5, Application US/08417551
; Patent No. 6326004
; GENERAL INFORMATION:
; APPLICANT: Greve, Jeffrey M.
; APPLICANT: McClelland, Alan
; APPLICANT: Davis, Gary
; TITLE OF INVENTION: Antiviral Methods Using Fragments
; OF Human Rhinovirus Receptor (ICAM-1)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 Mb storage
; COMPUTER: Dell Latitude CP
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417-551

```

STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb storage
COMPUTER: Dell Latitude CP
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316.385
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/103.303
FILING DATE: 6-AUG-1993
APPLICATION NUMBER: 07/631.313
FILING DATE: 20-DEC-1990
APPLICATION NUMBER: 07/556.238
FILING DATE: 20-JUL-1990
APPLICATION NUMBER: 07/390.662
FILING DATE: 10-AUG-1989
APPLICATION NUMBER: 07/262.428
FILING DATE: 25-OCT-1988
APPLICATION NUMBER: 07/239.571
FILING DATE: 1-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: SHIMEI, BARBARA A.
REGISTRATION NUMBER: 29,862
REFERENCE/DOCKET NUMBER: MTI 208.3C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 812-2786
TELEFAX: (203) 812-5492
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: yes
FEATURE:
NAME/KEY: XbaI site
LOCATION: bases 2-7
NAME/KEY: BamHI site
LOCATION: bases 8-13
NAME/KEY: complement to stop codon
LOCATION: bases 14-16 are complementary to stop
LOCATION: codon on sense strand
NAME/KEY: complement to codons for amino acids 81-
NAME/KEY: 88 of ICAM-1
LOCATION: bases 17-39 are complementary to
LOCATION: nucleotides on sense strand coding for amino acid
LOCATION: residues 81-88 of ICAM-1
PUBLICATION INFORMATION:
AUTHORS: Staunton, D.
AUTHORS: Marlin, S.
AUTHORS: Stratowa, C.
AUTHORS: Dustin, M.
AUTHORS: Springer, T.
TITLE: Primary structure of ICAM-1 demonstrates
TITLE: interaction between members of the immunoglobulin
TITLE: and integrin supergene families
JOURNAL: Cell
VOLUME: 52
PAGES: 925-933
DATE: 25-MAR-1988
RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 17 TO 39
US-08-316-385-5
Query Match 48.5%; Score 16; DB 4; Length 39;
Best Local Similarity 79.2%; Pred No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 TACTCACCCTCCGACACCACTA 29
Db 11 TCCTCACCCTCTGGAGTCCAGTA 34
RESULT 33
US-09-034-205-52/c
; Sequence 52, Application US/09034205
; Patent No. 6194149
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Nerl, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/034,205
; APPLICATION NUMBER: US/09/034,205
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-09-034-205-52
Query Match 46.7%; Score 15.4; DB 3; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 CCGTTCGCGACCACT 28
Db 17 CCGTTCGCGACCACT 1
RESULT 34
US-09-677-218B-52/c
; Sequence 52, Application US/09677218B
; Patent No. 6355437
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Nerl, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/677,218B

FILING DATE: 02-Oct-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/034,205

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-03268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 52:

US-09-677-218B-52

Query Match 46.7%; Score 15.4; DB 3; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGGTTCCGCGAGCCACT 28
DB 17 CGGTTCCGCGAGCCACT 1

RESULT 35

US-09-677-192-52/c

Sequence 52, Application US/09677192

Patent No. 6358691

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

APPLICANT: Brow, Mary Ann D.

APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING

TITLE OF INVENTION: OLIGONUCLEOTIDES

FILE REFERENCE: FORS-04708

CURRENT APPLICATION NUMBER: US/09/677,192

CURRENT FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: 09/034,205

PRIOR FILING DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 68

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 52

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-677-192-52

Query Match 46.7%; Score 15.4; DB 3; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGGTTCCGCGAGCCACT 28
DB 17 CGGTTCCGCGAGCCACT 1

RESULT 36

US-09-402-618B-52/c

Sequence 52, Application US/09402618B

Patent No. 6709815

GENERAL INFORMATION:

APPLICANT: Dong, Fang

APPLICANT: Lyamichev, Victor

APPLICANT: Prudent, James

APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce

APPLICANT: Brow, Mary Ann

APPLICANT: Anderson, Todd

APPLICANT: Dahlberg, James

TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotic

FILE REFERENCE: FORS-04012

CURRENT APPLICATION NUMBER: US/09/402,618B

CURRENT FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: PCT/US98/03194

PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 128

SOFTWARE: Patent In version 3.0

SEQ ID NO 52

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-09-402-618B-52

Query Match 46.7%; Score 15.4; DB 4; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGGTTCCGCGAGCCACT 28
DB 17 CGGTTCCGCGAGCCACT 1

RESULT 37

5166057-36

Patent No. 5166057

APPLICANT: PALESE, PETER; PARVIN, JEFFREY D.; KRYSTAL, MARK

TITLE OF INVENTION: RECOMBIANT NEGATIVE STRAND RNA VIRUS

EXPRESSION-SYSTEMS

NUMBER OF SEQUENCES: 43

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/527,237

FILING DATE: 22-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 440,053

FILING DATE: 21-NOV-1989

APPLICATION NUMBER: 399,728

FILING DATE: 28-AUG-1989

SEQ ID NO:36

LENGTH: 37

5166057-36

Query Match 46.7%; Score 15.4; DB 6; Length 37;
Best Local Similarity 76.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TACTCAGCTTCCGCGAGCCACTAT 30
DB 6 TACTCAGCTTCCGCGAGCCACTAT 30

RESULT 38

US-08-316-439A-21
; Sequence 21, Application US/08316439A
; Patent No. 5840520
; GENERAL INFORMATION:
; APPLICANT: CLARKE, DAVID KIRKWOOD
; APPLICANT: PALSESE, PETER M
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS EXPRESSION
; TITLE OF INVENTION: SYSTEMS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GORDWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316.439A
; FILING DATE: September 30, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/190,678
; FILING DATE: February 1, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,061
; FILING DATE: August 4, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/527,237
; FILING DATE: May 22, 1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/440,053
; FILING DATE: No. 5840520ember 21, 1989
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/399,728
; FILING DATE: August 28, 1989
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CSERR, LUANN
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-010/000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5165
; TELEFAX: (415) 857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 21:
; LENGTH: 38 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: SYNTHETIC DNA
US-08-316-439A-21
Query Match 46.7%; Score 15.4; DB 2; Length 38;
Best Local Similarity 76.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 TACTCACCGTTCGCGACCACTAT 30
Db 7 TACTCACCGTTCGCGCGCCGCTAT 31
RESULT 39
US-09-039-982A-54

; Sequence 54, Application US/09039982A
; Patent No. 6225042
; GENERAL INFORMATION:
; APPLICANT: Cai, Zeling
; APPLICANT: Sprunt, Jonathan
; APPLICANT: Brunmark, Anders
; APPLICANT: Jackson, Michael
; APPLICANT: Peterson, Per A
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-CELLS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Olson & Hierl, Ltd.
; STREET: 20 No. 6225042th Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,982A
; FILING DATE: 16-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Olson, Arne M.
; REGISTRATION NUMBER: 30,203
; REFERENCE/DOCKET NUMBER: TSRI4710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 580-1180
; TELEFAX: (312) 580-1189
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-039-982A-54
Query Match 46.1%; Score 15.2; DB 3; Length 33;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 4 TGTAACACCGTTCCGCGACCACTATG 31
Db 6 TGAGTCATGATCCCGAGTGCATATG 33
RESULT 40
US-09-039-762A-54
; Sequence 54, Application US/09039762A
; Patent No. 6255073
; GENERAL INFORMATION:
; APPLICANT: Cai, Zeling
; APPLICANT: Sprunt, Jonathan
; APPLICANT: Brunmark, Anders
; APPLICANT: Jackson, Michael
; APPLICANT: Peterson, Per A
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Olson & Hierl, Ltd.
; STREET: 20 No. 6255073th Wacker Drive, 36th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,762A
FILING DATE: 16-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OLSON, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-039-762A-54

Query Match : 46.1%; Score 15.2; DB 3; Length 33;
Best Local Similarity 71.4%; Pred.No.5.7e+02;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 TGTACTCACCCTTCGCGACGACCACTATG 31
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Db 6 TCAGCTCATGGATCCCCAGTGCCTATG 33

Search completed: November 23, 2004, 22:26:13
Job time : 47.191 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 18:47:33 ; Search time 154.742 Seconds
(without alignments)
1152.370 Million cell updates/sec

Title: US-10-087-631B-3

Perfect score: 33
Sequence: 1 cgggtactacccttcgcagaccatggc 33

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 1987578

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	33	100.0	33	15	US-10-419-022-3	Sequence 3, Appli
3	31	93.9	31	16	US-10-337-190-1	Sequence 1, Appli
4	22	66.7	41	17	US-10-451-882-42	Sequence 42, Appli
5	20	60.6	24	17	US-10-318-416B-34	Sequence 34, Appli
6	20	60.6	26	17	US-10-318-416B-32	Sequence 32, Appli
7	20	60.6	32	15	US-10-147-679A-20	Sequence 3, Appli
8	19	58.8	31	9	US-09-782-361-3	Sequence 11, Appli
9	19	57.6	19	9	US-09-747-419-11	Sequence 11, Appli
10	19	57.6	19	15	US-10-259-275-11	Sequence 11, Appli
11	19	57.6	19	18	US-10-667-271-78	Sequence 78, Appli
12	19	57.6	19	18	US-10-667-271-82	Sequence 82, Appli

86	15	45.5	18	10	US-09-935-338-191	Sequence 191, App	159	14	42.4	15	17	US-10-669-841-7337	Sequence 7337, Ap
87	15	45.5	18	10	US-09-935-338-228	Sequence 228, App	160	14	42.4	15	17	US-10-669-841-7341	Sequence 7341, Ap
88	15	45.5	18	17	US-10-451-882-31	Sequence 31, Appl	c 161	14	42.4	15	17	US-09-740-332-35	Sequence 35, Appl
c 89	15	45.5	19	18	US-10-667-271-77	Sequence 77, Appl	162	14	42.4	17	10	US-09-740-332-4521	Sequence 4521, Ap
c 90	15	45.5	19	18	US-10-667-271-773	Sequence 773, App	c 163	14	42.4	17	10	US-09-817-879-35	Sequence 35, Appl
c 91	15	45.5	21	16	US-10-441-830-1	Sequence 1, Appl	164	14	42.4	17	10	US-09-817-879-4521	Sequence 4521, Ap
c 92	15	45.5	21	17	US-10-639-150-3	Sequence 3, Appl	c 165	14	42.4	17	17	US-10-669-841-2628	Sequence 2628, Ap
c 93	15	45.5	26	13	US-10-029-907-19	Sequence 19, Appl	c 166	14	42.4	17	17	US-10-669-841-7114	Sequence 7114, Ap
c 94	15	45.5	26	15	US-10-309-561-19	Sequence 19, Appl	c 167	14	42.4	19	18	US-10-667-271-32	Sequence 32, Appl
c 95	15	45.5	26	17	US-10-789-355-19	Sequence 19, Appl	c 168	14	42.4	19	18	US-10-667-271-55	Sequence 55, Appl
c 96	15	45.5	26	18	US-10-686-835-19	Sequence 19, Appl	c 169	14	42.4	19	18	US-10-667-271-728	Sequence 728, App
c 97	15	45.5	34	16	US-10-182-936A-162	Sequence 162, App	170	14	42.4	19	18	US-10-667-271-751	Sequence 751, App
c 98	14.8	44.8	19	18	US-10-667-271-53	Sequence 53, Appl	171	14	42.4	19	18	US-10-667-271-780	Sequence 780, App
c 99	14.8	44.8	19	18	US-10-667-271-61	Sequence 61, Appl	172	14	42.4	25	15	US-10-098-263B-109400	Sequence 109400,
100	14.8	44.8	19	18	US-10-667-271-749	Sequence 749, App	c 173	14	42.4	25	15	US-10-098-263B-115307	Sequence 115307,
101	14.8	44.8	19	18	US-10-667-271-757	Sequence 757, App	c 174	14	42.4	26	15	US-10-198-680A-4	Sequence 4, Appl
c 102	14.8	44.8	21	18	US-10-444-853A-146	Sequence 146, App	c 175	14	42.4	26	15	US-10-320-978-3	Sequence 3, Appl
c 103	14.8	44.8	21	18	US-10-444-853A-153	Sequence 153, App	c 176	14	42.4	26	15	US-10-353-563-3	Sequence 3, Appl
c 104	14.8	44.8	21	18	US-10-444-853A-192	Sequence 192, App	c 177	14	42.4	26	15	US-10-353-589-3	Sequence 3, Appl
c 105	14.8	44.8	21	18	US-10-444-853A-193	Sequence 193, App	c 178	14	42.4	26	15	US-10-320-979-3	Sequence 3, Appl
c 106	14.8	44.8	21	18	US-10-444-853A-200	Sequence 200, App	c 179	14	42.4	26	15	US-10-353-894-3	Sequence 3, Appl
c 107	14.8	44.8	21	18	US-10-667-271-1424	Sequence 1424, Ap	c 180	14	42.4	26	15	US-10-198-259A-4	Sequence 4, Appl
c 108	14.8	44.8	21	18	US-10-667-271-1431	Sequence 1431, Ap	c 181	14	42.4	26	15	US-10-198-384A-4	Sequence 4, Appl
c 109	14.8	44.8	21	18	US-10-667-271-1449	Sequence 1449, Ap	c 182	14	42.4	26	18	US-10-791-318-3	Sequence 3, Appl
c 110	14.8	44.8	21	18	US-10-667-271-1450	Sequence 1450, Ap	c 183	14	42.4	37	10	US-09-770-158-1	Sequence 1, Appl
c 111	14.8	44.8	21	18	US-10-667-271-1457	Sequence 1457, Ap	c 184	14	42.4	37	10	US-09-848-754A-6140	Sequence 6140, Ap
c 112	14.8	44.8	23	18	US-10-667-271-1395	Sequence 1395, Ap	c 185	14	42.4	37	15	US-10-230-006-1523	Sequence 1523, Ap
c 113	14.8	44.8	23	18	US-10-667-271-1397	Sequence 1397, Ap	c 186	14	42.4	37	15	US-10-138-674-18274	Sequence 18274, A
c 114	14.8	44.8	25	13	US-10-033-297-121	Sequence 121, App	c 187	14	42.4	37	16	US-10-287-949A-18274	Sequence 18274, A
c 115	14.8	44.8	25	15	US-10-290-386-121	Sequence 121, App	c 188	14	42.4	37	17	US-10-825-805-1106	Sequence 1106, Ap
c 116	14.8	44.8	25	16	US-10-356-861-121	Sequence 121, App	c 189	14	42.4	38	10	US-10-211-069-27	Sequence 27, Appl
c 117	14.8	44.8	31	14	US-10-225-501-7	Sequence 7, Appl	c 190	14	42.4	47	14	US-10-667-271-54	Sequence 54, Appl
c 118	14.8	44.8	33	10	US-09-882-945A-63	Sequence 63, Appl	c 191	13.8	41.8	19	18	US-10-667-271-750	Sequence 750, App
c 119	14.8	44.8	50	16	US-10-062-188-191	Sequence 191, App	c 192	13.8	41.8	19	18	US-10-444-853A-144	Sequence 144, App
c 120	14.6	44.2	34	17	US-10-440-295-5	Sequence 5, Appl	c 193	13.8	41.8	21	18	US-10-444-853A-151	Sequence 151, App
c 121	14.6	44.2	34	17	US-10-204-070A-9	Sequence 9, Appl	194	13.8	41.8	21	18	US-10-444-853A-199	Sequence 199, App
c 122	14.4	43.6	17	10	US-09-740-332-34	Sequence 34, Appl	195	13.8	41.8	21	18	US-10-667-271-1422	Sequence 1422, Ap
c 123	14.4	43.6	17	10	US-09-740-332-4524	Sequence 4524, Ap	c 196	13.8	41.8	21	18	US-10-667-271-1429	Sequence 1429, Ap
c 124	14.4	43.6	17	10	US-09-817-879-34	Sequence 34, Appl	c 197	13.8	41.8	21	18	US-10-667-271-1456	Sequence 1456, Ap
c 125	14.4	43.6	17	10	US-09-817-879-4524	Sequence 4524, Ap	c 198	13.8	41.8	21	18	US-10-667-271-1456	Sequence 1456, Ap
c 126	14.4	43.6	17	17	US-10-669-841-2627	Sequence 2627, Ap	c 199	13.8	41.8	25	9	US-09-866-108-10985	Sequence 10985, A
c 127	14.4	43.6	17	17	US-10-669-841-7117	Sequence 7117, Ap	200	13.8	41.8	25	15	US-10-098-263B-117433	Sequence 117433,
c 128	14.4	43.6	19	18	US-10-667-271-57	Sequence 57, Appl	201	13.8	41.8	25	15	US-10-098-263B-117434	Sequence 117434,
c 129	14.4	43.6	19	18	US-10-667-271-58	Sequence 58, Appl	202	13.8	41.8	25	15	US-10-723-361-10985	Sequence 3, Appl
c 130	14.4	43.6	19	18	US-10-667-271-65	Sequence 65, Appl	c 203	13.8	41.8	28	9	US-09-955-286-3	Sequence 3, Appl
c 131	14.4	43.6	19	18	US-10-667-271-753	Sequence 753, App	c 204	13.8	41.8	31	9	US-09-801-274-816	Sequence 816, App
c 132	14.4	43.6	19	18	US-10-667-271-754	Sequence 754, App	c 205	13.8	41.8	39	17	US-10-318-416B-24	Sequence 24, Appl
c 133	14.4	43.6	19	18	US-10-667-271-761	Sequence 761, App	c 206	13.8	41.8	40	14	US-10-071-485-74	Sequence 74, Appl
c 134	14.4	43.6	22	9	US-09-464-426A-1	Sequence 1, Appl	c 207	13.8	41.8	40	14	US-09-884-465A-177	Sequence 177, App
c 135	14.4	43.6	22	9	US-09-981-215-1	Sequence 1, Appl	c 208	13.8	41.8	45	10	US-09-884-465A-178	Sequence 178, App
c 136	14.4	43.6	25	15	US-10-098-263B-94252	Sequence 94252, A	c 209	13.8	41.8	45	10	US-10-131-827-3328	Sequence 3328, Ap
c 137	14.4	43.6	32	16	US-10-688-272-25	Sequence 25, Appl	c 210	13.8	41.8	50	16	US-10-131-827-3328	Sequence 3827, Ap
c 138	14.4	43.6	41	14	US-10-043-573-79	Sequence 79, Appl	c 211	13.8	41.8	50	16	US-10-131-827-3827	Sequence 3827, Ap
c 139	14.4	43.6	50	16	US-10-131-827-3821	Sequence 3821, Ap	c 212	13.6	41.2	25	15	US-10-098-263B-64470	Sequence 64470, A
c 140	14.4	43.6	50	16	US-10-131-827-6034	Sequence 6034, Ap	c 213	13.6	41.2	31	10	US-09-912-263-170	Sequence 170, App
c 141	14.2	43.0	21	15	US-10-168-989-7	Sequence 7, Appl	c 214	13.6	41.2	37	15	US-10-156-306-2523	Sequence 2523, App
c 142	14.2	43.0	33	15	US-10-304-038-7	Sequence 7, Appl	c 215	13.6	41.2	37	16	US-10-138-674-20280	Sequence 20280, A
c 143	14.2	43.0	50	15	US-10-393-815-204	Sequence 204, App	c 216	13.6	41.2	37	16	US-10-138-674-20280	Sequence 20329, A
144	14	42.4	15	9	US-09-504-231A-1524	Sequence 1524, App	c 217	13.6	41.2	37	16	US-10-138-674-20407	Sequence 20407, A
145	14	42.4	15	9	US-09-274-553D-1524	Sequence 1524, Ap	c 218	13.6	41.2	37	17	US-10-287-949A-20329	Sequence 20329, A
c 146	14	42.4	15	10	US-09-740-332-4578	Sequence 4578, Ap	c 219	13.6	41.2	37	17	US-10-287-949A-20329	Sequence 20329, A
c 147	14	42.4	15	10	US-09-740-332-4625	Sequence 4625, Ap	c 220	13.6	41.2	37	17	US-10-287-949A-20329	Sequence 20329, A
c 148	14	42.4	15	10	US-09-740-332-4627	Sequence 4627, Ap	c 221	13.6	41.2	38	10	US-09-780-533A-4832	Sequence 4832, Ap
c 149	14	42.4	15	10	US-09-740-332-4744	Sequence 4744, Ap	c 222	13.6	41.2	38	10	US-09-780-164-1920	Sequence 1920, Ap
c 150	14	42.4	15	10	US-09-740-332-4748	Sequence 4748, Ap	c 223	13.6	41.2	47	15	US-10-170-097-708	Sequence 708, App
c 151	14	42.4	15	10	US-09-817-879-4578	Sequence 4578, Ap	c 224	13.6	41.2	50	16	US-10-131-827-3697	Sequence 3697, Ap
c 152	14	42.4	15	10	US-09-817-879-4625	Sequence 4625, Ap	c 225	13.4	40.6	15	9	US-09-504-231A-1557	Sequence 1557, Ap
c 153	14	42.4	15	10	US-09-817-879-4627	Sequence 4627, Ap	226	13.4	40.6	15	9	US-09-274-553D-1557	Sequence 1557, Ap
c 154	14	42.4	15	10	US-09-817-879-4744	Sequence 4744, Ap	227	13.4	40.6	15	10	US-09-740-332-4727	Sequence 4727, Ap
c 155	14	42.4	15	10	US-09-817-879-4748	Sequence 4748, Ap	228	13.4	40.6	15	10	US-09-817-879-4727	Sequence 4727, Ap
c 156	14	42.4	15	17	US-10-669-841-7171	Sequence 7171, Ap	229	13.4	40.6	15	17	US-10-669-841-7320	Sequence 7320, Ap
c 157	14	42.4	15	17	US-10-669-841-7218	Sequence 7218, Ap	c 230	13.4	40.6	18	17	US-10-318-416B-12	Sequence 12, Appl
c 158	14	42.4	15	17	US-10-669-841-7220	Sequence 7220, Ap	c 231	13.4	40.6	19	18	US-10-667-271-69	Sequence 69, Appl

232	13.4	40.6	19	18	US-10-667-271-765	Sequence 765, App.	305	13.	39.4	24	15	US-10-196-232-12	Sequence 12, Appl
233	13.4	40.6	25	15	US-10-098-263B-29535	Sequence 29535, A	306	13	39.4	24	16	US-10-210-281-191	Sequence 191, App
c 234	13.4	40.6	25	15	US-10-098-263B-99882	Sequence 99882, A	c 307	13	39.4	25	9	US-09-866-108-10981	Sequence 10981, A
235	13.4	40.6	25	15	US-10-098-263B-100331	Sequence 100331, A	c 308	13	39.4	25	9	US-09-866-108-10982	Sequence 10982, A
236	13.4	40.6	26	14	US-10-096-718-74	Sequence 74, Appl	c 309	13	39.4	25	9	US-09-866-108-10983	Sequence 10983, A
c 237	13.4	40.6	30	15	US-10-212-962-10	Sequence 10, Appl	c 310	13	39.4	25	9	US-09-866-108-10984	Sequence 10984, A
238	13.4	40.6	33	15	US-10-371-525-104	Sequence 104, App	c 311	13	39.4	25	9	US-09-866-108-10986	Sequence 10986, A
239	13.4	40.6	33	15	US-10-371-069-104	Sequence 104, App	c 312	13	39.4	25	9	US-09-866-108-10987	Sequence 10987, A
240	13.4	40.6	33	15	US-10-371-645-104	Sequence 104, App	c 313	13	39.4	25	9	US-09-866-108-10988	Sequence 10988, A
241	13.4	40.6	33	15	US-10-371-260-104	Sequence 104, App	c 314	13	39.4	25	9	US-09-866-108-10989	Sequence 10989, A
242	13.4	40.6	40	10	US-09-307-111-154	Sequence 154, App	315	13	39.4	25	15	US-10-098-263B-57742	Sequence 57742, A
c 243	13.4	40.6	47	16	US-10-349-143-1903	Sequence 1903, App	316	13	39.4	25	15	US-10-098-263B-84574	Sequence 84574, A
244	13.4	40.6	48	10	US-09-468-147-205	Sequence 205, App	c 317	13	39.4	25	15	US-10-098-263B-88868	Sequence 88868, A
245	13.4	40.6	48	15	US-10-319-745-205	Sequence 205, App	318	13	39.4	25	15	US-10-098-263B-89294	Sequence 89294, A
246	13.2	40.0	24	10	US-09-940-244-121	Sequence 121, App	319	13	39.4	25	15	US-10-098-263B-107433	Sequence 107433, A
247	13.2	40.0	24	18	US-10-309-584-121	Sequence 121, App	c 320	13	39.4	25	17	US-10-723-361-10981	Sequence 10981, A
c 248	13.2	40.0	25	15	US-10-098-263B-31785	Sequence 31785, A	c 321	13	39.4	25	17	US-10-723-361-10982	Sequence 10982, A
249	13.2	40.0	25	15	US-10-098-263B-68842	Sequence 68842, A	c 322	13	39.4	25	17	US-10-723-361-10983	Sequence 10983, A
c 250	13.2	40.0	25	15	US-10-098-263B-69789	Sequence 69789, A	c 323	13	39.4	25	17	US-10-723-361-10984	Sequence 10984, A
c 251	13.2	40.0	25	15	US-10-098-263B-78979	Sequence 78979, A	c 324	13	39.4	25	17	US-10-723-361-10986	Sequence 10986, A
c 252	13.2	40.0	25	15	US-10-098-263B-95278	Sequence 95278, A	c 325	13	39.4	25	17	US-10-723-361-10987	Sequence 10987, A
253	13.2	40.0	25	15	US-10-098-263B-104519	Sequence 104519, A	c 326	13	39.4	25	17	US-10-723-361-10988	Sequence 10988, A
254	13.2	40.0	29	15	US-10-229-346-26	Sequence 26, Appl	c 327	13	39.4	25	17	US-10-723-361-10989	Sequence 10989, A
c 255	13.2	40.0	29	18	US-10-487-846-26	Sequence 26, Appl	328	13	39.4	29	10	US-09-770-158-16	Sequence 16, Appl
c 256	13.2	40.0	31	18	US-10-422-588-4	Sequence 4, Appl	329	13	39.4	32	9	US-09-755-633-13	Sequence 13, Appl
257	13.2	40.0	32	9	US-09-745-605-21	Sequence 21, Appl	330	13	39.4	32	14	US-10-218-654-138	Sequence 138, App
258	13.2	40.0	33	9	US-09-745-605-35	Sequence 35, Appl	331	13	39.4	32	15	US-10-262-439-138	Sequence 138, App
c 259	13.2	40.0	33	16	US-10-385-662-18	Sequence 18, Appl	332	13	39.4	32	18	US-10-787-382-13	Sequence 13, Appl
260	13.2	40.0	41	16	US-10-035-833A-2069	Sequence 2069, App	c 333	13	39.4	36	10	US-09-848-754A-9535	Sequence 9535, App
261	13.2	40.0	41	16	US-10-035-833A-7326	Sequence 7326, App	c 334	13	39.4	37	10	US-09-827-395A-1596	Sequence 1596, App
c 262	13.2	40.0	47	16	US-10-349-143-3114	Sequence 3114, App	c 335	13	39.4	37	10	US-09-827-395A-1729	Sequence 1729, App
c 263	13.2	40.0	50	16	US-10-131-827-7901	Sequence 7901, App	c 336	13	39.4	37	10	US-09-827-395A-1737	Sequence 1737, App
c 264	13	39.4	13	10	US-09-740-332-4577	Sequence 4577, App	c 337	13	39.4	37	15	US-10-156-306-6253	Sequence 6253, App
c 265	13	39.4	13	10	US-09-740-332-4604	Sequence 4604, App	c 338	13	39.4	37	15	US-10-430-882-1596	Sequence 1596, App
c 266	13	39.4	13	10	US-09-740-332-4620	Sequence 4620, App	c 339	13	39.4	37	15	US-10-430-882-1729	Sequence 1729, App
c 267	13	39.4	13	10	US-09-740-332-4622	Sequence 4622, App	c 340	13	39.4	37	15	US-10-430-882-1737	Sequence 1737, App
c 268	13	39.4	13	10	US-09-740-332-4690	Sequence 4690, App	c 341	13	39.4	37	16	US-10-138-674-18388	Sequence 18388, A
269	13	39.4	13	10	US-09-740-332-4731	Sequence 4731, App	c 342	13	39.4	37	16	US-10-138-674-20606	Sequence 20606, A
270	13	39.4	13	10	US-09-740-332-4736	Sequence 4736, App	c 343	13	39.4	37	17	US-10-287-949A-18388	Sequence 18388, A
271	13	39.4	13	10	US-09-740-332-4737	Sequence 4737, App	c 344	13	39.4	37	17	US-10-287-949A-20606	Sequence 20606, A
c 272	13	39.4	13	10	US-09-817-879-4577	Sequence 4577, App	c 345	13	39.4	38	10	US-09-825-805-914	Sequence 914, App
c 273	13	39.4	13	10	US-09-817-879-4604	Sequence 4604, App	c 346	13	39.4	38	10	US-09-825-805-1159	Sequence 1159, App
c 274	13	39.4	13	10	US-09-817-879-4620	Sequence 4620, App	c 347	13	39.4	38	10	US-09-770-158-2	Sequence 2, Appl
c 275	13	39.4	13	10	US-09-817-879-4622	Sequence 4622, App	c 348	13	39.4	38	10	US-09-780-533A-4619	Sequence 4619, App
c 276	13	39.4	13	10	US-09-817-879-4690	Sequence 4690, App	c 349	13	39.4	38	10	US-09-930-423-3038	Sequence 3038, App
277	13	39.4	13	10	US-09-817-879-4731	Sequence 4731, App	c 350	13	39.4	38	10	US-09-780-164-1953	Sequence 1953, App
278	13	39.4	13	10	US-09-817-879-4736	Sequence 4736, App	c 351	13	39.4	38	10	US-09-745-237A-3038	Sequence 3038, App
279	13	39.4	13	10	US-09-817-879-4737	Sequence 4737, App	c 352	13	39.4	41	15	US-10-005-956-704	Sequence 704, App
c 280	13	39.4	13	17	US-10-669-841-7170	Sequence 7170, App	353	13	39.4	41	16	US-10-035-833A-526	Sequence 526, App
c 281	13	39.4	13	17	US-10-669-841-7197	Sequence 7197, App	354	13	39.4	41	16	US-10-035-833A-6079	Sequence 6079, App
c 282	13	39.4	13	17	US-10-669-841-7213	Sequence 7213, App	c 355	13	39.4	45	9	US-09-735-363A-77	Sequence 77, Appl
c 283	13	39.4	13	17	US-10-669-841-7215	Sequence 7215, App	356	13	39.4	47	16	US-10-349-143-3439	Sequence 3439, App
c 284	13	39.4	13	17	US-10-669-841-7283	Sequence 7283, App	c 357	13	39.4	50	16	US-10-131-827-953	Sequence 953, App
285	13	39.4	13	17	US-10-669-841-7324	Sequence 7324, App	c 358	12.8	38.8	16	10	US-09-825-805-7	Sequence 7, Appl
286	13	39.4	13	17	US-10-669-841-7329	Sequence 7329, App	359	12.8	38.8	17	10	US-09-740-332-4522	Sequence 4522, App
287	13	39.4	13	17	US-10-669-841-7330	Sequence 7330, App	360	12.8	38.8	17	10	US-09-817-879-4522	Sequence 4522, App
c 288	13	39.4	15	9	US-09-504-231A-7	Sequence 5, Appl	361	12.8	38.8	17	17	US-10-669-841-7115	Sequence 7115, App
c 289	13	39.4	15	9	US-09-504-231A-5	Sequence 7, Appl	c 362	12.8	38.8	19	9	US-09-969-373-2873	Sequence 2873, App
c 290	13	39.4	15	9	US-09-504-231A-1564	Sequence 1564, App	c 363	12.8	38.8	19	18	US-10-667-271-56	Sequence 56, Appl
c 291	13	39.4	15	9	US-09-274-553D-5	Sequence 5, Appl	364	12.8	38.8	19	18	US-10-667-271-752	Sequence 752, App
c 292	13	39.4	15	9	US-09-274-553D-7	Sequence 7, Appl	365	12.8	38.8	20	8	US-08-887-505-83	Sequence 83, Appl
293	13	39.4	15	9	US-09-274-553D-1564	Sequence 1564, App	c 366	12.8	38.8	21	9	US-09-747-419-16	Sequence 16, Appl
294	13	39.4	17	10	US-09-740-332-4520	Sequence 4520, App	c 367	12.8	38.8	21	15	US-10-259-275-16	Sequence 16, Appl
295	13	39.4	17	10	US-09-740-332-4527	Sequence 4527, App	c 368	12.8	38.8	21	16	US-10-467-000-13	Sequence 13, Appl
296	13	39.4	17	10	US-09-817-879-4520	Sequence 4520, App	c 369	12.8	38.8	23	18	US-10-667-271-1402	Sequence 1402, App
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298	13	39.4	17	17	US-10-669-841-7113	Sequence 7113, App	c 371	12.8	38.8	25	14	US-10-060-830-536	Sequence 536, App
299	13	39.4	17	17	US-10-669-841-7120	Sequence 7120, App	c 372	12.8	38.8	25	14	US-10-215-112-7462	Sequence 7462, App
300	13	39.4	19	18	US-10-667-271-64	Sequence 64, Appl	373	12.8	38.8	25	14	US-10-215-112-11011	Sequence 11011, A
c 301	13	39.4	19	18	US-10-667-271-72	Sequence 72, Appl	374	12.8	38.8	25	15	US-10-098-263B-8317	Sequence 8317, App
302	13	39.4	19	18	US-10-667-271-760	Sequence 760, App	c 375	12.8	38.8	25	15	US-10-098-263B-11276	Sequence 11276, A
303	13	39.4	19	18	US-10-667-271-768	Sequence 768, App	376	12.8	38.8	25	15	US-10-098-263B-14936	Sequence 14936, A
304	13	39.4	24	9	US-09-835-381-13	Sequence 13, Appl	377	12.8	38.8	25	15	US-10-098-263B-94251	Sequence 94251, A

378	12.8	38.8	25	17	US-10-717-597-450	Sequence 450, App	C 451	12.6	38.2	37	16	US-10-138-674-20666	Sequence 20666, A
379	12.8	38.8	26	15	US-10-171-319-80	Sequence 80, Appl	C 452	12.6	38.2	37	17	US-10-287-949A-20666	Sequence 20666, A
380	12.8	38.8	26	15	US-10-171-319-80	Sequence 84, Appl	C 453	12.6	38.2	38	10	US-09-825-805-1291	Sequence 1291, Ap
381	12.8	38.8	26	15	US-10-093-463-351	Sequence 351, App	C 454	12.6	38.2	38	10	US-09-825-805-1407	Sequence 1407, Ap
382	12.8	38.8	27	8	US-08-832-488-6	Sequence 6, Appl	C 455	12.6	38.2	38	10	US-09-825-805-1473	Sequence 1473, Ap
383	12.8	38.8	27	8	US-08-832-488-6	Sequence 10, Appl	C 456	12.6	38.2	38	10	US-09-848-754A-4752	Sequence 4752, Ap
384	12.8	38.8	30	9	US-09-946-678-19	Sequence 19, Appl	C 457	12.6	38.2	39	9	US-09-747-003-28	Sequence 28, Appl
385	12.8	38.8	31	15	US-10-435-608-18	Sequence 18, Appl	C 458	12.6	38.2	39	16	US-10-665-460A-58	Sequence 58, Appl
386	12.8	38.8	31	16	US-10-606-060A-34	Sequence 34, Appl	C 459	12.6	38.2	39	16	US-10-685-460A-58	Sequence 58, Appl
387	12.8	38.8	31	16	US-10-622-108-18	Sequence 18, Appl	C 460	12.6	38.2	42	9	US-09-388-089B-14	Sequence 14, Appl
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389	12.8	38.8	37	15	US-10-238-960-15	Sequence 15, Appl	C 462	12.6	38.2	45	16	US-10-380-533-91	Sequence 91, Appl
390	12.8	38.8	37	15	US-10-238-960-16	Sequence 16, Appl	C 463	12.6	38.2	45	16	US-09-848-616-152	Sequence 152, App
391	12.8	38.8	37	15	US-10-238-960-20	Sequence 20, Appl	C 464	12.6	38.2	47	10	US-09-918-728B-106	Sequence 106, App
392	12.8	38.8	38	9	US-09-814-292-17	Sequence 17, Appl	C 465	12.6	38.2	47	15	US-10-050-502-152	Sequence 152, App
393	12.8	38.8	39	9	US-09-730-893-11	Sequence 11, Appl	C 466	12.6	38.2	47	15	US-10-050-502-152	Sequence 152, App
394	12.8	38.8	39	10	US-09-940-173A-11	Sequence 11, Appl	C 467	12.6	38.2	47	15	US-10-349-143-3558	Sequence 3558, Ap
395	12.8	38.8	40	9	US-09-419-076-1	Sequence 1, Appl	C 468	12.6	38.2	47	16	US-10-289-456-152	Sequence 152, App
396	12.8	38.8	40	10	US-09-003-810-1	Sequence 1, Appl	C 469	12.6	38.2	47	16	US-10-622-124-95	Sequence 95, Appl
397	12.8	38.8	40	15	US-10-433-168-1	Sequence 1, Appl	C 470	12.6	38.2	47	17	US-10-622-087-65	Sequence 65, Appl
398	12.8	38.8	41	14	US-10-043-573-80	Sequence 80, Appl	C 471	12.6	38.2	50	16	US-10-131-827-705	Sequence 705, App
399	12.8	38.8	45	10	US-09-931-375A-85	Sequence 85, Appl	C 472	12.6	38.2	50	16	US-10-131-827-705	Sequence 1263, Ap
400	12.8	38.8	50	16	US-10-131-827-4773	Sequence 4773, Ap	C 473	12.6	38.2	50	16	US-10-131-827-1263	Sequence 1263, Ap
401	12.8	38.8	50	16	US-10-131-827-7864	Sequence 7864, Ap	C 474	12.4	37.6	15	9	US-09-504-231A-1525	Sequence 1525, Ap
402	12.6	38.2	20	9	US-09-734-836-16	Sequence 16, Appl	C 475	12.4	37.6	15	9	US-09-274-553D-1525	Sequence 1525, Ap
403	12.6	38.2	20	10	US-09-953-318-111	Sequence 11, App	C 476	12.4	37.6	15	9	US-09-274-553D-1525	Sequence 1525, Ap
404	12.6	38.2	20	15	US-10-446-373-111	Sequence 11, App	C 477	12.4	37.6	16	10	US-09-825-805-6	Sequence 6, Appl
405	12.6	38.2	20	15	US-10-446-373-111	Sequence 11, App	C 478	12.4	37.6	19	18	US-10-667-271-66	Sequence 66, Appl
406	12.6	38.2	23	9	US-10-188-470-59	Sequence 59, Appl	C 479	12.4	37.6	19	18	US-10-667-271-762	Sequence 762, App
407	12.6	38.2	23	9	US-09-730-989-13	Sequence 13, Appl	C 480	12.4	37.6	24	10	US-09-940-185-3340	Sequence 3340, App
408	12.6	38.2	24	15	US-10-441-729-2	Sequence 2, Appl	C 481	12.4	37.6	24	15	US-10-236-104-40	Sequence 40, Appl
409	12.6	38.2	25	9	US-09-866-108-10979	Sequence 10979, A	C 482	12.4	37.6	24	15	US-10-236-104-43	Sequence 43, Appl
410	12.6	38.2	25	9	US-09-866-108-10980	Sequence 10980, A	C 483	12.4	37.6	25	14	US-10-215-112-7969	Sequence 7969, Ap
411	12.6	38.2	25	14	US-10-112-12397	Sequence 12397, A	C 484	12.4	37.6	25	14	US-10-215-112-7969	Sequence 11261, A
412	12.6	38.2	25	15	US-10-098-263B-17396	Sequence 17396, A	C 485	12.4	37.6	25	14	US-10-215-112-12046	Sequence 12046, A
413	12.6	38.2	25	15	US-10-098-263B-47874	Sequence 47874, A	C 486	12.4	37.6	25	15	US-10-098-263B-3124	Sequence 3124, Ap
414	12.6	38.2	25	15	US-10-098-263B-105657	Sequence 105657, A	C 487	12.4	37.6	25	15	US-10-098-263B-20225	Sequence 20225, A
415	12.6	38.2	25	15	US-10-098-263B-107763	Sequence 107763, A	C 488	12.4	37.6	25	15	US-10-098-263B-23272	Sequence 23272, A
416	12.6	38.2	25	15	US-10-098-263B-108994	Sequence 108994, A	C 489	12.4	37.6	25	15	US-10-098-263B-36916	Sequence 36916, A
417	12.6	38.2	25	15	US-10-098-263B-117940	Sequence 117940, A	C 490	12.4	37.6	25	15	US-10-098-263B-43276	Sequence 43276, A
418	12.6	38.2	25	17	US-10-717-597-716	Sequence 716, App	C 491	12.4	37.6	25	15	US-10-098-263B-47999	Sequence 47999, A
419	12.6	38.2	25	17	US-10-723-361-10979	Sequence 10979, A	C 492	12.4	37.6	25	15	US-10-098-263B-50338	Sequence 50338, A
420	12.6	38.2	26	15	US-10-723-361-10980	Sequence 10980, A	C 493	12.4	37.6	25	15	US-10-098-263B-52446	Sequence 52446, A
421	12.6	38.2	26	15	US-10-378-168-56	Sequence 56, Appl	C 494	12.4	37.6	25	15	US-10-098-263B-60640	Sequence 60640, A
422	12.6	38.2	27	14	US-10-150-262-10	Sequence 10, Appl	C 495	12.4	37.6	25	15	US-10-098-263B-65249	Sequence 65249, A
423	12.6	38.2	28	9	US-09-927-767-1	Sequence 1, Appl	C 496	12.4	37.6	25	15	US-10-098-263B-65249	Sequence 65249, A
424	12.6	38.2	28	9	US-09-927-885-1	Sequence 1, Appl	C 497	12.4	37.6	25	15	US-10-098-263B-65250	Sequence 65250, A
425	12.6	38.2	28	9	US-09-927-788-1	Sequence 1, Appl	C 498	12.4	37.6	25	15	US-10-098-263B-84123	Sequence 84123, A
426	12.6	38.2	28	9	US-09-927-896-1	Sequence 1, Appl	C 499	12.4	37.6	25	15	US-10-098-263B-88883	Sequence 88883, A
427	12.6	38.2	28	9	US-09-928-227-1	Sequence 1, Appl	C 500	12.4	37.6	25	15	US-10-098-263B-88884	Sequence 88884, A
428	12.6	38.2	29	15	US-10-336-638-329	Sequence 329, App	C 501	12.4	37.6	25	15	US-10-098-263B-115308	Sequence 115308, A
429	12.6	38.2	34	10	US-10-336-638-856	Sequence 856, App	C 502	12.4	37.6	25	15	US-10-098-263B-115308	Sequence 115308, A
430	12.6	38.2	35	9	US-09-920-000-5	Sequence 5, Appl	C 503	12.4	37.6	26	8	US-08-911-824-19	Sequence 126787, A
431	12.6	38.2	35	10	US-09-790-398-15	Sequence 15, Appl	C 504	12.4	37.6	26	14	US-10-096-718-67	Sequence 19, Appl
432	12.6	38.2	35	10	US-08-825-805-303	Sequence 303, App	C 505	12.4	37.6	27	9	US-09-898-883-11	Sequence 67, Appl
433	12.6	38.2	36	17	US-10-441-925A-12	Sequence 12, Appl	C 506	12.4	37.6	27	10	US-09-151-376-49	Sequence 49, Appl
434	12.6	38.2	36	10	US-09-848-754A-9510	Sequence 9510, Ap	C 507	12.4	37.6	27	15	US-10-226-820-17	Sequence 17, Appl
435	12.6	38.2	36	10	US-09-261-329-25	Sequence 25, Appl	C 508	12.4	37.6	27	15	US-10-139-089-49	Sequence 49, Appl
436	12.6	38.2	37	10	US-09-825-805-304	Sequence 304, App	C 509	12.4	37.6	30	16	US-10-321-039-235	Sequence 235, App
437	12.6	38.2	37	10	US-09-848-616-150	Sequence 150, App	C 510	12.4	37.6	31	10	US-09-740-332-9320	Sequence 9320, Ap
438	12.6	38.2	37	10	US-09-927-454-3759	Sequence 3759, App	C 511	12.4	37.6	31	10	US-09-817-879-9320	Sequence 9320, Ap
439	12.6	38.2	37	10	US-09-848-754A-5925	Sequence 5925, Ap	C 512	12.4	37.6	31	17	US-10-669-841-15865	Sequence 15865, A
440	12.6	38.2	37	10	US-09-848-754A-6240	Sequence 6240, Ap	C 513	12.4	37.6	32	10	US-09-887-194A-20	Sequence 20, Appl
441	12.6	38.2	37	10	US-09-848-754A-6262	Sequence 6262, Ap	C 514	12.4	37.6	33	8	US-08-736-019-105	Sequence 105, App
442	12.6	38.2	37	10	US-09-827-395A-1670	Sequence 1670, Ap	C 515	12.4	37.6	37	9	US-08-864-785-1810	Sequence 1810, Ap
443	12.6	38.2	37	15	US-09-827-395A-1693	Sequence 1693, App	C 516	12.4	37.6	37	9	US-08-864-785-1924	Sequence 1924, Ap
444	12.6	38.2	37	15	US-10-289-454-371	Sequence 371, App	C 517	12.4	37.6	37	9	US-09-864-785-2004	Sequence 2004, Ap
445	12.6	38.2	37	15	US-10-050-902-150	Sequence 150, App	C 518	12.4	37.6	37	10	US-09-927-046-3653	Sequence 3653, Ap
446	12.6	38.2	37	15	US-10-050-898-150	Sequence 150, App	C 519	12.4	37.6	37	10	US-09-927-046-3873	Sequence 3873, Ap
447	12.6	38.2	37	15	US-10-230-006-1464	Sequence 1464, Ap	C 520	12.4	37.6	37	10	US-09-927-046-3901	Sequence 3901, Ap
448	12.6	38.2	37	15	US-10-430-882-1670	Sequence 1670, Ap	C 521	12.4	37.6	37	10	US-09-848-754A-5921	Sequence 5921, Ap
449	12.6	38.2	37	15	US-10-430-882-1693	Sequence 1693, Ap	C 522	12.4	37.6	37	10	US-09-848-754A-6012	Sequence 6012, Ap
450	12.6	38.2	37	15	US-10-346-390-151	Sequence 151, App	C 523	12.4	37.6	37	10	US-09-848-754A-6075	Sequence 6075, Ap

C 524	12.4	37.6	37	10	US-09-848-754A-6142	Sequence 6142, Ap	C 597	12.4	37.6	38	17	US-10-669-841-9232	Sequence 9232, Ap
C 525	12.4	37.6	37	10	US-09-848-754A-6407	Sequence 6407, Ap	C 598	12.4	37.6	38	17	US-10-669-841-9309	Sequence 9309, Ap
C 526	12.4	37.6	37	10	US-09-827-395A-1572	Sequence 1572, Ap	C 599	12.4	37.6	41	15	US-10-408-930-31	Sequence 31, Appl
C 527	12.4	37.6	37	10	US-09-827-395A-1789	Sequence 1789, Ap	C 600	12.4	37.6	41	16	US-10-035-833A-4120	Sequence 4120, Ap
C 528	12.4	37.6	37	15	US-10-156-306-2526	Sequence 2526, Ap	C 601	12.4	37.6	44	11	US-09-837-306-329	Sequence 329, App
C 529	12.4	37.6	37	15	US-10-156-306-6114	Sequence 6114, Ap	C 602	12.4	37.6	44	15	US-10-045-674-412	Sequence 412, App
C 530	12.4	37.6	37	15	US-10-156-306-6254	Sequence 6254, Ap	C 603	12.4	37.6	46	9	US-09-423-800-19	Sequence 19, Appl
C 531	12.4	37.6	37	15	US-10-230-006-1525	Sequence 1525, Ap	C 604	12.4	37.6	46	14	US-10-182-018-19	Sequence 19, Appl
C 532	12.4	37.6	37	15	US-10-230-006-1614	Sequence 1614, Ap	C 605	12.4	37.6	46	15	US-10-169-003-19	Sequence 19, Appl
C 533	12.4	37.6	37	15	US-10-230-006-1631	Sequence 1631, Ap	C 606	12.4	37.6	46	15	US-10-337-981-19	Sequence 19, Appl
C 534	12.4	37.6	37	15	US-10-430-882-1572	Sequence 1572, Ap	C 607	12.4	37.6	46	15	US-10-191-540-136	Sequence 136, App
C 535	12.4	37.6	37	15	US-10-430-882-1789	Sequence 1789, Ap	C 608	12.4	37.6	46	16	US-10-453-483-115	Sequence 115, App
C 536	12.4	37.6	37	16	US-10-138-674-18255	Sequence 18255, A	C 609	12.4	37.6	46	16	US-10-344-733-19	Sequence 19, Appl
C 537	12.4	37.6	37	16	US-10-138-674-18279	Sequence 18279, A	C 610	12.4	37.6	47	16	US-10-349-143-930	Sequence 930, App
C 538	12.4	37.6	37	16	US-10-138-674-18313	Sequence 18313, A	C 611	12.4	37.6	47	16	US-10-349-143-2410	Sequence 2410, Ap
C 539	12.4	37.6	37	16	US-10-138-674-18377	Sequence 18377, A	C 612	12.4	37.6	47	16	US-10-294-934-822	Sequence 822, Appl
C 540	12.4	37.6	37	16	US-10-138-674-18556	Sequence 18556, A	C 613	12.4	37.6	50	10	US-09-920-394-6	Sequence 6, Appl
C 541	12.4	37.6	37	16	US-10-138-674-18603	Sequence 18603, A	C 614	12.4	37.6	50	16	US-10-131-827-161	Sequence 161, App
C 542	12.4	37.6	37	16	US-10-138-674-18707	Sequence 18707, A	C 615	12.4	37.6	50	16	US-10-131-827-4631	Sequence 4631, Ap
C 543	12.4	37.6	37	16	US-10-138-674-18714	Sequence 18714, A	C 616	12.4	37.6	50	18	US-10-431-627-4	Sequence 4, Appl
C 544	12.4	37.6	37	16	US-10-138-674-18728	Sequence 18728, A	C 617	12.2	37.0	17	9	US-09-866-108-6089	Sequence 6089, Ap
C 545	12.4	37.6	37	16	US-10-138-674-18772	Sequence 18772, A	C 618	12.2	37.0	17	9	US-09-908-130-2	Sequence 2, Appl
C 546	12.4	37.6	37	16	US-10-138-674-20303	Sequence 20303, A	C 619	12.2	37.0	17	9	US-09-908-131-2	Sequence 2, Appl
C 547	12.4	37.6	37	16	US-10-138-674-20573	Sequence 20573, A	C 620	12.2	37.0	17	9	US-09-907-795-2	Sequence 2, Appl
C 548	12.4	37.6	37	16	US-10-138-674-20636	Sequence 20636, A	C 621	12.2	37.0	17	10	US-09-930-423-1581	Sequence 1581, Ap
C 549	12.4	37.6	37	17	US-10-287-949A-18255	Sequence 18255, A	C 622	12.2	37.0	17	10	US-09-745-237A-1581	Sequence 1581, Ap
C 550	12.4	37.6	37	17	US-10-287-949A-18279	Sequence 18279, A	C 623	12.2	37.0	17	13	US-10-041-856-81	Sequence 81, Appl
C 551	12.4	37.6	37	17	US-10-287-949A-18313	Sequence 18313, A	C 624	12.2	37.0	17	14	US-10-124-884-2	Sequence 2, Appl
C 552	12.4	37.6	37	17	US-10-287-949A-18377	Sequence 18377, A	C 625	12.2	37.0	17	15	US-10-230-006-45	Sequence 45, Appl
C 553	12.4	37.6	37	17	US-10-287-949A-18556	Sequence 18556, A	C 626	12.2	37.0	17	17	US-10-723-361-6089	Sequence 6089, Ap
C 554	12.4	37.6	37	17	US-10-287-949A-18603	Sequence 18603, A	C 627	12.2	37.0	18	17	US-10-250-997-1	Sequence 1, Appl
C 555	12.4	37.6	37	17	US-10-287-949A-18707	Sequence 18707, A	C 628	12.2	37.0	18	17	US-10-412-382-43	Sequence 43, Appl
C 556	12.4	37.6	37	17	US-10-287-949A-18714	Sequence 18714, A	C 629	12.2	37.0	20	9	US-09-816-079-7	Sequence 7, Appl
C 557	12.4	37.6	37	17	US-10-287-949A-18728	Sequence 18728, A	C 630	12.2	37.0	20	15	US-10-301-661A-21	Sequence 21, Appl
C 558	12.4	37.6	37	17	US-10-287-949A-18772	Sequence 18772, A	C 631	12.2	37.0	20	15	US-10-301-661A-88	Sequence 88, Appl
C 559	12.4	37.6	37	17	US-10-287-949A-20303	Sequence 20303, A	C 632	12.2	37.0	20	15	US-10-109-349A-245	Sequence 245, App
C 560	12.4	37.6	37	17	US-10-287-949A-20573	Sequence 20573, A	C 633	12.2	37.0	20	17	US-10-619-739-310	Sequence 310, App
C 561	12.4	37.6	37	17	US-10-287-949A-20636	Sequence 20636, A	C 634	12.2	37.0	20	18	US-10-660-122-21	Sequence 21, Appl
C 562	12.4	37.6	38	10	US-09-825-805-919	Sequence 919, App	C 635	12.2	37.0	21	18	US-10-786-720-13148	Sequence 13148, A
C 563	12.4	37.6	38	10	US-09-825-805-938	Sequence 938, App	C 636	12.2	37.0	24	10	US-09-940-185-2746	Sequence 2746, Ap
C 564	12.4	37.6	38	10	US-09-825-805-954	Sequence 954, App	C 637	12.2	37.0	25	9	US-09-866-108-14601	Sequence 14601, A
C 565	12.4	37.6	38	10	US-09-825-805-979	Sequence 979, App	C 638	12.2	37.0	25	9	US-09-866-108-14602	Sequence 14602, A
C 566	12.4	37.6	38	10	US-09-825-805-1006	Sequence 1006, Ap	C 639	12.2	37.0	25	9	US-09-925-796-18	Sequence 18, Appl
C 567	12.4	37.6	38	10	US-09-825-805-1085	Sequence 1085, Ap	C 640	12.2	37.0	25	9	US-09-941-450-18	Sequence 18, Appl
C 568	12.4	37.6	38	10	US-09-825-805-1098	Sequence 1098, Ap	C 641	12.2	37.0	25	9	US-09-942-090-18	Sequence 18, Appl
C 569	12.4	37.6	38	10	US-09-825-805-1236	Sequence 1236, Ap	C 642	12.2	37.0	25	14	US-10-060-830-534	Sequence 534, App
C 570	12.4	37.6	38	10	US-09-825-805-1255	Sequence 1255, Ap	C 643	12.2	37.0	25	14	US-10-215-112-5708	Sequence 5708, Ap
C 571	12.4	37.6	38	10	US-09-825-805-1403	Sequence 1403, Ap	C 644	12.2	37.0	25	14	US-10-215-112-13906	Sequence 13906, A
C 572	12.4	37.6	38	10	US-09-877-478-4281	Sequence 4281, Ap	C 645	12.2	37.0	25	15	US-10-098-263B-7683	Sequence 7683, Ap
C 573	12.4	37.6	38	10	US-09-877-478-4341	Sequence 4341, Ap	C 646	12.2	37.0	25	15	US-10-098-263B-7683	Sequence 7683, Ap
C 574	12.4	37.6	38	10	US-09-877-478-4418	Sequence 4418, Ap	C 647	12.2	37.0	25	15	US-10-098-263B-35813	Sequence 35813, A
C 575	12.4	37.6	38	10	US-09-776-474-2073	Sequence 2073, Ap	C 648	12.2	37.0	25	15	US-10-098-263B-64615	Sequence 64615, A
C 576	12.4	37.6	38	10	US-09-776-474-2149	Sequence 2149, Ap	C 649	12.2	37.0	25	15	US-10-098-263B-66594	Sequence 66594, A
C 577	12.4	37.6	38	10	US-09-930-423-2939	Sequence 2939, Ap	C 650	12.2	37.0	25	15	US-10-098-263B-67026	Sequence 67026, A
C 578	12.4	37.6	38	10	US-09-930-423-2977	Sequence 2977, Ap	C 651	12.2	37.0	25	15	US-10-098-263B-67338	Sequence 67338, A
C 579	12.4	37.6	38	10	US-09-930-423-2991	Sequence 2991, Ap	C 652	12.2	37.0	25	15	US-10-098-263B-78907	Sequence 78907, A
C 580	12.4	37.6	38	10	US-09-930-423-2998	Sequence 2998, Ap	C 653	12.2	37.0	25	15	US-10-098-263B-86270	Sequence 86270, A
C 581	12.4	37.6	38	10	US-09-930-423-3000	Sequence 3000, Ap	C 654	12.2	37.0	25	15	US-10-098-263B-87898	Sequence 87898, A
C 582	12.4	37.6	38	10	US-09-930-423-3171	Sequence 3171, Ap	C 655	12.2	37.0	25	15	US-10-098-263B-92652	Sequence 92652, A
C 583	12.4	37.6	38	10	US-09-780-164-1841	Sequence 1841, Ap	C 656	12.2	37.0	25	15	US-10-098-263B-13184	Sequence 13184, A
C 584	12.4	37.6	38	10	US-09-745-237A-2939	Sequence 2939, Ap	C 657	12.2	37.0	25	15	US-10-098-263B-130640	Sequence 130640, A
C 585	12.4	37.6	38	10	US-09-745-237A-2977	Sequence 2977, Ap	C 658	12.2	37.0	25	15	US-10-060-998-1585	Sequence 1585, Ap
C 586	12.4	37.6	38	10	US-09-745-237A-2991	Sequence 2991, Ap	C 659	12.2	37.0	25	17	US-10-723-361-14601	Sequence 14601, A
C 587	12.4	37.6	38	10	US-09-745-237A-2998	Sequence 2998, Ap	C 660	12.2	37.0	25	17	US-10-723-361-14602	Sequence 14602, A
C 588	12.4	37.6	38	10	US-09-745-237A-3000	Sequence 3000, Ap	C 661	12.2	37.0	25	18	US-10-843-944-18	Sequence 18, Appl
C 589	12.4	37.6	38	10	US-09-745-237A-3171	Sequence 3171, Ap	C 662	12.2	37.0	26	9	US-09-732-618-35	Sequence 35, Appl
C 590	12.4	37.6	38	15	US-10-191-540-137	Sequence 137, App	C 663	12.2	37.0	26	15	US-10-218-567-12	Sequence 12, Appl
C 591	12.4	37.6	38	15	US-10-453-483-116	Sequence 116, App	C 664	12.2	37.0	27	9	US-09-770-967-8	Sequence 8, Appl
C 592	12.4	37.6	38	16	US-10-342-902-4281	Sequence 4281, Ap	C 665	12.2	37.0	27	9	US-09-858-369-8	Sequence 8, Appl
C 593	12.4	37.6	38	16	US-10-342-902-4341	Sequence 4341, Ap	C 666	12.2	37.0	27	9	US-09-819-522-8	Sequence 8, Appl
C 594	12.4	37.6	38	16	US-10-342-902-4418	Sequence 4418, Ap	C 667	12.2	37.0	27	9	US-09-828-061A-9	Sequence 9, Appl
C 595	12.4	37.6	38	16	US-10-469-304-13	Sequence 13, Appl	C 668	12.2	37.0	27	9	US-09-757-251-9	Sequence 9, Appl
C 596	12.4	37.6	38	17	US-10-669-841-9172	Sequence 9172, Ap	C 669	12.2	37.0	27	9	US-09-784-897A-8	Sequence 8, Appl

c 670	12.2	37.0	27	9	US-09-770-983-8	Sequence 8, Appli	c 743	12	36.4	22	16	US-10-461-790-119	Sequence 119, App
c 671	12.2	37.0	27	9	US-09-828-325A-9	Sequence 9, Appli	744	12	36.4	22	18	US-10-660-122-19	Sequence 19, Appl
c 672	12.2	37.0	27	9	US-09-757-217A-9	Sequence 9, Appli	745	12	36.4	24	9	US-09-973-451-18	Sequence 18, Appl
c 673	12.2	37.0	27	9	US-09-828-255A-9	Sequence 9, Appli	746	12	36.4	24	10	US-09-940-185-2633	Sequence 2633, Ap
c 674	12.2	37.0	27	9	US-09-784-818-8	Sequence 8, Appli	c 747	12	36.4	25	9	US-09-866-108-10990	Sequence 10990, A
c 675	12.2	37.0	27	10	US-09-756-248-8	Sequence 8, Appli	c 748	12	36.4	25	14	US-10-215-112-12413	Sequence 12413, A
c 676	12.2	37.0	27	11	US-09-828-317A-9	Sequence 9, Appli	c 749	12	36.4	25	15	US-10-098-263B-50355	Sequence 50355, A
c 677	12.2	37.0	27	15	US-10-244-215-74	Sequence 74, Appli	c 750	12	36.4	25	15	US-10-098-263B-50355	Sequence 50355, A
c 678	12.2	37.0	28	9	US-09-779-881-2	Sequence 2, Appli	c 751	12	36.4	25	15	US-10-098-263B-54146	Sequence 54146, A
c 679	12.2	37.0	29	18	US-10-687-402-16	Sequence 16, Appli	752	12	36.4	25	15	US-10-098-263B-55238	Sequence 55238, A
c 680	12.2	37.0	30	16	US-10-412-382-54	Sequence 54, Appli	753	12	36.4	25	15	US-10-098-263B-57444	Sequence 57444, A
c 681	12.2	37.0	32	9	US-09-837-644-4	Sequence 4, Appli	754	12	36.4	25	15	US-10-098-263B-64469	Sequence 64469, A
c 682	12.2	37.0	32	14	US-10-027-760-4	Sequence 4, Appli	755	12	36.4	25	15	US-10-098-263B-84004	Sequence 84004, A
c 683	12.2	37.0	32	16	US-10-622-108-36	Sequence 36, Appli	c 756	12	36.4	25	15	US-10-098-263B-95095	Sequence 95095, A
c 684	12.2	37.0	33	10	US-09-981-002-22	Sequence 22, Appli	c 757	12	36.4	25	15	US-10-098-263B-95095	Sequence 95095, A
c 685	12.2	37.0	36	16	US-10-682-595-8	Sequence 8, Appli	c 758	12	36.4	25	15	US-10-098-263B-96197	Sequence 96197, A
c 686	12.2	37.0	37	10	US-09-405-032-36	Sequence 36, Appli	759	12	36.4	25	15	US-10-098-263B-99822	Sequence 99822, A
c 687	12.2	37.0	37	10	US-09-405-032-38	Sequence 38, Appli	760	12	36.4	25	15	US-10-098-263B-100302	Sequence 100302, A
c 688	12.2	37.0	39	14	US-10-086-156-41	Sequence 41, Appli	761	12	36.4	25	15	US-10-098-263B-103785	Sequence 103785, A
c 689	12.2	37.0	39	18	US-10-031-123B-28	Sequence 28, Appli	762	12	36.4	25	15	US-10-098-263B-111921	Sequence 111921, A
c 690	12.2	37.0	40	9	US-09-245-802-54	Sequence 54, Appli	c 763	12	36.4	25	15	US-10-098-263B-117644	Sequence 117644, A
c 691	12.2	37.0	40	9	US-09-780-929-67	Sequence 67, Appli	c 764	12	36.4	25	15	US-10-278-455-33	Sequence 33, Appl
c 692	12.2	37.0	40	9	US-09-780-929-72	Sequence 72, Appli	c 765	12	36.4	25	15	US-10-278-437-33	Sequence 33, Appl
c 693	12.2	37.0	40	9	US-09-780-929-78	Sequence 78, Appli	c 766	12	36.4	25	17	US-10-723-361-10990	Sequence 10990, A
c 694	12.2	37.0	40	9	US-09-780-929-81	Sequence 81, Appli	767	12	36.4	26	9	US-09-784-911-21	Sequence 21, Appl
c 695	12.2	37.0	40	9	US-09-780-929-82	Sequence 82, Appli	768	12	36.4	27	17	US-10-716-359-29	Sequence 29, Appl
c 696	12.2	37.0	40	9	US-09-759-508B-4	Sequence 4, Appli	769	12	36.4	29	9	US-09-982-308-14	Sequence 14, Appl
c 697	12.2	37.0	40	9	US-09-759-508B-9	Sequence 9, Appli	770	12	36.4	29	13	US-10-145-014-14	Sequence 14, Appl
c 698	12.2	37.0	40	10	US-09-963-827B-54	Sequence 54, Appli	771	12	36.4	29	13	US-10-336-638-748	Sequence 748, App
c 699	12.2	37.0	40	15	US-10-230-576-3	Sequence 3, Appli	772	12	36.4	29	15	US-10-235-079B-11	Sequence 11, Appl
c 700	12.2	37.0	41	16	US-10-035-833A-6184	Sequence 6184, Ap	773	12	36.4	30	15	US-10-772-656-69	Sequence 69, Appl
c 701	12.2	37.0	42	14	US-10-181-836-14	Sequence 14, Appli	774	12	36.4	31	17	US-10-314-861-20	Sequence 20, Appl
c 702	12.2	37.0	45	18	US-10-031-123B-10	Sequence 10, Appli	775	12	36.4	32	15	US-10-706-466-9	Sequence 9, Appli
c 703	12.2	37.0	46	16	US-10-406-027-131	Sequence 131, App	776	12	36.4	32	16	US-09-894-839-42	Sequence 42, Appl
c 704	12.2	37.0	47	16	US-10-349-143-319	Sequence 519, App	c 777	12	36.4	33	15	US-10-176-255-18	Sequence 18, Appl
c 705	12.2	37.0	47	16	US-10-349-143-3353	Sequence 3353, Ap	c 778	12	36.4	33	15	US-10-176-255-19	Sequence 19, Appl
c 706	12.2	37.0	47	16	US-10-294-934-776	Sequence 776, App	c 779	12	36.4	33	15	US-10-055-555-18	Sequence 18, Appl
c 707	12.2	37.0	47	16	US-10-333-429-109	Sequence 109, App	c 780	12	36.4	33	15	US-10-055-555-19	Sequence 19, Appl
c 708	12.2	37.0	48	15	US-10-230-006-2248	Sequence 2248, Ap	c 781	12	36.4	33	16	US-10-392-837A-49	Sequence 49, Appl
c 709	12.2	37.0	49	16	US-10-380-705-27	Sequence 27, Appli	782	12	36.4	33	18	US-10-815-495-10	Sequence 10, Appl
c 710	12.2	37.0	50	16	US-10-131-827-3371	Sequence 3371, Ap	783	12	36.4	35	9	US-09-982-308-11	Sequence 11, Appl
c 711	12	36.4	12	8	US-08-887-505-98	Sequence 98, Appli	c 784	12	36.4	35	10	US-09-825-805-207	Sequence 207, App
c 712	12	36.4	13	10	US-09-740-332-4720	Sequence 4720, Ap	785	12	36.4	35	13	US-10-145-014-11	Sequence 11, Appl
c 713	12	36.4	13	10	US-09-817-879-4720	Sequence 4720, Ap	c 786	12	36.4	36	9	US-09-504-231A-2882	Sequence 2882, Ap
c 714	12	36.4	13	17	US-10-669-841-7313	Sequence 7313, Ap	787	12	36.4	36	9	US-09-274-553D-2882	Sequence 2882, Ap
c 715	12	36.4	14	16	US-10-461-790-122	Sequence 122, App	c 788	12	36.4	36	10	US-09-848-754A-9561	Sequence 9561, Ap
c 716	12	36.4	15	9	US-09-504-231A-1526	Sequence 1526, Ap	c 789	12	36.4	37	9	US-09-864-785-1748	Sequence 1748, Ap
c 717	12	36.4	15	9	US-09-274-553D-1526	Sequence 1526, Ap	c 790	12	36.4	37	9	US-09-864-785-1798	Sequence 1798, Ap
c 718	12	36.4	15	10	US-09-740-332-4708	Sequence 4707, Ap	c 791	12	36.4	37	10	US-09-825-805-208	Sequence 208, App
c 719	12	36.4	15	10	US-09-740-332-4708	Sequence 4708, Ap	c 792	12	36.4	37	10	US-09-848-616-149	Sequence 149, App
c 720	12	36.4	15	10	US-09-740-332-4723	Sequence 4723, Ap	c 793	12	36.4	37	10	US-09-927-046-3796	Sequence 3796, Ap
c 721	12	36.4	15	10	US-09-817-879-4708	Sequence 4707, Ap	c 794	12	36.4	37	10	US-09-848-754A-6001	Sequence 6001, Ap
c 722	12	36.4	15	10	US-09-817-879-4708	Sequence 4708, Ap	c 795	12	36.4	37	10	US-09-848-754A-6301	Sequence 6301, Ap
c 723	12	36.4	15	10	US-09-817-879-4723	Sequence 4723, Ap	c 796	12	36.4	37	10	US-09-848-754A-6328	Sequence 6328, Ap
c 724	12	36.4	15	17	US-10-669-841-7300	Sequence 7300, Ap	c 797	12	36.4	37	10	US-09-848-754A-6345	Sequence 6345, Ap
c 725	12	36.4	15	17	US-10-669-841-7301	Sequence 7301, Ap	c 798	12	36.4	37	10	US-09-848-754A-6398	Sequence 6398, Ap
c 726	12	36.4	15	17	US-10-669-841-7316	Sequence 7316, Ap	c 799	12	36.4	37	10	US-09-827-395A-1780	Sequence 1780, Ap
c 727	12	36.4	17	10	US-09-740-332-38	Sequence 28, Appli	c 800	12	36.4	37	15	US-10-156-306-2576	Sequence 2576, Ap
c 728	12	36.4	17	10	US-09-740-332-36	Sequence 36, Appli	c 801	12	36.4	37	15	US-10-156-306-2638	Sequence 2638, Ap
c 729	12	36.4	17	10	US-09-817-879-28	Sequence 28, Appli	c 802	12	36.4	37	15	US-10-156-306-6076	Sequence 6076, Ap
c 730	12	36.4	17	10	US-09-817-879-36	Sequence 36, Appli	c 803	12	36.4	37	15	US-10-156-306-6120	Sequence 6120, Ap
c 731	12	36.4	17	17	US-10-669-841-2621	Sequence 2621, Ap	c 804	12	36.4	37	15	US-10-156-306-6122	Sequence 6122, Ap
c 732	12	36.4	17	17	US-10-669-841-2629	Sequence 2629, Ap	c 805	12	36.4	37	15	US-10-156-306-6178	Sequence 6178, Ap
c 733	12	36.4	19	18	US-10-667-271-67	Sequence 67, Appli	c 806	12	36.4	37	15	US-10-156-306-6308	Sequence 6308, Ap
c 734	12	36.4	19	18	US-10-667-271-70	Sequence 70, Appli	c 807	12	36.4	37	15	US-10-289-454-370	Sequence 370, App
c 735	12	36.4	19	18	US-10-667-271-763	Sequence 763, App	c 808	12	36.4	37	15	US-10-050-902-149	Sequence 149, App
c 736	12	36.4	19	18	US-10-667-271-766	Sequence 766, App	c 809	12	36.4	37	15	US-10-050-898-149	Sequence 149, App
c 737	12	36.4	20	8	US-08-887-505-84	Sequence 84, Appli	c 810	12	36.4	37	15	US-10-230-006-1453	Sequence 1453, Ap
c 738	12	36.4	20	8	US-08-944-410-9	Sequence 9, Appli	c 811	12	36.4	37	15	US-10-430-882-1780	Sequence 1780, Ap
c 739	12	36.4	20	10	US-09-882-945A-60	Sequence 60, Appli	c 812	12	36.4	37	15	US-10-346-190-150	Sequence 150, App
c 740	12	36.4	20	16	US-10-300-288-42	Sequence 42, Appli	c 813	12	36.4	37	16	US-10-289-456-149	Sequence 149, App
c 741	12	36.4	21	15	US-10-258-746-4	Sequence 4, Appli	c 814	12	36.4	37	16	US-10-622-124-92	Sequence 92, Appl
c 742	12	36.4	22	15	US-10-136-728-126	Sequence 126, App	815	12	36.4	37	16	US-10-622-124-93	Sequence 93, Appl

C 816	12	36.4	37	16	US-10-138-674-18165	Sequence 18165, A	889	12	36.4	38	17	US-10-287-949A-15929	Sequence 15929, A
C 817	12	36.4	37	16	US-10-138-674-18193	Sequence 18193, A	890	12	36.4	38	17	US-10-669-841-8115	Sequence 8115, Ap
C 818	12	36.4	37	16	US-10-138-674-18339	Sequence 18339, A	891	12	36.4	38	17	US-10-669-841-8389	Sequence 8389, Ap
C 819	12	36.4	37	16	US-10-138-674-18389	Sequence 18389, A	892	12	36.4	38	17	US-10-669-841-8732	Sequence 8732, Ap
C 820	12	36.4	37	16	US-10-138-674-18408	Sequence 18408, A	C 893	12	36.4	38	17	US-10-669-841-9372	Sequence 9372, Ap
C 821	12	36.4	37	16	US-10-138-674-18453	Sequence 18453, A	C 894	12	36.4	39	15	US-10-323-069A-83	Sequence 83, Appl
C 822	12	36.4	37	16	US-10-138-674-18473	Sequence 18473, A	C 895	12	36.4	40	9	US-09-245-802-13	Sequence 13, Appl
C 823	12	36.4	37	16	US-10-138-674-18486	Sequence 18486, A	C 896	12	36.4	40	10	US-09-963-827B-144	Sequence 144, App
C 824	12	36.4	37	16	US-10-138-674-20261	Sequence 20261, A	C 897	12	36.4	40	18	US-10-469-851-230	Sequence 230, Appl
C 825	12	36.4	37	16	US-10-138-674-20387	Sequence 20387, A	C 898	12	36.4	41	15	US-10-296-616-13	Sequence 13, Appl
C 826	12	36.4	37	16	US-10-138-674-20431	Sequence 20431, A	C 899	12	36.4	41	15	US-10-296-616-14	Sequence 14, Appl
C 827	12	36.4	37	16	US-10-138-674-20473	Sequence 20473, A	C 900	12	36.4	41	16	US-10-035-833A-941	Sequence 941, App
C 828	12	36.4	37	16	US-10-138-674-20512	Sequence 20512, A	C 901	12	36.4	41	16	US-10-035-833A-2057	Sequence 2057, Ap
C 829	12	36.4	37	16	US-10-138-674-20516	Sequence 20516, A	C 902	12	36.4	41	16	US-10-035-833A-6951	Sequence 6951, Ap
C 830	12	36.4	37	16	US-10-138-674-20627	Sequence 20627, A	C 903	12	36.4	41	16	US-10-035-833A-7314	Sequence 7314, Ap
C 831	12	36.4	37	17	US-10-287-949A-18165	Sequence 18165, A	C 904	12	36.4	42	9	US-09-101-807-5	Sequence 5, Appl
C 832	12	36.4	37	17	US-10-287-949A-18193	Sequence 18193, A	C 905	12	36.4	44	15	US-10-370-071-3	Sequence 3, Appl
C 833	12	36.4	37	17	US-10-287-949A-18339	Sequence 18339, A	C 906	12	36.4	44	15	US-10-251-215-29	Sequence 29, Appl
C 834	12	36.4	37	17	US-10-287-949A-18389	Sequence 18389, A	C 907	12	36.4	45	14	US-10-146-835-18	Sequence 18, Appl
C 835	12	36.4	37	17	US-10-287-949A-18408	Sequence 18408, A	C 908	12	36.4	47	16	US-10-294-934-712	Sequence 712, App
C 836	12	36.4	37	17	US-10-287-949A-18453	Sequence 18453, A	C 909	12	36.4	48	14	US-10-165-857-4	Sequence 4, Appl
C 837	12	36.4	37	17	US-10-287-949A-18473	Sequence 18473, A	C 910	12	36.4	48	15	US-10-295-798-16	Sequence 16, Appl
C 838	12	36.4	37	17	US-10-287-949A-18486	Sequence 18486, A	C 911	12	36.4	48	15	US-10-244-142A-18	Sequence 18, Appl
C 839	12	36.4	37	17	US-10-287-949A-20261	Sequence 20261, A	C 912	12	36.4	48	15	US-10-165-748B-4	Sequence 4, Appl
C 840	12	36.4	37	17	US-10-287-949A-20387	Sequence 20387, A	C 913	12	36.4	48	17	US-10-165-856A-4	Sequence 1356, Ap
C 841	12	36.4	37	17	US-10-287-949A-20431	Sequence 20431, A	C 914	12	36.4	50	16	US-10-131-827-1356	Sequence 1558, Ap
C 842	12	36.4	37	17	US-10-287-949A-20473	Sequence 20473, A	C 915	11.8	35.8	15	9	US-09-504-231A-1558	Sequence 1558, Ap
C 843	12	36.4	37	17	US-10-287-949A-20512	Sequence 20512, A	C 916	11.8	35.8	15	9	US-09-274-553D-1558	Sequence 6087, Ap
C 844	12	36.4	37	17	US-10-287-949A-20516	Sequence 20516, A	C 917	11.8	35.8	17	9	US-09-866-108-6087	Sequence 6088, Ap
C 845	12	36.4	37	17	US-10-287-949A-20627	Sequence 20627, A	C 918	11.8	35.8	17	9	US-09-866-108-6088	Sequence 3194, Ap
C 846	12	36.4	37	17	US-10-622-087-62	Sequence 62, Appl	C 919	11.8	35.8	17	10	US-09-818-875-3194	Sequence 3195, Ap
C 847	12	36.4	37	17	US-10-622-087-63	Sequence 63, Appl	C 920	11.8	35.8	17	10	US-09-818-875-3195	Sequence 152, App
C 848	12	36.4	38	10	US-09-825-805-936	Sequence 936, App	C 921	11.8	35.8	17	10	US-09-940-925A-152	Sequence 152, App
C 849	12	36.4	38	10	US-09-825-805-987	Sequence 987, App	C 922	11.8	35.8	17	10	US-09-941-193A-152	Sequence 33, Appl
C 850	12	36.4	38	10	US-09-825-805-1332	Sequence 1332, Ap	C 923	11.8	35.8	17	10	US-09-740-332-33	Sequence 33, Appl
C 851	12	36.4	38	10	US-09-825-805-1361	Sequence 1361, Ap	C 924	11.8	35.8	17	15	US-10-230-006-535	Sequence 535, App
C 852	12	36.4	38	10	US-09-730-289B-2596	Sequence 2596, Ap	C 925	11.8	35.8	17	15	US-10-230-006-536	Sequence 536, App
C 853	12	36.4	38	10	US-09-730-289B-2803	Sequence 2803, Ap	C 926	11.8	35.8	17	15	US-10-209-787-3194	Sequence 3194, Ap
C 854	12	36.4	38	10	US-09-780-533A-3211	Sequence 3211, Ap	C 927	11.8	35.8	17	15	US-10-209-787-3195	Sequence 3195, Ap
C 855	12	36.4	38	10	US-09-780-533A-4514	Sequence 4514, Ap	C 928	11.8	35.8	17	15	US-10-209-787-3195	Sequence 3194, Ap
C 856	12	36.4	38	10	US-09-780-533A-4514	Sequence 4514, Ap	C 929	11.8	35.8	17	16	US-10-261-185-3194	Sequence 3194, Ap
C 857	12	36.4	38	10	US-09-877-478-3498	Sequence 3498, Ap	C 930	11.8	35.8	17	16	US-10-261-185-3195	Sequence 3195, Ap
C 858	12	36.4	38	10	US-09-877-478-3498	Sequence 3498, Ap	C 931	11.8	35.8	17	17	US-10-669-841-2626	Sequence 2626, Ap
C 859	12	36.4	38	10	US-09-877-478-4481	Sequence 4481, Ap	C 932	11.8	35.8	17	17	US-10-723-361-6087	Sequence 6087, Ap
C 860	12	36.4	38	10	US-09-776-474-2132	Sequence 2132, Ap	C 933	11.8	35.8	17	17	US-10-723-361-6088	Sequence 6088, Ap
C 861	12	36.4	38	10	US-09-930-423-2567	Sequence 2567, Ap	C 934	11.8	35.8	17	17	US-10-681-074-3194	Sequence 3194, Ap
C 862	12	36.4	38	10	US-09-930-423-2719	Sequence 2719, Ap	C 935	11.8	35.8	17	17	US-10-681-074-3195	Sequence 3195, Ap
C 863	12	36.4	38	10	US-09-930-423-3050	Sequence 3050, Ap	C 936	11.8	35.8	17	18	US-10-660-122-23	Sequence 23, Appl
C 864	12	36.4	38	10	US-09-930-423-3089	Sequence 3089, Ap	C 937	11.8	35.8	19	18	US-10-667-271-62	Sequence 62, Appl
C 865	12	36.4	38	10	US-09-930-423-3194	Sequence 3194, Ap	C 938	11.8	35.8	19	18	US-10-667-271-758	Sequence 758, App
C 866	12	36.4	38	10	US-09-780-164-1243	Sequence 1243, Ap	C 939	11.8	35.8	20	9	US-09-855-797A-36	Sequence 36, Appl
C 867	12	36.4	38	10	US-09-780-164-1243	Sequence 1243, Ap	C 940	11.8	35.8	20	9	US-09-855-797A-36	Sequence 11, Appl
C 868	12	36.4	38	10	US-09-780-164-1243	Sequence 1243, Ap	C 941	11.8	35.8	20	9	US-09-855-797A-36	Sequence 43, Appl
C 869	12	36.4	38	10	US-09-780-164-1243	Sequence 1243, Ap	C 942	11.8	35.8	20	9	US-09-855-797A-36	Sequence 36, Appl
C 870	12	36.4	38	10	US-09-780-164-1243	Sequence 1243, Ap	C 943	11.8	35.8	20	9	US-09-907-900-36	Sequence 36, Appl
C 871	12	36.4	38	10	US-09-745-237A-2567	Sequence 2567, Ap	C 944	11.8	35.8	20	10	US-09-909-595-36	Sequence 36, Appl
C 872	12	36.4	38	10	US-09-745-237A-2567	Sequence 2567, Ap	C 945	11.8	35.8	20	10	US-09-909-595-36	Sequence 36, Appl
C 873	12	36.4	38	10	US-09-745-237A-2719	Sequence 2719, Ap	C 946	11.8	35.8	20	15	US-10-196-842-9	Sequence 9, Appl
C 874	12	36.4	38	10	US-09-745-237A-3050	Sequence 3050, Ap	C 947	11.8	35.8	20	15	US-10-196-842-9	Sequence 18, Appl
C 875	12	36.4	38	10	US-09-745-237A-3089	Sequence 3089, Ap	C 948	11.8	35.8	20	15	US-10-197-026A-18	Sequence 18, Appl
C 876	12	36.4	38	15	US-10-156-306-1802	Sequence 1802, Ap	C 949	11.8	35.8	20	15	US-10-300-892-36	Sequence 36, Appl
C 877	12	36.4	38	15	US-10-342-902-3224	Sequence 3224, Ap	C 950	11.8	35.8	20	15	US-10-331-109-1	Sequence 1, Appl
C 878	12	36.4	38	16	US-10-342-902-3224	Sequence 3224, Ap	C 951	11.8	35.8	20	15	US-10-331-109-2	Sequence 2, Appl
C 879	12	36.4	38	16	US-10-342-902-3498	Sequence 3498, Ap	C 952	11.8	35.8	20	15	US-10-159-834-33	Sequence 33, Appl
C 880	12	36.4	38	16	US-10-342-902-3498	Sequence 3498, Ap	C 953	11.8	35.8	20	16	US-10-159-834-101	Sequence 101, App
C 881	12	36.4	38	16	US-10-342-902-4481	Sequence 4481, Ap	C 954	11.8	35.8	20	16	US-10-289-762-5638	Sequence 5638, Ap
C 882	12	36.4	38	16	US-10-138-674-13539	Sequence 13539, A	C 955	11.8	35.8	20	16	US-10-303-199A-3	Sequence 3, Appl
C 883	12	36.4	38	16	US-10-138-674-13697	Sequence 13697, A	C 956	11.8	35.8	20	17	US-10-815-730-36	Sequence 36, Appl
C 884	12	36.4	38	16	US-10-138-674-13836	Sequence 13836, A	C 957	11.8	35.8	20	17	US-10-815-730-36	Sequence 36, Appl
C 885	12	36.4	38	16	US-10-138-674-15929	Sequence 15929, A	C 958	11.8	35.8	22	15	US-10-820-133-36	Sequence 36, Appl
C 886	12	36.4	38	17	US-10-287-949A-13539	Sequence 13539, A	C 959	11.8	35.8	24	10	US-10-419-034-5	Sequence 5, Appl
C 887	12	36.4	38	17	US-10-287-949A-13697	Sequence 13697, A	C 960	11.8	35.8	25	9	US-09-327-737-90	Sequence 90, Appl
C 888	12	36.4	38	17	US-10-287-949A-13836	Sequence 13836, A	C 961	11.8	35.8	25	14	US-10-060-830-537	Sequence 537, App

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962 11.8 35.8 25 14 US-10-215-112-14238 Sequence 14238, A
c 963 11.8 35.8 25 15 US-10-098-263B-1847 Sequence 1847, Ap
964 11.8 35.8 25 15 US-10-098-263B-4640 Sequence 4640, Ap
965 11.8 35.8 25 15 US-10-098-263B-4953 Sequence 4953, Ap
966 11.8 35.8 25 15 US-10-098-263B-6720 Sequence 6720, Ap
967 11.8 35.8 25 15 US-10-098-263B-17151 Sequence 17151, A
968 11.8 35.8 25 15 US-10-098-263B-29536 Sequence 29536, A
969 11.8 35.8 25 15 US-10-098-263B-32755 Sequence 32755, A
c 970 11.8 35.8 25 15 US-10-098-263B-34577 Sequence 34577, A
c 971 11.8 35.8 25 15 US-10-098-263B-35380 Sequence 35380, A
c 972 11.8 35.8 25 15 US-10-098-263B-35471 Sequence 35471, A
973 11.8 35.8 25 15 US-10-098-263B-36188 Sequence 36188, A
974 11.8 35.8 25 15 US-10-098-263B-38311 Sequence 38311, A
c 975 11.8 35.8 25 15 US-10-098-263B-41441 Sequence 41441, A
c 976 11.8 35.8 25 15 US-10-098-263B-43815 Sequence 43815, A
c 977 11.8 35.8 25 15 US-10-098-263B-47317 Sequence 47317, A
c 978 11.8 35.8 25 15 US-10-098-263B-48106 Sequence 48106, A
c 979 11.8 35.8 25 15 US-10-098-263B-60065 Sequence 60065, A
c 980 11.8 35.8 25 15 US-10-098-263B-63611 Sequence 63611, A
c 981 11.8 35.8 25 15 US-10-098-263B-75329 Sequence 75329, A
c 982 11.8 35.8 25 15 US-10-098-263B-75688 Sequence 75688, A
c 983 11.8 35.8 25 15 US-10-098-263B-82516 Sequence 82516, A
984 11.8 35.8 25 15 US-10-098-263B-88417 Sequence 88417, A
985 11.8 35.8 25 15 US-10-098-263B-91620 Sequence 91620, A
986 11.8 35.8 25 15 US-10-098-263B-97615 Sequence 97615, A
c 987 11.8 35.8 25 15 US-10-098-263B-99881 Sequence 99881, A
988 11.8 35.8 25 15 US-10-098-263B-100332 Sequence 100332, A
989 11.8 35.8 25 15 US-10-098-263B-100369 Sequence 100369, A
990 11.8 35.8 25 15 US-10-098-263B-104724 Sequence 104724, A
c 991 11.8 35.8 25 15 US-10-098-263B-112256 Sequence 112256, A
c 992 11.8 35.8 25 15 US-10-098-263B-114794 Sequence 114794, A
c 993 11.8 35.8 25 15 US-10-098-263B-118102 Sequence 118102, A
994 11.8 35.8 25 15 US-10-098-263B-128255 Sequence 128255, A
c 995 11.8 35.8 25 15 US-10-098-263B-128409 Sequence 128409, A
c 996 11.8 35.8 25 15 US-10-098-263B-130429 Sequence 130429, A
997 11.8 35.8 25 17 US-10-775-169-1828 Sequence 1828, Ap
998 11.8 35.8 26 9 US-09-117-860-47 Sequence 47, Appl
c 999 11.8 35.8 26 9 US-09-732-618-34 Sequence 34, Appl
1000 11.8 35.8 29 9 US-09-884-566-5 Sequence 5, Appli
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ALIGNMENTS

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RESULT 1
US-10-087-631B-3
; Sequence 3, Application US/10087631B
; Publication No. US20030054372A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; TITLE OF INVENTION: CONTROL
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/087,631B
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ST650 HCV specific probe
US-10-087-631B-3
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Query Match 100.0%; Score 33; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGGTGTACTACCGTTCGCGAGACCACCTATGCG 33
Db 1 CGGTGTACTACCGTTCGCGAGACCACCTATGCG 33
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RESULT 2
US-10-419-022-3
; Sequence 3, Application US/10419022
; Publication No. US20030165982A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; TITLE OF INVENTION: CONTROL
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/419,022
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/10/087,631B
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ST650 HCV specific probe
US-10-419-022-3
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Query Match 100.0%; Score 33; DB 15; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGGTGTACTACCGTTCGCGAGACCACCTATGCG 33
Db 1 CGGTGTACTACCGTTCGCGAGACCACCTATGCG 33
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RESULT 3
US-10-337-190-1
; Sequence 1, Application US/10337190
; Publication No. US20040014070A1
; GENERAL INFORMATION:
; APPLICANT: Pansl, Judith
; APPLICANT: Wenzig, Peter
; APPLICANT: Schoenbrunner, Ralf
; APPLICANT: O'Donnell, Patrick
; APPLICANT: Kyger, Erich
; APPLICANT: Malhotra, Kushbeer
; APPLICANT: Weindel, Kurt
; APPLICANT: Bartl, Knut
; TITLE OF INVENTION: Use of Silica Material in an Amplification Reaction
; FILE REFERENCE: 21255-US
; CURRENT APPLICATION NUMBER: US/10/337,190
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: 60/347,3237
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: HCV specific probe
US-10-337-190-1
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Query Match 93.9%; Score 31; DB 16; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGGTGTACTACCGTTCGCGAGACCACCTATG 31
Db 1 CGGTGTACTACCGTTCGCGAGACCACCTATG 31
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RESULT 4
US-10-451-882-42
; Sequence 42, Application US/10451882
; Publication No. US20040185455A1
; GENERAL INFORMATION:
; APPLICANT: Takara Shuzo Co., Ltd.
; TITLE OF INVENTION: Method for detection of virulent organisms
; FILE REFERENCE: 662981
; CURRENT APPLICATION NUMBER: US/10/451,882
; CURRENT FILING DATE: 2004-01-05
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: JP 2000-396321
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: JP 2000-396222
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: JP 2001-199552
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: JP 2001-278920
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 42
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer area to amplify a portion of HCV.
US-10-451-882-42

Query Match 66.7%; Score 22; DB 17; Length 41;
Best Local Similarity 97.1%; Pred. No. 6.6;
Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGGTGTACTCACC-GTTCGCGAGACCACTATGGC 33
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DB 5 CGGTGTACTCACC GTTCGCGAGACCACTATGGC 38
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RESULT 5
US-10-318-416B-34/c
; Sequence 34, Application US/10318416B
; Publication No. US20040115643A1
; GENERAL INFORMATION:
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Gribanov, Oleg G.
; TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF
; FILE REFERENCE: 25006.0012U1
; CURRENT APPLICATION NUMBER: US/10/318,416B
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /note =
; OTHER INFORMATION: synthetic construct
US-10-318-416B-34

Query Match 60.6%; Score 20; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCGCGAGACCACTATGGC 33
|||||
DB 24 GTTCGCGAGACCACTATGGC 5
|||||

RESULT 6
US-10-318-416B-32
; Sequence 32, Application US/10318416B
; Publication No. US20040115643A1
; GENERAL INFORMATION:

; APPLICANT: Lizardi, Paul M.
; APPLICANT: Gribanov, Oleg G.
; TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF
; FILE REFERENCE: 25006.0012U1
; CURRENT APPLICATION NUMBER: US/10/318,416B
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /note =
; OTHER INFORMATION: synthetic construct
US-10-318-416B-32

Query Match 60.6%; Score 20; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCGCGAGACCACTATGGC 33
|||||
DB 1 GTTCGCGAGACCACTATGGC 20
|||||

RESULT 7
US-10-147-679A-20
; Sequence 20, Application US/10147679A
; Publication No. US20030224366A1
; GENERAL INFORMATION:
; APPLICANT: Weindel, Kurt
; APPLICANT: Riedling, Michael
; APPLICANT: Geiger, Albert
; TITLE OF INVENTION: Magnetic glass particles, method for their preparation
; TITLE OF INVENTION: and uses thereof
; FILE REFERENCE: 1803-344-999
; CURRENT APPLICATION NUMBER: US/10/147,679A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: EP99122853.7
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe (HCV)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: derivatisation with a
; OTHER INFORMATION: Pentamethine-di-indocarbocyanine via a
; OTHER INFORMATION: alkylphosphatidyl-linker (Pharmacia Biotech
; OTHER INFORMATION: Cy5-N-ethyl-phosphoramidite)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)
; OTHER INFORMATION: N represents a
; OTHER INFORMATION: 2-(amino-cyclohexyl)-propane-1,3-diol-linker
; OTHER INFORMATION: derivatised with 6-carboxy-fluorescein (Biogenex
; OTHER INFORMATION: CX-FAM-phosphoramidite)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (31)
; OTHER INFORMATION: derivatisation with a 3'-terminal phosphate group
US-10-147-679A-20

Query Match 60.6%; Score 20; DB 15; Length 32;
Best Local Similarity 96.9%; Pred. No. 51;

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Matches 31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CGGTGTACTCAGG-TTCCGCAGACCACTATG 31
DB 1 CGGTGTACTCAGGTTCCGCAGACCACTATG 32
RESULT 8
US-09-782-361-3/c
; Sequence 3, Application US/09782361
; Patent No. US20020064778A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yu-Wen
; TITLE OF INVENTION: PRIMER-SPECIFIC AND MISPAIR EXTENSION ASSAY FOR IDENTIFYING GEN
; FILE REFERENCE: 2883-4757US
; CURRENT APPLICATION NUMBER: US/09/782,361
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: sense universal primer for PCR (second round)
US-09-782-361-3
Query Match 58.8%; Score 19.4; DB 9; Length 31;
Best Local Similarity 95.2%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CGGTCCGCAGACCACTATGG 32
DB 21 CGGTCCGCAGACCACTATGG 1
RESULT 9
US-09-747-419-11
; Sequence 11, Application US/09747419
; Patent No. US20020155582A1
; GENERAL INFORMATION:
; APPLICANT: Lemon, Stanley
; APPLICANT: Yi, Minkyung
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
; FILE REFERENCE: 265.0007 0101
; CURRENT APPLICATION NUMBER: US/09/747,419
; CURRENT FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: US 60/171,909
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-747-419-11
Query Match 57.6%; Score 19; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 GTTCCGCAGACCACTATGG 32
DB 1 GTTCCGCAGACCACTATGG 19
RESULT 10
US-10-259-275-11
; Sequence 11, Application US/10259275
; Publication No. US20030125541A1
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; GENERAL INFORMATION:
; APPLICANT: Lemon, Stanley M.
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
; FILE REFERENCE: 265.0007 0120
; CURRENT APPLICATION NUMBER: US/10/259,275
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/171,909
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 09/747,419
; PRIOR FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: US 60/325,236
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/338,123
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 19
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Primer
US-10-259-275-11
Query Match 57.6%; Score 19; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 GTTCCGCAGACCACTATGG 32
DB 1 GTTCCGCAGACCACTATGG 19
RESULT 11
US-10-667-271-78/c
; Sequence 78, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-7638)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78
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; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-78

Query Match      57.6%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCAGACCACTATGGC 33
      |||||
Db 19 TTCCGCAGACCACTATGGC 1

RESULT 12
US-10-667-271-82/c
; Sequence 82, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-82

Query Match      57.6%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GTTCCGCAGACCACTATGG 32
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Db 19 GTTCCGCAGACCACTATGG 1

RESULT 13
US-10-667-271-774
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; Sequence 774, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 774
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-774

Query Match      57.6%; Score 19; DB 18; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.4e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCAGACCACTATGGC 33
      :|||:|||||:|:|:|
Db 1  UUCGCGACCAUUGGC 19

RESULT 14
US-10-667-271-778
; Sequence 778, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
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; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 778
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:  s1NA antisense region
US-10-667-271-778

Query Match          57.6%; Score 19; DB 18; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.4e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCCGCAGACCACTATGG 32
Db 1 GUUCCGCAGACCACTATGG 19

RESULT 15
US-10-471-351-1/c
; Sequence 1, Application US/10471351
; Publication No. US20040115685A1
; GENERAL INFORMATION:
; APPLICANT: Tercero, Juan Carlos
; APPLICANT: Garcia, Lucia
; APPLICANT: Guisan, Jose Manuel
; APPLICANT: Fernandez, Roberto
; APPLICANT: Fuentes, Manuel
; TITLE OF INVENTION: IMMOBILISATION OF LIGANDS
; FILE REFERENCE: 14620-025US1
; CURRENT APPLICATION NUMBER: US/10/471,351
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: PCT/GB02/01059
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: GB 0105745.4
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: this sequence has an aminated 3'-terminus
; FEATURE:
; OTHER INFORMATION: Probe sequence
US-10-471-351-1

Query Match          57.6%; Score 19; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCAGACCACTATGGC 33
Db 25 TTCCGCAGACCACTATGGC 7

US-10-087-631b-3.max.rnpb
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US-10-318-416B-35/c
; Sequence 35, Application US/10318416B
; Publication No. US20040115643A1
; GENERAL INFORMATION:
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Gribanov, Oleg G.
; TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF
; TITLE OF INVENTION: PRIMERS
; FILE REFERENCE: 25006.0012U1
; CURRENT APPLICATION NUMBER: US/10/318,416B
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
US-10-318-416B-35

Query Match          55.8%; Score 18.4; DB 17; Length 24;
Best Local Similarity 95.0%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTTCCGCAGACCACTATGGC 33
Db 24 GTTCCGCAGACCACTATGGC 5

RESULT 17
US-10-318-416B-33
; Sequence 33, Application US/10318416B
; Publication No. US20040115643A1
; GENERAL INFORMATION:
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Gribanov, Oleg G.
; TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF
; TITLE OF INVENTION: PRIMERS
; FILE REFERENCE: 25006.0012U1
; CURRENT APPLICATION NUMBER: US/10/318,416B
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
US-10-318-416B-33

Query Match          55.8%; Score 18.4; DB 17; Length 26;
Best Local Similarity 95.0%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTTCCGCAGACCACTATGGC 33
Db 1 GTTCCGCAGACCACTATGGC 20

RESULT 18
US-10-008-140B-11
; Sequence 11, Application US/10008140B
; Publication No. US20030124512A1
; GENERAL INFORMATION:
; APPLICANT: Pharmasset, Ltd.
; APPLICANT: Stuyver, Lieven
```

; TITLE OF INVENTION: Simultaneous Quantification of Nucleic Acids in Diseased Cells
; FILE REFERENCE: 08841. 105021
; CURRENT APPLICATION NUMBER: US/10/008,140B
; CURRENT FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotides used to amplify HCV (primers) antisense
US-10-008-140B-11

Query Match 54.5%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCAGACCACTATGG 32
Db 1 TTCCGCAGACCACTATGG 18
|||||

RESULT 19

US-10-667-271-80/c
; Sequence 80, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-80
Query Match 54.5%; Score 18; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 TTCCGCAGACCACTATGG 32
Db 1 TTCCGCAGACCACTATGG 18
|||||
RESULT 21
US-10-667-271-776
; Sequence 776, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-80

Query Match 54.5%; Score 18; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GTTCCGACCACTATG 31
Db 18 GTTCCGACCACTATG 1
|||||

RESULT 20

US-10-667-271-81/c
; Sequence 81, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-81

Query Match 54.5%; Score 18; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 TCCGCAGACCACTATGG 33
Db 19 TCCGCAGACCACTATGG 2
|||||

RESULT 21

US-10-667-271-776
; Sequence 776, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-80

Query Match 54.5%; Score 18; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 776
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense region
US-10-667-271-776

Query Match 54.5%; Score 18; DB 18; Length 19;
Best Local Similarity 77.8%; Pred. No. 3.9e+02;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCCGCAGACCACTATG 31
Db 2 GUUCCGCAGACCACTAUG 19

RESULT 22
US-10-667-271-777
; Sequence 777, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 777
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense region
US-10-667-271-777

Query Match 54.5%; Score 18; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 16 TCCGCAGACCACTATGGC 33
Db 1 UCCGCAGACCACTAUGGC 18

RESULT 23
US-10-240-460-8/c
; Sequence 8, Application US/10240460
; Publication No. US20030207292A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030207292A1omi, Tsunumori
; APPLICANT: Nagamine, Kentaro
; TITLE OF INVENTION: METHOD FOR AMPLIFYING NUCLEIC ACID BY USING
; TITLE OF INVENTION: DOUBLE-STRANDED NUCLEIC ACID AS TEMPLATE
; FILE REFERENCE: 201487/1110
; CURRENT APPLICATION NUMBER: US/10/240,460
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/JPO1/02771
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-111939
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificially
; OTHER INFORMATION: synthesized primer sequence
US-10-240-460-8

Query Match 54.5%; Score 18; DB 15; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TCCGCAGACCACTATGGC 33
Db 46 TCCGCAGACCACTATGGC 29

RESULT 24
US-10-667-271-76/c
; Sequence 76, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29

```
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region
US-10-667-271-772

Query Match          52.7%; Score 17.4; DB 18; Length 19;
Best Local Similarity 94.7%; Pred. No. 7.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      12  CCGTTCGCGAGACCACTAT 30
          ||:|||||
Db      19  CCGTTCGCGAGACCACTAT 1

RESULT 25
US-10-667-271-772
; Sequence 772, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region
US-10-667-271-772
```

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; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 772
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-772

Query Match          52.7%; Score 17.4; DB 18; Length 19;
Best Local Similarity 73.7%; Pred. No. 7.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy      12  CCGTTCGCGAGACCACTAT 30
          ||:|||||
Db      1  CCGUUCGCGAGACCAUAU 19

RESULT 26
US-10-667-271-1401/c
; Sequence 1401, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1401
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region
US-10-667-271-1401

Query Match          52.7%; Score 17.4; DB 18; Length 23;
Best Local Similarity 94.7%; Pred. No. 7.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 12 CCGTTCGCGAGACCACTAT 30
Db 19 CCGTTCGCGAGACCACTAT 1

RESULT 27
US-09-740-332-30/c
; Sequence 30, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-30

Query Match 51.5%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TCCGCGAGACCACTATGG 32
Db 17 TCCGCGAGACCACTATGG 1

RESULT 28
US-09-740-332-4525
; Sequence 4525, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4525
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4525

Query Match 51.5%; Score 17; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCGAGACCACTATG 31
Db 1 UUCCGCGAGACCACTAUG 17

RESULT 29
US-09-817-879-30/c
; Sequence 30, Application US/09817879
```

```
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MH800-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-30

Query Match 51.5%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TCCGCGAGACCACTATGG 32
Db 17 TCCGCGAGACCACTATGG 1

RESULT 30
US-09-817-879-4525
; Sequence 4525, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MH800-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4525
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4525

Query Match 51.5%; Score 17; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCGAGACCACTATG 31
Db 1 UUCCGCGAGACCACTAUG 17

RESULT 31
US-10-669-841-2623/c
; Sequence 2623, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
```

```
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS C VIRUS
; FILE REFERENCE: 400/042US (MEHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2623
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-2623

Query Match 51.5%; Score 17; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 TCCGCAGACCACTATGG 32
Db 17 TCCGCAGACCACTATGG 1

RESULT 32
US-10-669-841-7118
; Sequence 7118, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS C VIRUS
; FILE REFERENCE: 400/042US (MEHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
```

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; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7118
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-7118

Query Match 51.5%; Score 17; DB 17; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCGCAGACCACTATG 31
Db 1 UCCGCAGACCACTAUG 17

RESULT 33
US-10-667-271-73/c
; Sequence 73, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
```

17 CCGCAGACCACTATGGC 33
|||||||:|:|
1 CCGCAGACCAUAUGG 17

DB

RESULT 35
US-09-882-945A-237/c
; Sequence 237, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 237
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-237

Query Match 51.5%; Score 17; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CCGCAGACCACTATGGC 33
|||||||:|:|
DB 24 CCGCAGACCACTATGGC 8

RESULT 36
US-10-667-271-75/c
; Sequence 75, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH802-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2

SEQ ID NO 75
LENGTH: 19

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region
US-10-667-271-75

Query Match 49.7%; Score 16.4; DB 18; Length 19;

Best Local Similarity 94.4%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTA 29

Db 18 CGGTTCGCGACCACTA 1

RESULT 37

US-10-667-271-771

Sequence 771, Application US/10667271

Publication No. US20040209831A1

GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics

APPLICANT: McSwiggen, James

APPLICANT: Macejak, Dennis

APPLICANT: Beigelman, Leonid

APPLICANT: Morrissey, David

TITLE OF INVENTION: RNA interference Mediated Inhibition of Hepatitis C Virus (HCV)

TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)

FILE REFERENCE: 400/129 (MBHB02-763B)

CURRENT APPLICATION NUMBER: US/10/667,271

CURRENT FILING DATE: 2003-09-16

PRIOR APPLICATION NUMBER: US 10/444,853

PRIOR FILING DATE: 2003-05-23

PRIOR APPLICATION NUMBER: PCT / US03/05043

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: PCT / US02/09187

PRIOR FILING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: USSN 60/401,104

PRIOR FILING DATE: 2002-08-05

PRIOR APPLICATION NUMBER: USSN 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: USSN 60/363,124

PRIOR FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: USSN 60/386,782

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: USSN 60/406,784

PRIOR FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: USSN 60/408,378

PRIOR FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: USSN 60/409,293

PRIOR FILING DATE: 2002-09-09

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1705

SOFTWARE: PatentIn version 3.2

SEQ ID NO 771

LENGTH: 19

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-771

Query Match 49.7%; Score 16.4; DB 18; Length 19;

Best Local Similarity 77.8%; Pred. No. 2e+03;

Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTA 29

Db 2 CGGUUCCGACCACTA 19

RESULT 38

US-09-825-805-24/c

Sequence 24, Application US/09825805

Publication No. US20030004122A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Beigelman, Leo

APPLICANT: Beaudry, Amber

APPLICANT: Karpeisky, Alex

APPLICANT: Adamic, Jasenka Matulic

APPLICANT: Sweedler, Dave

APPLICANT: Zinnen, Shawn

TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotids

FILE REFERENCE: MBHB00-831-F (400/009)

CURRENT APPLICATION NUMBER: US/09/825,805

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: 09/578,223

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 09/476,387

PRIOR FILING DATE: 1999-12-30

PRIOR APPLICATION NUMBER: 09/474,432

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/301,511

PRIOR FILING DATE: 1999-04-28

PRIOR APPLICATION NUMBER: 09/186,675

PRIOR FILING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: 60/083,727

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/064,866

PRIOR FILING DATE: 1997-11-05

NUMBER OF SEQ ID NOS: 1558

SOFTWARE: PatentIn version 3.0

SEQ ID NO 24

LENGTH: 16

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Hepatitis C Virus
US-09-825-805-24

Query Match 48.5%; Score 16; DB 10; Length 16;

Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCGCGACCACTAT 30

Db 16 TTCGCGACCACTAT 1

RESULT 39

US-09-740-332-4526

Sequence 4526, Application US/09740332

Publication No. US20030125270A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

FILE REFERENCE: RFI 400/003

CURRENT APPLICATION NUMBER: US/09/740,332

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9704

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4526

LENGTH: 17

TYPE: RNA

ORGANISM: artificial sequence

FEATURE:

NAME/KEY: misc_feature

LOCATION:

OTHER INFORMATION: oligonucleotide substrate

US-09-740-332-4526

Query Match 48.5%; Score 16; DB 10; Length 17;
Best Local Similarity 87.5%; Pred. No. 3e+03; 0; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACCTATGGC 33
|||||:|:|:
DB 1 CGCAGACCACCUAUGGC 16

RESULT 40

US-09-817-879-4526
; Sequence 4526, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4526
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4526

Query Match 48.5%; Score 16; DB 10; Length 17;
Best Local Similarity 87.5%; Pred. No. 3e+03; 0; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACCTATGGC 33
|||||:|:|:
DB 1 CGCAGACCACCUAUGGC 16

Search completed: November 24, 2004, 03:42:14
Job time : 164.842 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1582.15 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-3

Perfect score: 33
Sequence: 1 cgggtactcacggtccgcagaccattatggc 33

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hlc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_ges1:*
- 9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.8	47.9	47	8	AZ759762 1M0552A19
C 2	15.2	46.1	47	8	BH848576 SALK 0685
C 3	14.4	43.6	37	7	H03404 Y148c01.81
C 4	14.2	43.0	50	1	AU106643 AU106643
C 5	14	42.4	46	7	T56929 Y483f08.12
C 6	14	42.4	50	1	AU102254 AU102254
C 7	13.8	41.8	32	8	BH861153 SALK 0345
C 8	13.8	41.8	45	8	AZ331523 1M0059F01
C 9	13.6	41.2	41	9	CR403035 Arabidops
C 10	13.6	41.2	43	9	CR403034 Arabidops
C 11	13.6	41.2	45	2	BZ251857 601115885
C 12	13.6	41.2	47	8	BZ763121 SALK 1135
C 13	13.4	40.6	28	9	CG719689 11190580
C 14	13.4	40.6	36	8	AZ498025 1M0335B09
C 15	13.4	40.6	39	9	TA3H02P
C 16	13.4	40.6	44	8	BH620252 1007061G0
C 17	13.2	40.0	41	8	AZ785555 2M0029G04
C 18	13.2	40.0	42	8	AZ812045 2M0078A04
C 19	13.2	40.0	44	8	BH102544 602889548
C 20	13.2	40.0	45	8	BZ660777 SALK 0242
C 21	13.2	40.0	50	1	AU102740 AU102740
C 22	13.2	40.0	50	1	AU105906 AU105906
C 23	13	39.4	38	8	AZ786726 2M0032H20
C 24	13	39.4	42	9	AL765117 Arabidops

c 98	11.8	35.8	46	9	TA68B01Q	AL465151 T. brucei	c 171	11.4	34.5	50	1	AU105781	AU105781
c 99	11.8	35.8	47	9	CL423878	CL423878 01S0750-0	c 172	11.4	34.5	50	1	AU105838	AU105838
c 100	11.8	35.8	49	1	AI527771	AI527771 yJ28H01.Y	c 173	11.4	34.5	50	1	AU107272	AU107272
c 101	11.8	35.8	49	7	CF642375	CF642375 D50.H06.F	c 174	11.4	34.5	50	1	AU107274	AU107274
c 102	11.8	35.8	49	9	AL771898	AL771898 Arabidops	c 175	11.4	34.5	50	1	AU107281	AU107281
c 103	11.8	35.8	50	1	AU102330	AU102330 AU102330	c 176	11.4	34.5	50	1	AU107284	AU107284
c 104	11.6	35.2	31	8	AZ481726	AZ481726 1M0306K11	c 177	11.4	34.5	50	1	AU107285	AU107285
c 105	11.6	35.2	34	1	AA889919	AA889919 aJ87G07.s	c 178	11.4	34.5	50	1	AU107287	AU107287
c 106	11.6	35.2	34	1	AI051365	AI051365 0W25F10.X	c 179	11.4	34.5	50	1	AU107288	AU107288
c 107	11.6	35.2	36	2	BE255223	BE255223 601115777	c 180	11.4	34.5	50	1	AU107290	AU107290
c 108	11.6	35.2	37	1	AV833600	AV833600 AV833600	c 181	11.4	34.5	50	1	AU107291	AU107291
c 109	11.6	35.2	37	2	AW250626	AW250626 2822256.S	c 182	11.4	34.5	50	1	AU107293	AU107293
c 110	11.6	35.2	37	8	AZ827785	AZ827785 2M0104J23	c 183	11.4	34.5	50	1	AU107294	AU107294
c 111	11.6	35.2	40	1	AA903929	AA903929 0e73C02.s	c 184	11.4	34.5	50	1	AU107295	AU107295
c 112	11.6	35.2	40	1	AA928240	AA928240 0n87C07.S	c 185	11.4	34.5	50	1	AU107400	AU107400
c 113	11.6	35.2	40	1	AV842793	AV842793 AV842793	c 186	11.4	34.5	50	1	AU108027	AU108027
c 114	11.6	35.2	40	8	BH900992	BH900992 KG08154-S	c 187	11.4	34.5	50	2	AW689452	AW689452
c 115	11.6	35.2	43	8	BH853202	BH853202 SALK_0761	c 188	11.4	34.5	50	8	AZ643903	AZ643903
c 116	11.6	35.2	43	8	BZ762248	BZ762248 SALK_0925	c 189	11.4	34.5	50	8	AZ787909	AZ787909
c 117	11.6	35.2	44	8	BH805848	BH805848 1008062F0	c 190	11.2	33.9	19	6	CF298891	CF298891
c 118	11.6	35.2	46	1	AA828900	AA828900 0d75H11.S	c 191	11.2	33.9	25	1	AA948130	AA948130
c 119	11.6	35.2	46	2	BE612731	BE612731 601452593	c 192	11.2	33.9	26	8	AZ445551	AZ445551
c 120	11.6	35.2	46	8	CC326487	CC326487 XN729.B8Y	c 193	11.2	33.9	27	1	AL045548	AL045548
c 121	11.6	35.2	47	8	AZ766816	AZ766816 1M0564E10	c 194	11.2	33.9	29	7	HI5932	HI5932
c 122	11.6	35.2	49	1	AI424311	AI424311 1e90B05.X	c 195	11.2	33.9	30	4	BI915618	BI915618
c 123	11.6	35.2	50	1	AU104929	AU104929 AU104929	c 196	11.2	33.9	31	4	BI915569	BI915569
c 124	11.6	35.2	50	1	AU107670	AU107670 AU107670	c 197	11.2	33.9	32	9	CL300541	CL300541
c 125	11.6	35.2	50	1	AU108094	AU108094 AU108094	c 198	11.2	33.9	33	8	AZ379585	AZ379585
c 126	11.6	35.2	50	2	AW18967	AW18967 un10B04.Y	c 199	11.2	33.9	34	7	N57329	N57329
c 127	11.6	35.2	50	6	CB192172	CB192172 PY25G04.Y	c 200	11.2	33.9	37	8	AZ960486	AZ960486
c 128	11.6	35.2	50	9	TA284A04P	TA284A04P T. brucei	c 201	11.2	33.9	39	9	CG722883	CG722883
c 129	11.4	34.5	25	9	TA296B02Q	TA296B02Q T. brucei	c 202	11.2	33.9	41	9	CL437876	CL437876
c 130	11.4	34.5	26	8	AZ386054	AZ386054 1M0145A05	c 203	11.2	33.9	42	8	AZ3939796	AZ3939796
c 131	11.4	34.5	28	1	AA713615	AA713615 vt90H08.S	c 204	11.2	33.9	42	9	DR26M14S	DR26M14S
c 132	11.4	34.5	28	1	AI354551	AI354551 qt98G05.X	c 205	11.2	33.9	43	9	TA119G10P	TA119G10P
c 133	11.4	34.5	32	9	CG733270	CG733270 1119155C0	c 206	11.2	33.9	43	1	AA894519	AA894519
c 134	11.4	34.5	32	9	AJ622328	AJ622328 Drosophila	c 207	11.2	33.9	45	6	CA968495	CA968495
c 135	11.4	34.5	34	1	AA176515	AA176515 2P37A12.R	c 208	11.2	33.9	45	9	CG728115	CG728115
c 136	11.4	34.5	34	8	AZ482003	AZ482003 1M0306D16	c 209	11.2	33.9	47	8	AZ775202	AZ775202
c 137	11.4	34.5	34	8	AZ941539	AZ941539 2M0201N13	c 210	11.2	33.9	47	9	AG189046	AG189046
c 138	11.4	34.5	37	1	AL043032	AL043032 DXFp434P	c 211	11.2	33.9	48	1	AJ646947	AJ646947
c 139	11.4	34.5	37	8	AZ374579	AZ374579 1M0127M20	c 212	11.2	33.9	48	8	AZ462540	AZ462540
c 140	11.4	34.5	37	8	AZ596892	AZ596892 1M0410M24	c 213	11.2	33.9	48	8	BH253038	BH253038
c 141	11.4	34.5	38	9	AL495780	AL495780 T. brucei	c 214	11.2	33.9	48	8	BH740754	BH740754
c 142	11.4	34.5	38	9	CL310548	CL310548 03S4741-0	c 215	11.2	33.9	48	9	CG719583	CG719583
c 143	11.4	34.5	38	9	AX002721	AX002721 Arabidops	c 216	11.2	33.9	49	1	AZ738220	AZ738220
c 144	11.4	34.5	39	8	AZ825899	AZ825899 2M0101P13	c 217	11.2	33.9	49	1	AA605689	AA605689
c 145	11.4	34.5	41	8	AZ606010	AZ606010 1M0427K11	c 218	11.2	33.9	49	7	CN752134	CN752134
c 146	11.4	34.5	42	8	AZ816309	AZ816309 2M0085D01	c 219	11.2	33.9	49	8	AZ601892	AZ601892
c 147	11.4	34.5	43	7	R07765	R07765 VF15G07.s1	c 220	11.2	33.9	49	9	AX660891	AX660891
c 148	11.4	34.5	43	8	AZ875350	AZ875350 2M0189M19	c 221	11.2	33.9	50	1	AU102811	AU102811
c 149	11.4	34.5	43	9	CL436351	CL436351 FST2795-N	c 222	11.2	33.9	50	1	AU103483	AU103483
c 150	11.4	34.5	44	1	AV833798	AV833798 AV833798	c 223	11.2	33.9	50	1	AU103978	AU103978
c 151	11.4	34.5	44	8	AQ025716	AQ025716 1(2)K0280	c 224	11.2	33.9	50	1	AU104105	AU104105
c 152	11.4	34.5	46	1	AA814610	AA814610 0b97D06.S	c 225	11.2	33.9	50	1	AU104116	AU104116
c 153	11.4	34.5	46	1	AA485011	AA485011 aa39e10.R	c 226	11.2	33.9	50	1	AU104118	AU104118
c 154	11.4	34.5	46	1	AA591686	AA591686 v113G08.R	c 227	11.2	33.9	50	1	AU104128	AU104128
c 155	11.4	34.5	46	2	BE336269	BE336269 601062658	c 228	11.2	33.9	50	1	AU104131	AU104131
c 156	11.4	34.5	46	2	BE336269	BE336269 601062658	c 229	11.2	33.9	50	1	AU104203	AU104203
c 157	11.4	34.5	47	9	CL309826	CL309826 03S2012-0	c 230	11.2	33.9	50	1	AU104204	AU104204
c 158	11.4	34.5	49	1	AA871018	AA871018 vq29C04.R	c 231	11.2	33.9	50	1	AU104237	AU104237
c 159	11.4	34.5	49	5	BQ585216	BQ585216 S011421-0	c 232	11.2	33.9	50	1	AU104238	AU104238
c 160	11.4	34.5	49	7	H92807	H92807 vt90a12.r1	c 233	11.2	33.9	50	1	AU105452	AU105452
c 161	11.4	34.5	49	8	BH608645	BH608645 611.LL18N	c 234	11.2	33.9	50	1	AU107600	AU107600
c 162	11.4	34.5	49	8	BH902910	BH902910 SALK_1015	c 235	11.2	33.9	50	6	CB064335	CB064335
c 163	11.4	34.5	49	9	AL757297	AL757297 Arabidops	c 236	11.2	33.9	50	6	CB191277	CB191277
c 164	11.4	34.5	50	1	AU102594	AU102594 AU102594	c 237	11.2	33.9	50	6	CB191839	CB191839
c 165	11.4	34.5	50	1	AU103659	AU103659 AU103659	c 238	11.2	33.9	50	8	AZ597958	AZ597958
c 166	11.4	34.5	50	1	AU103666	AU103666 AU103666	c 239	11.2	33.9	50	9	AL765665	AL765665
c 167	11.4	34.5	50	1	AU104973	AU104973 AU104973	c 240	11.2	33.9	50	9	DMES46715	DMES46715
c 168	11.4	34.5	50	1	AU105080	AU105080 AU105080	c 241	11.2	33.9	50	9	CL685441	CL685441
c 169	11.4	34.5	50	1	AU105723	AU105723 AU105723	c 242	11	33.3	19	8	AZ626779	AZ626779
c 170	11.4	34.5	50	1	AU105774	AU105774 AU105774	c 243	11	33.3	22	8	AZ603594	AZ603594

C 244	11	33.3	23	9	TA120H10P	AL462505	T. brucei	C 317	10.8	32.7	34	7	T90379	T90379 yd43e08.s1
C 245	11	33.3	25	1	AT000229	AI000229	oc04b07.s	C 318	10.8	32.7	36	1	AI223280	AI223280 gg53f04.x
C 246	11	33.3	25	8	A2871659	AZ871659	2M0184G07.s	C 319	10.8	32.7	36	1	AZ331632	AZ331632 1M0059N10
C 247	11	33.3	29	9	A2961088	AZ961088	2M0229G21	C 320	10.8	32.7	36	9	TA345F06Q	TA345F06Q T. brucei
C 248	11	33.3	29	9	AG192228	AG192228	Pan trogl	C 321	10.8	32.7	37	9	DR18M6T	DR18M6T AL745793 Danilo rer
C 249	11	33.3	31	9	AL757862	AL757862	ArabiDops	C 322	10.8	32.7	38	1	AJ652144	AJ652144 AJ652144
C 250	11	33.3	31	9	BX532709	BX532709	ArabiDops	C 323	10.8	32.7	39	2	BF339449	BF339449 602039103
C 251	11	33.3	33	8	BZ661231	BZ661231	SALK 0246	C 324	10.8	32.7	39	2	BF342092	BF342092 602012848
C 252	11	33.3	33	8	BZ767418	BZ767418	SALK 1388	C 325	10.8	32.7	39	8	AZ595333	AZ595333 1M0407F23
C 253	11	33.3	33	8	BZ767420	BZ767420	SALK 1388	C 326	10.8	32.7	40	1	AI003400	AI003400 am78h01.s
C 254	11	33.3	33	9	DME545177	AJ545177	Drosophil	C 327	10.8	32.7	40	1	AA589938	AA589938 v181f04.r
C 255	11	33.3	34	9	CL610141	CL610141	EY03538-3	C 328	10.8	32.7	40	8	AZ453043	AZ453043 1M0254A13
C 256	11	33.3	36	8	BH846810	BH846810	SALK 0105	C 329	10.8	32.7	41	8	AZ765994	AZ765994 1M0563D16
C 257	11	33.3	36	9	CG728704	CG728704	1113102F0	C 330	10.8	32.7	41	9	CL439311	CL439311 PST902-3
C 258	11	33.3	37	1	AA873944	AZ873944	vm86a07.r	C 331	10.8	32.7	42	6	CF032091	CF032091 QCE13h07
C 259	11	33.3	37	1	AA974682	AA974682	op29b04.s	C 332	10.8	32.7	42	6	CF281741	CF281741 14ETL--08
C 260	11	33.3	37	8	BH847357	BH847357	SALK 0528	C 333	10.8	32.7	42	6	AZ735068	AZ735068 1M0128B15
C 261	11	33.3	38	9	AG213121	AG213121	Oryza sat	C 334	10.8	32.7	42	9	AJ594706	AJ594706 Arabidops
C 262	11	33.3	39	7	CF642114	CF642114	D47_H04 F	C 335	10.8	32.7	42	9	AI696963	AI696963 wc76c08.x
C 263	11	33.3	39	8	AZ793656	AZ793656	2M047J004	C 336	10.8	32.7	43	1	AA621647	AA621647 af54a06.s
C 264	11	33.3	39	9	CG894914	CG894914	OZS4734-0	C 337	10.8	32.7	43	8	AZ778700	AZ778700 2M0014P03
C 265	11	33.3	39	9	CL234238	CL234238	OZS0288-0	C 338	10.8	32.7	44	1	AJ680183	AJ680183 AJ680183
C 266	11	33.3	39	9	CL234495	CL234495	OZS0422-0	C 339	10.8	32.7	44	4	BI829988	BI829988 603080234
C 267	11	33.3	40	8	AZ486679	AZ486679	1M0314B23	C 340	10.8	32.7	44	9	DME546976	DME546976 Drosophil
C 268	11	33.3	40	8	CC043523	CC043523	3591_1_15	C 341	10.8	32.7	45	8	AZ773590	AZ773590 2M0001C07
C 269	11	33.3	41	8	AZ475800	AZ475800	1M0294G10	C 342	10.8	32.7	45	8	CC455309	CC455309 SALK 0805
C 270	11	33.3	41	8	BH626346	BH626346	1007112H0	C 343	10.8	32.7	46	7	W89234	W89234 mf39c11.r1
C 271	11	33.3	42	1	AA553224	AA553224	vk89c09.s	C 344	10.8	32.7	46	7	W91341	W91341 mg17d01.r1
C 272	11	33.3	42	8	AQ025866	AQ025866	1(2)k0870	C 345	10.8	32.7	46	8	B2355101	B2355101 SALK 1263
C 273	11	33.3	42	9	CG716838	CG716838	1119046D0	C 346	10.8	32.7	46	9	CS941127	CS941127 01S0649-0
C 274	11	33.3	42	9	AG227149	AG227149	Lotus cor	C 347	10.8	32.7	46	9	CF339432	CF339432 BCL1--04-
C 275	11	33.3	43	1	AI445286	AI445286	188h03.x	C 348	10.8	32.7	47	6	CO780863	CO780863 RLO10D_D0
C 276	11	33.3	43	4	BH397324	BH397324	5009-0-31	C 349	10.8	32.7	47	7	CH445507	CH445507 EYL2526-5
C 277	11	33.3	43	8	BH902203	BH902203	SALK 0914	C 350	10.8	32.7	47	9	BL846659	BL846659 SALK 0095
C 278	11	33.3	43	9	CL309631	CL309631	03S2012-0	C 351	10.8	32.7	47	9	CL303536	CL303536 M041A07 G
C 279	11	33.3	44	1	AU014001	AU014001		C 352	10.8	32.7	48	7	T93941	T93941 Ye06f04.r1
C 280	11	33.3	44	6	CB275423	CB275423	WLR151-15	C 353	10.8	32.7	48	9	AL763935	AL763935 Arabidops
C 281	11	33.3	44	8	BH624958	BH624958	1007091C0	C 354	10.8	32.7	48	9	CL234325	CL234325 OZS0422-0
C 282	11	33.3	44	9	CL569510	CL569510	AN0535_Sa	C 355	10.8	32.7	48	9	CL844507	CL844507 EYL2526-5
C 283	11	33.3	45	8	AZ640312	AZ640312	1M0502G18	C 356	10.8	32.7	49	1	AI188903	AI188903 Qd36C11.x
C 284	11	33.3	46	1	AA790759	AA790759	vm18g12.r	C 357	10.8	32.7	49	9	H28255	H28255 Y160e03.r1
C 285	11	33.3	47	1	AV855281	AV855281		C 358	10.8	32.7	49	9	DME546181	DME546181 Drosophil
C 286	11	33.3	47	4	BM046304	BM046304	603626308	C 359	10.8	32.7	49	9	CC886568	CC886568 SALK 1487
C 287	11	33.3	47	4	BM047185	BM047185	603627544	C 360	10.8	32.7	50	1	AA907197	AA907197 01S0604.s
C 288	11	33.3	47	8	AZ997109	AZ997109	2M0283H01	C 361	10.8	32.7	50	1	AU102575	AU102575 AU102575
C 289	11	33.3	47	8	BH813635	BH813635	SALK 0645	C 362	10.8	32.7	50	1	AU102576	AU102576 AU102576
C 290	11	33.3	48	1	AI168820	AI168820	ox67d03.s	C 363	10.8	32.7	50	1	AU102741	AU102741 AU102741
C 291	11	33.3	48	2	AW247978	AW247978	2819657.5	C 364	10.8	32.7	50	1	AU103004	AU103004 AU103004
C 292	11	33.3	48	8	AZ916239	AZ916239	PstI_4_b1	C 365	10.8	32.7	50	1	AU103644	AU103644 AU103644
C 293	11	33.3	48	8	BH851849	BH851849	SALK 0736	C 366	10.8	32.7	50	1	AU103647	AU103647 AU103647
C 294	11	33.3	49	8	AZ470342	AZ470342	1M0284E22	C 367	10.8	32.7	50	1	AU104156	AU104156 AU104156
C 295	11	33.3	49	8	CC178559	CC178559	NPX468_Ba	C 368	10.8	32.7	50	1	AU104947	AU104947 AU104947
C 296	11	33.3	50	1	AU102242	AU102242		C 369	10.8	32.7	50	1	AU105919	AU105919 AU105919
C 297	11	33.3	50	1	AU102580	AU102580		C 370	10.8	32.7	50	1	AU105921	AU105921 AU105921
C 298	11	33.3	50	1	AU102994	AU102994		C 371	10.8	32.7	50	1	AU106375	AU106375 AU106375
C 299	11	33.3	50	1	AU104458	AU104458		C 372	10.8	32.7	50	1	AU106379	AU106379 AU106379
C 300	11	33.3	50	1	AU105285	AU105285		C 373	10.8	32.7	50	1	AU106383	AU106383 AU106383
C 301	11	33.3	50	1	AU105578	AU105578		C 374	10.8	32.7	50	1	AU106949	AU106949 AU106949
C 302	11	33.3	50	1	AU106968	AU106968		C 375	10.8	32.7	50	1	AU107469	AU107469 AU107469
C 303	11	33.3	50	1	AU107280	AU107280		C 376	10.8	32.7	50	5	EX734506	EX734506 BX734506
C 304	11	33.3	50	1	AU107282	AU107282		C 377	10.8	32.7	50	8	BZ769278	BZ769278 SALK 1419
C 305	11	33.3	50	9	TA101G05P	TA101G05P		C 378	10.8	32.7	50	9	DR121L1T	DR121L1T DanLo rer
C 306	11	33.3	50	9	CL309184	CL309184	0362010-0	C 379	10.6	32.1	24	8	AZ314869	AZ314869 1M0031D19
C 307	10.8	32.7	19	8	AZ804253	AZ804253	2M0065008	C 380	10.6	32.1	25	1	AA565870	AA565870 nj32f03.s
C 308	10.8	32.7	24	8	AZ804253	AZ804253	2M0065008	C 381	10.6	32.1	25	9	PCH303928	PCH303928 Plasmodi
C 309	10.8	32.7	25	1	AL039948	AL039948	DK2P434J	C 382	10.6	32.1	28	4	BM398821	BM398821 5009-0-5-
C 310	10.8	32.7	25	8	AZ507387	AZ507387	1M0349D04	C 383	10.6	32.1	28	8	BH861193	BH861193 SALK 0347
C 311	10.8	32.7	26	8	AZ507387	AZ507387	1M0349D04	C 384	10.6	32.1	28	8	BH906920	BH906920 SALK 0366
C 312	10.8	32.7	26	9	TA199A09P	TA199A09P		C 385	10.6	32.1	28	9	TA216E09Q	TA216E09Q T. brucei
C 313	10.8	32.7	29	8	AZ799919	AZ799919	2M0057J08	C 386	10.6	32.1	30	7	T94314	T94314 Ye37g03.s1
C 314	10.8	32.7	30	8	AZ582016	AZ582016	1M0374C01	C 387	10.6	32.1	30	8	AZ326805	AZ326805 1M0049820
C 315	10.8	32.7	33	8	AZ602767	AZ602767	1M0421M07	C 388	10.6	32.1	31	1	AI769915	AI769915 wj30d08.x
C 316	10.8	32.7	34	1	AV8333590	AV8333590	AV8333590	C 389	10.6	32.1	31	1	AV848542	AV848542 AV848542

C 390	10.6	32.1	31	8	AZ380740	AZ380740	1M0136N14	C 463	10.6	32.1	50	1	AU104890	AU104890	AU104890
C 391	10.6	32.1	32	1	AV962980	AV962980	AV962980	C 464	10.6	32.1	50	1	AU104926	AU104926	AU104926
C 392	10.6	32.1	32	9	BX895415	ArabiDops	BX895415	C 465	10.6	32.1	50	1	AU105181	AU105181	AU105181
C 393	10.6	32.1	33	4	BI593580	603341963	BI593580	C 466	10.6	32.1	50	1	AU106313	AU106313	AU106313
C 394	10.6	32.1	33	8	BH256406	KG00828-5	BH256406	C 467	10.6	32.1	50	1	AU106314	AU106314	AU106314
C 395	10.6	32.1	33	9	BH256406	KG00828-5	BH256406	C 468	10.6	32.1	50	1	AU106316	AU106316	AU106316
C 396	10.6	32.1	34	1	AA934127	on95d08.s	AA934127	C 469	10.6	32.1	50	1	AU106870	AU106870	AU106870
C 397	10.6	32.1	34	1	AA934127	on95d08.s	AA934127	C 470	10.6	32.1	50	1	AU106878	AU106878	AU106878
C 398	10.6	32.1	36	8	BH848296	SALK_0677	BH848296	C 471	10.6	32.1	50	1	AU106952	AU106952	AU106952
C 399	10.6	32.1	36	8	BZ597107	SALK_0994	BZ597107	C 472	10.6	32.1	50	1	AU106957	AU106957	AU106957
C 400	10.6	32.1	37	1	AA972482	Op4d03.s	AA972482	C 473	10.6	32.1	50	1	AU107027	AU107027	AU107027
C 401	10.6	32.1	37	1	AA972482	Op4d03.s	AA972482	C 474	10.6	32.1	50	1	AU107275	AU107275	AU107275
C 402	10.6	32.1	38	9	AG216229	Drosophi1	AG216229	C 475	10.6	32.1	50	1	AU108025	AU108025	AU108025
C 403	10.6	32.1	38	9	AG216229	Drosophi1	AG216229	C 476	10.6	32.1	50	1	AU108028	AU108028	AU108028
C 404	10.6	32.1	39	1	AU008671	AU008671	AU008671	C 477	10.6	32.1	50	1	AU108029	AU108029	AU108029
C 405	10.6	32.1	39	8	BZ291057	SALK_1123	BZ291057	C 478	10.6	32.1	50	2	BZ368091	601221989	BZ368091
C 406	10.6	32.1	39	9	CL661199	PRIO140b_	CL661199	C 479	10.6	32.1	50	8	BZ763937	SALK_1228	BZ763937
C 407	10.6	32.1	39	9	CL661199	PRIO140b_	CL661199	C 480	10.6	32.1	50	9	CNS07FCJ	Anopheles	AL608293
C 408	10.6	32.1	40	1	AI337481	AI337481	AI337481	C 481	10.6	32.1	50	9	HSMC39C08	X88091 H.sapient	D
C 409	10.6	32.1	40	7	T49499	Ya76a12.r1	T49499	C 482	10.6	32.1	50	9	TA215A01P	AL479508 T. brucei	AL479508
C 410	10.6	32.1	42	2	AW455805	2DZ Neuro	AW455805	C 483	10.6	32.1	50	9	CG799492	1118002G1	CG799492
C 411	10.6	32.1	42	6	CF299124	7LEAF-02	CF299124	C 484	10.4	31.5	19	6	CF298023	7LEAF--01	CF298023
C 412	10.6	32.1	42	8	AZ768020	1M0567G18	AZ768020	C 485	10.4	31.5	21	1	AJ648125	AJ648125	AJ648125
C 413	10.6	32.1	42	9	CC799365	01S0473-0	CC799365	C 486	10.4	31.5	21	6	CF315101	HD--03-00	CF315101
C 414	10.6	32.1	43	2	BF161778	601770701	BF161778	C 487	10.4	31.5	21	9	TA185E09P	AL474070 T. brucei	AL474070
C 415	10.6	32.1	43	4	BJ076110	BJ076110	BJ076110	C 488	10.4	31.5	23	8	AZ806411	AZ806411	AZ806411
C 416	10.6	32.1	43	4	AJ2773579	2M0001006	AJ2773579	C 489	10.4	31.5	25	9	AG204424	Pan trogl	AG204424
C 417	10.6	32.1	43	8	AZ809933	2M0074K07	AZ809933	C 490	10.4	31.5	26	9	AG203073	Pan trogl	AG203073
C 418	10.6	32.1	43	9	AL762950	ArabiDops	AL762950	C 491	10.4	31.5	31	1	AA968474	AA968474	AA968474
C 419	10.6	32.1	44	8	BH000259	2M0288A03	BH000259	C 492	10.4	31.5	31	1	AA968474	AA968474	AA968474
C 420	10.6	32.1	44	8	BH000259	2M0288A03	BH000259	C 493	10.4	31.5	31	7	H30580	AL174157 vz84e01.r	AL174157
C 421	10.6	32.1	44	8	BH000259	2M0288A03	BH000259	C 494	10.4	31.5	32	8	AZ513928	1M0360G15	AZ513928
C 422	10.6	32.1	44	8	BZ382740	SALK_1187	BZ382740	C 495	10.4	31.5	33	9	BZ660509	SALK_0239	BZ660509
C 423	10.6	32.1	45	1	AV962808	AV962808	AV962808	C 496	10.4	31.5	33	9	AL759548	ArabiDops	AL759548
C 424	10.6	32.1	45	8	AZ460870	1M0286M23	AZ460870	C 497	10.4	31.5	34	1	AA906611	ok79h09.s	AA906611
C 425	10.6	32.1	45	8	AJ2796865	2M0052117	AJ2796865	C 498	10.4	31.5	34	1	AV832421	AV832421	AV832421
C 426	10.6	32.1	45	9	AJ2796865	2M0052117	AJ2796865	C 499	10.4	31.5	34	2	BF301588	602029966	BF301588
C 427	10.6	32.1	45	9	AX943362	ArabiDops	AX943362	C 500	10.4	31.5	34	6	CF302742	7LEAF--08	CF302742
C 428	10.6	32.1	45	9	TA1260P0P	TA1260P0P	TA1260P0P	C 501	10.4	31.5	34	7	N63645	N63645	N63645
C 429	10.6	32.1	46	1	AA674366	VP99a11.r	AA674366	C 502	10.4	31.5	34	8	AZ820869	2M0093E20	AZ820869
C 430	10.6	32.1	46	8	AZ802293	2M0063E08	AZ802293	C 503	10.4	31.5	34	8	BZ357538	SALK_1308	BZ357538
C 431	10.6	32.1	46	8	BZ382796	SALK_1188	BZ382796	C 504	10.4	31.5	34	9	TA348D07Q	AL496178 T. brucei	AL496178
C 432	10.6	32.1	46	9	AX948932	ArabiDops	AX948932	C 505	10.4	31.5	35	7	R87898	R87898	R87898
C 433	10.6	32.1	47	1	AV672363	AV672363	AV672363	C 506	10.4	31.5	35	8	AZ666583	1M0548N17	AZ666583
C 434	10.6	32.1	47	1	AV672363	AV672363	AV672363	C 507	10.4	31.5	37	1	AI051308	cx24d05.x	AI051308
C 435	10.6	32.1	47	8	AZ767816	1M0567H24	AZ767816	C 508	10.4	31.5	37	1	AJ746682	AJ746682	AJ746682
C 436	10.6	32.1	47	8	AZ785454	2M0029A21	AZ785454	C 509	10.4	31.5	37	8	AZ796238	2M0051E23	AZ796238
C 437	10.6	32.1	47	9	TA248H10Q	TA248H10Q	TA248H10Q	C 510	10.4	31.5	37	8	BH789296	SALK_0016	BH789296
C 438	10.6	32.1	48	2	BF507294	BF507294	BF507294	C 511	10.4	31.5	37	9	AL953736	ArabiDops	AL953736
C 439	10.6	32.1	48	8	BZ762247	SALK_0925	BZ762247	C 512	10.4	31.5	38	1	AU267032	AU267032	AU267032
C 440	10.6	32.1	48	8	CC026876	3591_1.55	CC026876	C 513	10.4	31.5	38	4	BG256610	602370273	BG256610
C 441	10.6	32.1	48	9	AL944927	ArabiDops	AL944927	C 514	10.4	31.5	39	1	AV834039	AV834039	AV834039
C 442	10.6	32.1	48	9	AB082911	AB082911	AB082911	C 515	10.4	31.5	39	7	D74282	CELK079A5F	D74282
C 443	10.6	32.1	49	1	AA691190	vt34c05.r	AA691190	C 516	10.4	31.5	39	8	AZ586761	1M0392024	AZ586761
C 444	10.6	32.1	49	1	AA320052	vy63h11.r	AA320052	C 517	10.4	31.5	39	9	AL754052	ArabiDops	AL754052
C 445	10.6	32.1	49	1	AI093925	ga27e01.s	AI093925	C 518	10.4	31.5	40	1	AA972484	Op42602.s	AA972484
C 446	10.6	32.1	49	1	AI444379	fb26f01.x	AI444379	C 519	10.4	31.5	40	1	AI180630	uc67f04.r	AI180630
C 447	10.6	32.1	49	1	AA576898	nm78g10.s	AA576898	C 520	10.4	31.5	40	7	H87885	H87885	H87885
C 448	10.6	32.1	49	2	AW733869	sk78e03.y	AW733869	C 521	10.4	31.5	40	8	BZ290948	SALK_0932	BZ290948
C 449	10.6	32.1	49	8	BH213269	SALK_0089	BH213269	C 522	10.4	31.5	41	7	H58496	yr21f01.s1	H58496
C 450	10.6	32.1	49	8	BZ593434	SALK_0704	BZ593434	C 523	10.4	31.5	41	8	AZ442277	1M0234P50	AZ442277
C 451	10.6	32.1	49	8	CC040332	3591_1.13	CC040332	C 524	10.4	31.5	42	8	CN750518	ApDt-XV1-	CN750518
C 452	10.6	32.1	49	9	AL755450	ArabiDops	AL755450	C 525	10.4	31.5	42	8	AZ803563	2M0064I03	AZ803563
C 453	10.6	32.1	50	1	AI000832	oe56d03.s	AI000832	C 526	10.4	31.5	42	8	AZ810624	2M0076H13	AZ810624
C 454	10.6	32.1	50	1	AI000832	oe56d03.s	AI000832	C 527	10.4	31.5	42	8	BH913376	3526_1.39	BH913376
C 455	10.6	32.1	50	1	AU102312	AU102312	AU102312	C 528	10.4	31.5	43	1	AA724794	ai05e05.s	AA724794
C 456	10.6	32.1	50	1	AU102318	AU102318	AU102318	C 529	10.4	31.5	43	1	AA780094	af36b09.s	AA780094
C 457	10.6	32.1	50	1	AU102545	AU102545	AU102545	C 530	10.4	31.5	43	1	AA926972	cm26a12.s	AA926972
C 458	10.6	32.1	50	1	AU102574	AU102574	AU102574	C 531	10.4	31.5	43	1	AI496775	fb1b09.y	AI496775
C 459	10.6	32.1	50	1	AU102574	AU102574	AU102574	C 532	10.4	31.5	43	7	D19179	MUSGS00488	D19179
C 460	10.6	32.1	50	1	AU102576	AU102576	AU102576	C 533	10.4	31.5	43	8	AZ760136	1M0553P02	AZ760136
C 461	10.6	32.1	50	1	AU103363	AU103363	AU103363	C 534	10.4	31.5	43	8	BZ583819	3590_1.46	BZ583819
C 462	10.6	32.1	50	1	AU103654	AU103654	AU103654	C 535	10.4	31.5	44	8	BZ382706	SALK_1187	BZ382706

682	10.2	30.9	42	8	BH799740	1008109H1	755	10.2	30.9	50	1	AU104073
C 683	10.2	30.9	42	9	AL936639	Arabidops	C 756	10.2	30.9	50	1	AU104084
C 684	10.2	30.9	42	9	BX535511	Arabidops	C 757	10.2	30.9	50	1	AU104152
C 685	10.2	30.9	43	1	AX902242	0107f02.s	C 758	10.2	30.9	50	1	AU104242
C 686	10.2	30.9	43	4	BG915507	602815734	759	10.2	30.9	50	1	AU104293
C 687	10.2	30.9	43	8	BH903344	SALK_1024	760	10.2	30.9	50	1	AU104594
C 688	10.2	30.9	43	9	CL520077	DAH8G05.F	761	10.2	30.9	50	1	AU104617
C 689	10.2	30.9	44	6	CD747102	S202.G02	762	10.2	30.9	50	1	AU104620
C 690	10.2	30.9	44	8	AZ340483	1M0072N19	763	10.2	30.9	50	1	AU104631
C 691	10.2	30.9	44	8	AZ514943	1M0361024	764	10.2	30.9	50	1	AU104683
C 692	10.2	30.9	44	8	CC458522	SALK_1194	C 765	10.2	30.9	50	1	AU104964
C 693	10.2	30.9	44	8	AL758939	Arabidops	C 766	10.2	30.9	50	1	AU105688
C 694	10.2	30.9	44	9	BX285481	Arabidops	C 767	10.2	30.9	50	1	AU105697
C 695	10.2	30.9	45	7	TC9111		C 768	10.2	30.9	50	1	AU106367
C 696	10.2	30.9	45	8	AZ2885975	2M0268F01	C 769	10.2	30.9	50	1	AU106372
C 697	10.2	30.9	45	8	BH850110		C 770	10.2	30.9	50	1	AU106382
C 698	10.2	30.9	45	8	BZ353391	SALK_1202	C 771	10.2	30.9	50	1	AU106746
C 699	10.2	30.9	45	9	CL246803	0250715-0	C 772	10.2	30.9	50	1	AU106802
C 700	10.2	30.9	45	9	CL528502	ASV17E02.	C 773	10.2	30.9	50	1	AU107130
C 701	10.2	30.9	46	1	AA681479	vr37h02.r	C 774	10.2	30.9	50	1	AU107136
C 702	10.2	30.9	46	1	AL185186	qe35f12.s	C 775	10.2	30.9	50	1	AU107137
C 703	10.2	30.9	46	1	AL612864	tz57h05.x	C 776	10.2	30.9	50	1	AU107139
C 704	10.2	30.9	46	1	AA511536	vj24e05.r	C 777	10.2	30.9	50	1	AU107140
C 705	10.2	30.9	46	8	AZ351893	1M0090G11	C 778	10.2	30.9	50	1	AU107141
C 706	10.2	30.9	46	8	AZ503840	1M0343H16	C 779	10.2	30.9	50	1	AU107142
C 707	10.2	30.9	46	8	BH909511	SALK_0541	C 780	10.2	30.9	50	1	AU107329
C 708	10.2	30.9	46	9	AJ588695	Arabidops	C 781	10.2	30.9	50	1	AU108040
C 709	10.2	30.9	47	6	CF337893	JMT--08-I	C 782	10.2	30.9	50	4	BG554327
C 710	10.2	30.9	47	8	BH752851	SALK_0189	C 783	10.2	30.9	50	4	BG554327
C 711	10.2	30.9	47	8	BH792501		C 784	10.2	30.9	50	6	CA583669
C 712	10.2	30.9	47	8	BH849777	SALK_0702	C 785	10.2	30.9	50	6	CA583669
C 713	10.2	30.9	47	8	BH851581	SALK_0732	C 786	10.2	30.9	50	8	AF149676
C 714	10.2	30.9	47	8	BH901058	KG08639-3	C 787	10.2	30.9	50	8	AZ307590
C 715	10.2	30.9	47	9	BX130256	Danio rer	C 788	10.2	30.9	50	8	AZ307590
C 716	10.2	30.9	47	9	BX130256	Danio rer	C 789	10.2	30.9	50	8	AZ307590
C 717	10.2	30.9	47	9	CNS07FA0		C 790	10.2	30.9	50	8	AZ307590
C 718	10.2	30.9	47	9	CL310999	03S4743-0	C 791	10.2	30.9	50	9	AZ307590
C 719	10.2	30.9	47	9	AB081891	Drosophil	C 792	10.2	30.9	50	9	AZ307590
C 720	10.2	30.9	48	1	AU256785	AU256785	C 793	10.2	30.9	50	9	AZ307590
C 721	10.2	30.9	48	1	AA399365	zt50d07.s	C 794	10.2	30.9	50	9	AZ307590
C 722	10.2	30.9	48	1	AA501194	vh75d02.r	C 795	10.2	30.9	50	9	AZ307590
C 723	10.2	30.9	48	1	AA501194		C 796	10.2	30.9	50	9	AZ307590
C 724	10.2	30.9	48	6	BZ298019	7LEAF--01	C 797	10.2	30.9	50	9	AZ307590
C 725	10.2	30.9	48	6	BZ298019		C 798	10.2	30.9	50	9	AZ307590
C 726	10.2	30.9	48	8	BZ355275	SALK_1265	C 799	10.2	30.9	50	9	AZ307590
C 727	10.2	30.9	48	8	BZ355275	SALK_1265	C 800	10.2	30.9	50	9	AZ307590
C 728	10.2	30.9	48	8	BZ762165	SALK_0918	C 801	10.2	30.9	50	9	AZ307590
C 729	10.2	30.9	48	8	BZ765295	SALK_1297	C 802	10.2	30.9	50	9	AZ307590
C 730	10.2	30.9	48	9	BX945139	Arabidops	C 803	10.2	30.9	50	9	AZ307590
C 731	10.2	30.9	49	1	AA933611	Oh87e12.s	C 804	10.2	30.9	50	9	AZ307590
C 732	10.2	30.9	49	1	AI096140	SWOVL3CAN	C 805	10.2	30.9	50	9	AZ307590
C 733	10.2	30.9	49	1	AI198147	qi51b10.x	C 806	10.2	30.9	50	9	AZ307590
C 734	10.2	30.9	49	1	AI198147		C 807	10.2	30.9	50	9	AZ307590
C 735	10.2	30.9	49	1	AA478678		C 808	10.2	30.9	50	9	AZ307590
C 736	10.2	30.9	49	7	H02223	Yj38e10.s1	C 809	10.2	30.9	50	9	AZ307590
C 737	10.2	30.9	49	7	H02223	Yj38e10.s1	C 810	10.2	30.9	50	9	AZ307590
C 738	10.2	30.9	49	7	W39290	zc76g04.r1	C 811	10.2	30.9	50	9	AZ307590
C 739	10.2	30.9	49	7	W39290		C 812	10.2	30.9	50	9	AZ307590
C 740	10.2	30.9	49	7	W39290		C 813	10.2	30.9	50	9	AZ307590
C 741	10.2	30.9	49	8	AZ7833979	2M026K08	C 814	10.2	30.9	50	9	AZ307590
C 742	10.2	30.9	49	8	BH791118		C 815	10.2	30.9	50	9	AZ307590
C 743	10.2	30.9	49	8	BH809509	KG06021-3	C 816	10.2	30.9	50	9	AZ307590
C 744	10.2	30.9	49	8	BH907122	SALK_0383	C 817	10.2	30.9	50	9	AZ307590
C 745	10.2	30.9	49	9	CG715750	1119043C0	C 818	10.2	30.9	50	9	AZ307590
C 746	10.2	30.9	49	9	AG190566	Pan trogl	C 819	10.2	30.9	50	9	AZ307590
C 747	10.2	30.9	50	1	AU102366		C 820	10.2	30.9	50	9	AZ307590
C 748	10.2	30.9	50	1	AU102572		C 821	10.2	30.9	50	9	AZ307590
C 749	10.2	30.9	50	1	AU102578		C 822	10.2	30.9	50	9	AZ307590
C 750	10.2	30.9	50	1	AU103250		C 823	10.2	30.9	50	9	AZ307590
C 751	10.2	30.9	50	1	AU104034		C 824	10.2	30.9	50	9	AZ307590
C 752	10.2	30.9	50	1	AU104050		C 825	10.2	30.9	50	9	AZ307590
C 753	10.2	30.9	50	1	AU104054		C 826	10.2	30.9	50	9	AZ307590
C 754	10.2	30.9	50	1	AU104055		C 827	10.2	30.9	50	9	AZ307590

C 828	10	30.3	34	8	BH907784	BH907784	SALK_0440	901	10	30.3	47	8	AZ835122	AZ835122	2M0129M08
C 829	10	30.3	35	1	AJ237255	AJ237255	SALK_0793	902	10	30.3	47	8	BH856671	BH856671	CC326500
C 830	10	30.3	35	2	AJ245489	AJ245489	2822716.5	C 903	10	30.3	47	8	CC326500	CC326500	XXN701 Bay
C 831	10	30.3	35	7	N70888	N70888	z889f11.81	904	10	30.3	47	9	BX285002	BX285002	Arabidops
C 832	10	30.3	35	8	AZ594762	AZ594762	1M0406M23	C 905	10	30.3	47	9	CL519316	CL519316	DAG1H09 F
C 833	10	30.3	35	8	AZ788299	AZ788299	2M0035U17	C 906	10	30.3	48	1	AA930605	AA930605	VY63e08.r
C 834	10	30.3	35	8	CC060475	CC060475	EY02581-3	C 907	10	30.3	48	1	AV840907	AV840907	AV840907
C 835	10	30.3	36	1	AA706884	AA706884	2J26H10.8	C 908	10	30.3	48	1	AA402658	AA402658	zu49e08.s
C 836	10	30.3	36	8	AZ581836	AZ581836	1M0370Q13	C 909	10	30.3	48	4	BI459090	BI459090	603199445
C 837	10	30.3	37	1	AA934082	AA934082	0n27g11.8	C 910	10	30.3	48	8	AZ772295	AZ772295	1M0583M04
C 838	10	30.3	37	1	AI198787	AI198787	qf79c02.x	C 911	10	30.3	48	8	AZ991463	AZ991463	2M0275K10
C 839	10	30.3	37	1	AI208266	AI208266	q959e08.x	C 912	10	30.3	48	9	CR397288	CR397288	Arabidops
C 840	10	30.3	37	4	BG722105	BG722105	602698519	C 913	10	30.3	49	1	AA715207	AA715207	nu63g10.s
C 841	10	30.3	37	7	H43693	H43693	Y080B05.81	C 914	10	30.3	49	1	AA813480	AA813480	ai67a09.s
C 842	10	30.3	37	8	BZ383683	BZ383683	SALK_1342	C 915	10	30.3	49	1	AI208610	AI208610	q945h02.x
C 843	10	30.3	37	8	BZ597109	BZ597109	SALK_0994	C 916	10	30.3	49	1	AI244893	AI244893	qJ98f06.x
C 844	10	30.3	37	9	AJ597362	AJ597362	Arabidops	C 917	10	30.3	49	1	AA154290	AA154290	ms01g03.x
C 845	10	30.3	37	9	CG724253	CG724253	1119080D0	C 918	10	30.3	49	1	AA232796	AA232796	zr47a03.x
C 846	10	30.3	37	9	AG201808	AG201808	Pan trogl	C 919	10	30.3	49	1	AV966624	AV966624	AV966624
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C 850	10	30.3	38	8	AZ863007	AZ863007	2M0170N23	C 923	10	30.3	49	8	BH916381	BH916381	3526_1.52
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C 853	10	30.3	39	8	BH855773	BH855773	SALK_0846	C 926	10	30.3	50	1	AU102616	AU102616	AU102616
C 854	10	30.3	39	9	AL937027	AL937027	Arabidops	C 927	10	30.3	50	1	AU102658	AU102658	AU102658
C 855	10	30.3	39	9	AA726265	AA726265	vu89c01.x	C 928	10	30.3	50	1	AU102723	AU102723	AU102723
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C 862	10	30.3	40	2	BE900485	BE900485	601673731	C 935	10	30.3	50	1	AU103788	AU103788	AU103788
C 863	10	30.3	40	7	H97838	H97838	Yw09C01.81	C 936	10	30.3	50	1	AU104168	AU104168	AU104168
C 864	10	30.3	40	9	CG846786	CG846786	CMHD-GT.7	C 937	10	30.3	50	1	AU104205	AU104205	AU104205
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C 866	10	30.3	41	8	BH611871	BH611871	SALK_0318	C 939	10	30.3	50	1	AU104715	AU104715	AU104715
C 867	10	30.3	41	9	CG781503	CG781503	1123045E0	C 940	10	30.3	50	1	AU104866	AU104866	AU104866
C 868	10	30.3	42	4	BG113593	BG113593	602284072	C 941	10	30.3	50	1	AU105411	AU105411	AU105411
C 869	10	30.3	42	4	BI553162	BI553162	603197760	C 942	10	30.3	50	1	AU105690	AU105690	AU105690
C 870	10	30.3	42	4	BI562641	BI562641	603256577	C 943	10	30.3	50	1	AU105770	AU105770	AU105770
C 871	10	30.3	42	9	BI141156	BI141156	Dario rer	C 944	10	30.3	50	1	AU105771	AU105771	AU105771
C 872	10	30.3	43	1	AA877060	AA877060	nz43g09.s	C 945	10	30.3	50	1	AU105775	AU105775	AU105775
C 873	10	30.3	43	1	AJ786712	AJ786712	uj56b03.x	C 946	10	30.3	50	1	AU105780	AU105780	AU105780
C 874	10	30.3	43	1	AA549203	AA549203	vk85d08.s	C 947	10	30.3	50	1	AU105781	AU105781	AU105781
C 875	10	30.3	43	7	R71759	R71759	YJ85g09.81	C 948	10	30.3	50	1	AU105782	AU105782	AU105782
C 876	10	30.3	43	8	AZ639598	AZ639598	1M0501L07	C 949	10	30.3	50	1	AU105905	AU105905	AU105905
C 877	10	30.3	43	9	AL944631	AL944631	Arabidops	C 950	10	30.3	50	1	AU106028	AU106028	AU106028
C 878	10	30.3	43	9	AL947531	AL947531	Arabidops	C 951	10	30.3	50	1	AU106303	AU106303	AU106303
C 879	10	30.3	44	4	BG928099	BG928099	HNC46-1-B	C 952	10	30.3	50	1	AU106345	AU106345	AU106345
C 880	10	30.3	44	5	BQ588161	BQ588161	E012337-0	C 953	10	30.3	50	1	AU106346	AU106346	AU106346
C 881	10	30.3	44	8	AZ778327	AZ778327	2M0013016	C 954	10	30.3	50	1	AU106406	AU106406	AU106406
C 882	10	30.3	44	8	BH847111	BH847111	SALK_0132	C 955	10	30.3	50	1	AU106424	AU106424	AU106424
C 883	10	30.3	44	8	BH850740	BH850740	SALK_0717	C 956	10	30.3	50	1	AU106529	AU106529	AU106529
C 884	10	30.3	44	8	BH913151	BH913151	3526_1.38	C 957	10	30.3	50	1	AU106614	AU106614	AU106614
C 885	10	30.3	44	8	BZ591723	BZ591723	3590_1.64	C 958	10	30.3	50	1	AU106648	AU106648	AU106648
C 886	10	30.3	44	8	BZ595035	BZ595035	SALK_0855	C 959	10	30.3	50	1	AU106965	AU106965	AU106965
C 887	10	30.3	44	9	CR399731	CR399731	Arabidops	C 960	10	30.3	50	1	AU107197	AU107197	AU107197
C 888	10	30.3	45	4	BI158736	BI158736	602921522	C 961	10	30.3	50	1	AU107216	AU107216	AU107216
C 889	10	30.3	45	4	BI218941	BI218941	602938541	C 962	10	30.3	50	1	AU107233	AU107233	AU107233
C 890	10	30.3	45	8	BH913356	BH913356	3526_1.39	C 963	10	30.3	50	1	AU107574	AU107574	AU107574
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C 892	10	30.3	45	9	AG195118	AG195118	Pan trogl	C 965	10	30.3	50	1	AU107588	AU107588	AU107588
C 893	10	30.3	46	1	AA954628	AA954628	o83e04.s	C 966	10	30.3	50	1	AU107673	AU107673	AU107673
C 894	10	30.3	46	1	AI000080	AI000080	o850e04.s	C 967	10	30.3	50	1	AU108020	AU108020	AU108020
C 895	10	30.3	46	1	AI284041	AI284041	qt72d04.x	C 968	10	30.3	50	1	AU108091	AU108091	AU108091
C 896	10	30.3	46	1	AV954130	AV954130	AV954130	C 969	10	30.3	50	1	AV952032	AV952032	AV952032
C 897	10	30.3	46	7	R94481	R94481	VQ40g11.81	C 970	10	30.3	50	4	BG113114	BG113114	602283773
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C 899	10	30.3	46	9	DMES45047	DMES45047	Drosophila	C 972	10	30.3	50	8	AZ416047	AZ416047	1M0191E11
C 900	10	30.3	47	7	H55083	H55083	CHR220022 C	C 973	10	30.3	50	8	BH847539	BH847539	SALK_0547

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c 974 10 30.3 50 9 CR267426 Forward s
975 10 30.3 50 9 CG721449 111906780
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c 977 9.8 29.7 20 8 AZ788491 2M0035D10
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979 9.8 29.7 22 9 CL670003 PRI0161a
980 9.8 29.7 22 9 CL682717 PRI0134d
981 9.8 29.7 23 8 BH848405 SALK 0681
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989 9.8 29.7 27 7 H77342 yu12a10.sl
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993 9.8 29.7 28 8 AZ834553 2M0117N13
c 994 9.8 29.7 28 9 AJ595741 Arabidops
995 9.8 29.7 29 8 AZ623273 1M0460M13
c 996 9.8 29.7 29 8 AZ766277 1M0563A15
997 9.8 29.7 29 8 AZ777646 2M0012N22
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ALIGNMENTS

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RESULT 1
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LOCUS 47 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0552A19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0552A19 R, genomic survey sequence.
ACCESSION AZ759762 GI:12866879
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0552 row: A column: 19
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 47.
Location/Qualifiers
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FEATURES

source

FEATURES

source

Class: TDNA tagged.

Location/Qualifiers

1. 47

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/mol_type="Genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK 068548.14.75.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

/lab host="E. Coli strain XL10-Gold, Tl-resistant, P-"
 /clone lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

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Query Match 47.9%; Score 15.8; DB 8; Length 47;
Best Local Similarity 74.1%; Pred. No. 3.6e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 6 TACTCACCCTTCGCGACGACCTACTGG 32
|||||
DB 28 TACTCTGTTTCCCCGAGACTACTATGG 2
|||||

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RESULT 2

BH848576/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. 47

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/mol_type="Genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

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/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion


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Best Local Similarity 72.0%; Pred. No. 2.6e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 5 TACTCACCATTACCAATGCAATAT 29
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DEFINITION 1M0059F01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0059F01 R, genomic survey sequence.
ACCESSION AZ331523
VERSION AZ331523.1 GI:10394300
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 45)
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiser, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: F column: 01
Seq primer: CACACAGGAACAGTGATGACC
Class: plasmid ends
High quality sequence stop: 45.
FEATURES
Location/Qualifiers
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/clone="UUGC1M0059F01"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 41.8%; Score 13.8; DB 8; Length 45;

Best Local Similarity 72.0%; Pred. No. 2.6e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 GTACTCACCCTTCGCGACGACCACTA 29
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Db 1 GTACTCACCCTACCTCTCTCCACCA 25
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RESULT 9
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LOCUS 41 bp DNA linear GSS 02-MAY-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-860A07-025973,
genomic survey sequence.
ACCESSION CR403035
VERSION CR403035.1 GI:46943763
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weishaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755929
PUBMED 12874060
REFERENCE 2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weishaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weishaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 41)
Rosso, M.G., Strizhov, N., Li, Y. and Weishaar, B.
AUTHORS Direct Submission
TITLE Submitted (01-MAY-2004) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
JOURNAL This sequence has been recovered from the left border of the T-DNA.
COMMENT It indicates an insertion within the locus defined by BAC clone
T15D22. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
Location/Qualifiers
1..41
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-860A07-025973"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

```



```

survey sequence.
BZ763121
VERSION BZ763121.1 GI:289335674
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Arabidopsis thaliana; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 47)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A sequence-indexed library of insertion mutations in the
Arabidopsis Genome
JOURNAL Arabidopsis
COMMENT Contact: Joseph R. Ecker
Salik Institute Genomic Analysis Laboratory (SIGAL)
The Salik Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salik.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of Atig07240.
Class: TDNA tagged.
FEATURES
source
Location/Qualifiers
1..47
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_lib="SALK_113559.16.10.x"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"
ORIGIN
Query Match 41.2%; Score 13.6; DB 8; Length 47;
Best Local Similarity 80.0%; Pred. No. 3.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 7 ACTACCGTTCGCAGACCA 26
Db 47 ACACAGTTCGGCGCCA 28
RESULT 13
CG719689/c
LOCUS CG719689 28 bp DNA linear GSS 20-OCT-2003
DEFINITION 119058G03.2EL.y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.
ACCESSION CG719689
VERSION CG719689.1 GI:37751846
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Zea mays
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
JOURNAL clade; Panicoideae; Andropogoneae; Zea.
COMMENT 1 (bases 1 to 28)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227

survey sequence.
BZ763121
VERSION BZ763121.1 GI:289335674
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Arabidopsis thaliana; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 47)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A sequence-indexed library of insertion mutations in the
Arabidopsis Genome
JOURNAL Arabidopsis
COMMENT Contact: Joseph R. Ecker
Salik Institute Genomic Analysis Laboratory (SIGAL)
The Salik Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salik.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of Atig07240.
Class: TDNA tagged.
FEATURES
source
Location/Qualifiers
1..47
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_lib="SALK_113559.16.10.x"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"
ORIGIN
Query Match 41.2%; Score 13.6; DB 8; Length 47;
Best Local Similarity 80.0%; Pred. No. 3.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 7 ACTACCGTTCGCAGACCA 26
Db 47 ACACAGTTCGGCGCCA 28
RESULT 13
CG719689/c
LOCUS CG719689 28 bp DNA linear GSS 20-OCT-2003
DEFINITION 119058G03.2EL.y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.
ACCESSION CG719689
VERSION CG719689.1 GI:37751846
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Zea mays
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
JOURNAL clade; Panicoideae; Andropogoneae; Zea.
COMMENT 1 (bases 1 to 28)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227

Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119058 row: G column: 03
Class: transposon-tagged.
FEATURES
source
Location/Qualifiers
1..28
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
ORIGIN
Query Match 40.6%; Score 13.4; DB 9; Length 28;
Best Local Similarity 73.9%; Pred. No. 3.8e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 8 CTCACCGTTCGCAGACCACTAT 30
Db 25 CTCACCGTTCGGGAATCATCAT 3
RESULT 14
AZ498025
LOCUS AZ498025 36 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0335B09F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0335B09 F, genomic survey sequence.
ACCESSION AZ498025
VERSION AZ498025.1 GI:10675499
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 36)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0335 row: B column: 09
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 36.
FEATURES
Location/Qualifiers

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1..36
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0335809"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: PW042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 40.6%; Score 13.4; DB 8; Length 36;
Best Local Similarity 73.9%; Pred. No. 3.9e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 9 TCACGTTCCGACCACTATG 31
Db 12 TCAGTGTCTGGGACCAATAAG 34

RESULT 15
TA3H02P
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 3h02, forward sequence, genomic survey sequence.
ACCESSION AL451569
VERSION AL451569.1 GI:11854297
KEYWORDS
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 39)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREGU27/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nleay@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers

FEATURES
source
1..44
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1007 - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdd.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match 40.6%; Score 13.4; DB 8; Length 44;
Best Local Similarity 64.5%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

1..39
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="3h02"

source
1..39
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="3h02"

ORIGIN
Query Match 40.6%; Score 13.4; DB 9; Length 39;
Best Local Similarity 73.9%; Pred. No. 3.9e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 10 CACCGTTCCGACCACTATGG 32
Db 2 CAACGCTCGAATACCACTGG 24

RESULT 16
BH620252
LOCUS
DEFINITION
1007061G07.2EL y1 1007 - RescueMu Grid H Zea mays genomic, genomic survey sequence.
ACCESSION BH620252
VERSION BH620252.1 GI:18431908
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001).
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence.
Plate: 1007061 column: 18
Class: transposon-tagged.
Location/Qualifiers
1..44
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1007 - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdd.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

```


QY 2 GGTGTAATCAGCGTTCGCGAGACCACTATGG 32
 DB 1 GTTGTCTTTCGTCCTCCGCCCTCAAAGG 31

RESULT 17
 AZ785555/c
 LOCUS
 DEFINITION 2M0029G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0029G04 R, genomic survey sequence.
 ACCESSION AZ785555
 VERSION AZ785555.1 GI:12922431
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 41)
 Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0029 row: G column: 04
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 41.
 Location/Qualifiers
 1. 41
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0029G04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source
 1. 41
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0029G04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 40.0%; Score 13.2; DB 8; Length 41;
 Best Local Similarity 69.2%; Pred. No. 4.8e+05;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 8 CTCACCGTTCGCGAGACCACTATGCG 33
 DB 34 CCCACCGTATGTCACAGCAGTGTGCG 9

RESULT 18
 AZ812045/c
 LOCUS
 DEFINITION 2M0078A04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0078A04 R, genomic survey sequence.
 ACCESSION AZ812045
 VERSION AZ812045.1 GI:12980903
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 42)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0078 row: A column: 04
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 42.
 Location/Qualifiers
 1. 42
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0078A04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source
 1. 42
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0078A04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 40.0%; Score 13.2; DB 8; Length 42;
 Best Local Similarity 69.2%; Pred. No. 4.8e+05;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 4 TGTACTCACGGTTCGACGACCACTA 29
  ||||| ||||| ||||| |||||
Db 29 TTTCCCACTGTTGAGCATATCACTA 4

RESULT 19
B1102544
LOCUS
DEFINITION B1102544 45 bp mRNA linear EST 26-JUN-2001
5' mRNA sequence.
ACCESSION B1102544
VERSION B1102544.1 GI:14553437
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 45)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1122 row: p column: 12
High quality sequence stop: 45.
Location/Qualifiers
1..45
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5044859"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Kid14"
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library. |"

ORIGIN
Query Match 40.0%; Score 13.2; DB 4; Length 45;
Best Local Similarity 69.2%; Pred. No. 4.8e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 8 CTCACGGTTCGACGACCACTATGCG 33
  ||||| ||||| ||||| |||||
Db 8 CTGCCCGTCCAGACCACTATGTCG 33

RESULT 20
B2660777/c
LOCUS
DEFINITION B2660777 45 bp DNA linear GSS 31-JAN-2003
SALK 024235.56.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_024235.56.00.x, genomic
survey sequence.
ACCESSION B2660777
VERSION B2660777.1 GI:28173924
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 45)
Alonso J.M., Leisse T.J., Barajas P., Chen H., Cheuk R.,
Gadrinab C., Jeske A., Karnes M., Kim C.J., Parker H., Prednis L.,

QY 4 TGTACTCACGGTTCGACGACCACTA 29
  ||||| ||||| ||||| |||||
Db 29 TTTCCCACTGTTGAGCATATCACTA 4

RESULT 19
B1102544
LOCUS
DEFINITION B1102544 45 bp mRNA linear EST 26-JUN-2001
5' mRNA sequence.
ACCESSION B1102544
VERSION B1102544.1 GI:14553437
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 45)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1122 row: p column: 12
High quality sequence stop: 45.
Location/Qualifiers
1..45
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5044859"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Kid14"
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library. |"

ORIGIN
Query Match 40.0%; Score 13.2; DB 4; Length 45;
Best Local Similarity 69.2%; Pred. No. 4.8e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 8 CTCACGGTTCGACGACCACTATGCG 33
  ||||| ||||| ||||| |||||
Db 8 CTGCCCGTCCAGACCACTATGTCG 33

RESULT 20
B2660777/c
LOCUS
DEFINITION B2660777 45 bp DNA linear GSS 31-JAN-2003
SALK 024235.56.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_024235.56.00.x, genomic
survey sequence.
ACCESSION B2660777
VERSION B2660777.1 GI:28173924
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 45)
Alonso J.M., Leisse T.J., Barajas P., Chen H., Cheuk R.,
Gadrinab C., Jeske A., Karnes M., Kim C.J., Parker H., Prednis L.,

Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At3g51890.
Class: TDNA tagged.
Location/Qualifiers
1..45
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_024235.56.00.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 40.0%; Score 13.2; DB 8; Length 45;
Best Local Similarity 69.2%; Pred. No. 4.8e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 7 ACTCACGGTTCGACGACCACTATGG 32
  ||||| ||||| ||||| |||||
Db 44 ATTCTCGTGTACGAAACCACTGTGG 19

RESULT 21
AUI02740/c
LOCUS
DEFINITION AUI02740 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC13229, mRNA sequence.
ACCESSION AUI02740
VERSION AUI02740.1 GI:13552261
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"

```

REFERENCE	1-4 (bases 1 to 38)	REFERENCE	1-4 (bases 1 to 38)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingley,A., von Niederhausern,A. and Wright,D.,Weiss,R.	AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingley,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)	JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0032 row: H column: 20 Seq primer: CGTTGTAACGACGCGCAGT Class: plasmid ends High quality sequence stop: 38.	COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0032 row: H column: 20 Seq primer: CGTTGTAACGACGCGCAGT Class: plasmid ends High quality sequence stop: 38.
FEATURES	Location/Qualifiers 1..38 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [G14732114]gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	FEATURES	Location/Qualifiers 1..38 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [G14732114]gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN	Query Match 39.4%; Score 13; DB 8; Length 38; Best Local Similarity 76.2%; Pred. No. 5.8e+05; Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0; QY 4 TGTACTACCGTTCGGCAGAC 24 DB 31 TGTTCACCGGTACAGCAGTC 11	ORIGIN	Query Match 39.4%; Score 13; DB 8; Length 38; Best Local Similarity 76.2%; Pred. No. 5.8e+05; Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0; QY 4 TGTACTACCGTTCGGCAGAC 24 DB 31 TGTTCACCGGTACAGCAGTC 11
RESULT 24	AL765117	RESULT 24	AL765117
LOCUS	Arabidopsis thaliana T-DNA flanking sequence GK-135908-012755, genomic survey sequence.	LOCUS	Arabidopsis thaliana T-DNA flanking sequence GK-135908-012755, genomic survey sequence.
DEFINITION	Arabidopsis thaliana (thale cress)	DEFINITION	Arabidopsis thaliana (thale cress)
ACCESSION	AL765117	ACCESSION	AL765117
VERSION	AL765117.1	VERSION	AL765117.1
KEYWORDS	GSS.	KEYWORDS	GSS.
SOURCE	Arabidopsis thaliana	SOURCE	Arabidopsis thaliana
ORGANISM	Arabidopsis thaliana	ORGANISM	Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weissshaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
 Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL MEDLINE PUBLISHED 22755829 12874060

REFERENCE 2

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weissshaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

JOURNAL MEDLINE PUBLISHED 21117147 14756321

REFERENCE 3

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weissshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL MEDLINE PUBLISHED 14682050

REFERENCE 4

AUTHORS Strizhov, N., Li, Y., Rosso, M.G. and Weissshaar, B.

TITLE Direct Submission

JOURNAL MEDLINE PUBLISHED 14682050

COMMENT Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany. This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T209. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES source

1. .42
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-135B08-012755"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA-derived sequences were removed."

ORIGIN

Query Match 39.4%; Score 13; DB 9; Length 42;
 Best Local Similarity 65.5%; Pred. No. 5.9e+05;
 Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 TGTACTCCGTCGTCGACACCATATGG 32
 |||||
 DB 12 TGGACTGGCCATGACGAGGAGACTATGG 40
 |||||

RESULT 25

AG192231 45 bp DNA linear GSS 06-MAR-2004

LOCUS AG192231

DEFINITION Pan troglodytes DNA, clone: RP43-068K06.TJ, genomic survey sequence.

ACCESSION AG192231

VERSION AG192231.1 GI:45224407

KEYWORDS

SOURCE Pan troglodytes (chimpanzee)

ORGANISM

REFERENCE 1

AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE BAC end sequences of Library RP-43

JOURNAL MEDLINE PUBLISHED Unpublished

REFERENCE 2

AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE Direct Submission

JOURNAL MEDLINE PUBLISHED Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC) 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea (E-mail: redstone@mail.kribb.re.kr, URL: <http://phs.grc.kribb.re.kr/>, Tel: 82-42-866-7181, Fax: 82-42-860-4409)

COMMENT Clones are derived from the chimpanzee BAC library RP-43. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: TJ

LIBRARY

Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI

FEATURES source

1. .45
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-068K06.TJ"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 39.4%; Score 13; DB 9; Length 45;
 Best Local Similarity 76.2%; Pred. No. 5.9e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGGTGTACTCACCGTTCGCA 21
 |||||
 DB 13 CGGTGTGTCTCCCTTCCCA 33
 |||||

RESULT 26

AU102583 50 bp mRNA linear EST 28-JAN-2004

LOCUS AU102583

DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HBWA420069, mRNA sequence.

ACCESSION AU102583

VERSION AU102583.1 GI:13552104

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL MEDLINE PUBLISHED EMBO Rep. 2 (5), 388-393 (2001)

COMMENT 21270072
 11375929
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and Sugano.S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HBMA420069"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 39.4%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 6e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 8 CTCACCGTCCGACAGCACT 28
| |||| | |||| | ||||
DB 15 CGCACCCCTCCCAGAGCACT 35

RESULT 27
CR396867
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-381B06-026791,
genomic survey sequence.
DEFINITION CR396867
VERSION CR396867.1 GI:46937590
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
1 Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060

REFERENCE 2
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321

REFERENCE 3
Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
Weisshaar,B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)

JOURNAL
MEDLINE 14682050
PUBMED

REFERENCE
AUTHORS Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At2g18420.
Details on the protocols used for generations of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
Location/Qualifiers

FEATURES
source Location/Qualifiers
1..50
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-381B06-026791"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (Ti) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match 39.4%; Score 13; DB 9; Length 50;
Best Local Similarity .65.5%; Pred. No. 6e+05;
Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 4 TGTAATCATCCGTCCGACAGCACTATGG 32
| |||| | |||| | |||| | ||||
DB 1 TGTCTCGACTTCCTCCATGCCATATGG 29

RESULT 28
A2773640
LOCUS Arabidopsis thaliana T-DNA linear GSS 16-FEB-2001
DEFINITION 2M0001P11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0001P11 F, genomic survey sequence.
ACCESSION A2773640
VERSION A2773640.1 GI:12898212
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 32)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0001 row: P column: 11
Seq primer: CGTTGTAAACGACGCAGCT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers

FEATURES
source Location/Qualifiers
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0001P11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 38.8%; Score 12.8; DB 8; Length 32;
Best Local Similarity 70.8%; Pred. No. 7e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 8 CTCACCGTCCGACACCATG 31
Db 4 CTCACGTATCCGCGTCCGTATG 27

RESULT 29

BI695278/c

LOCUS 36 bp mRNA linear EST 18-SEP-2001
DEFINITION 603345135F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5372912 5',
mRNA sequence.

ACCESSION BI695278

VERSION BI695278.1 GI:15657907

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 36)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999).

Contact: Robert Strausberg, Ph.D.

Email: cgaps@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11949 row: e column: 09

High quality sequence stop: 36.

Location/Qualifiers

FEATURES

source

1..36

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N-3"

/db_xref="taxon:10090"

/clone="IMAGE:5372912"

/tissue_type="tumor, biopsy sample"

/dev_stage="5 months"

/lab_host="DH10B"

/clone_lib="NCI CGAP Mam2"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigator

providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match

Best Local Similarity 38.8%; Score 12.8; DB 4; Length 36;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY

Db

RESULT 30

BI695278/c

LOCUS 46 bp DNA linear GSS 02-APR-2004

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-386C04-018253,

genomic survey sequence.

ACCESSION BX285871

VERSION BX285871.1 GI:28884867

KEYWORDS GSS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1

AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., and Weisshaar, B.

TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for

the identification of T-DNA insertion mutants in Arabidopsis

thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE 22755829

PUBMED 12874060

REFERENCE 2

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and

Weisshaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for

flanking sequence tag-based reverse genetics

Plant Mol. Biol. 53 (1-2), 247-259 (2003)

MEDLINE 23117147

PUBMED 14756321

REFERENCE 3

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and

Weisshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA

mutagenized Arabidopsis thaliana lines

Biotechniques 35 (6), 1164-1168 (2003)

JOURNAL 14682050

PUBMED 14682050

REFERENCE 4 (bases 1 to 46)

AUTHORS Rosso, M.G., Li, Y., Strizhov, N. and Weisshaar, B.

TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At5g39070.

Details on the protocols used for generation of the sequence are

described in References 1-3. The sequences are generated at the MPI

for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated

'GABI'. Information on line availability can be found at:

<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

Location/Qualifiers

1..46

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-386C04-018253"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecovPe="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana

plants (T1) which were transformed with the T-DNA from

vector pAC161 (GenBank accession number: AJ537514). The

lines contain one or more T-DNA insertions. The DNA

fragment(s) resulting from the PCR were directly sequenced

to determine the genomic sequence flanking the insertion.

T-DNA derived sequences were removed."

ORIGIN

```

Query Match      38.8%; Score 12.8; DB 9; Length 46;
Best Local Similarity 62.5%; Pred. No. 7.2e+05;
Matches 20; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 GGTGTACTACCGTTCGACGACCACTATGGC 33
    |||||
Db 38 GCTATACTAGCAATCCCAATCACTACAGTGGC 7

RESULT 31
LOCUS CR397300
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-417A05-026074,
genomic survey sequence.
ACCESSION CR397300
VERSION CR397300.1 GI:46938028
SOURCE GSS.
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weissshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weissshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
Weissshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
MEDLINE 14682050
PUBMED
REFERENCE 4
AUTHORS Strizhov,N., Rosso,M.G., Li,Y. and Weissshaar,B.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2004) Weissshaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT It indicates an insertion close to or within gene At2g36200.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
source
Location/Qualifiers
1..47
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strains="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-417A05-026074"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.

Query Match      38.8%; Score 12.8; DB 9; Length 46;
Best Local Similarity 62.5%; Pred. No. 7.2e+05;
Matches 20; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 GGTGTACTACCGTTCGACGACCACTATGGC 33
    |||||
Db 38 GCTATACTAGCAATCCCAATCACTACAGTGGC 7

RESULT 32
LOCUS AU104159/c
DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT00274, mRNA sequence.
ACCESSION AU104159
VERSION AU104159.1 GI:13553680
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT00274"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      38.8%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 7.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CGGTGTACTACCGTTCGACGAC 24
    |||||
Db 24 CCGGGAGCGACGCTTCACAGAC 1

RESULT 33
LOCUS AU106328/c
DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT00883, mRNA sequence.
ACCESSION AU106328
VERSION AU106328.1 GI:13555849
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS (bases 1 to 50)

```


/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M023G09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 38.2%; Score 12.6; DB 8; Length 37;
Best Local Similarity 78.9%; Pred. No. 8.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GTACTCACCCTCCGACGA 23
|||||
Db 28 GTACTCACCCTATCCGAC 10

RESULT 36

BZ767361/c
LOCUS 44 bp DNA linear GSS 13-MAR-2003
DEFINITION SALK_138740.35.70.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_138740.35.70.x, genomic survey sequence.

ACCESSION BZ767361
VERSION BZ767361.1 GI:28939914
KEYWORDS GSS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednisi,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu

TITLE

JOURNAL A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
COMMENT Unpublished (2001)

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g00560.
Class: TDNA tagged.

FEATURES

Location/Qualifiers
1..44
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"

/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_138740.35.70.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 38.2%; Score 12.6; DB 8; Length 44;
Best Local Similarity 78.9%; Pred. No. 8.8e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 15 TTCGCGACACCACTATGCG 33
|||||
Db 40 TTCGCGCGCAACTATGCG 22

RESULT 37

TA82D010/c
LOCUS 46 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 82d01, reverse sequence, genomic survey sequence.

ACCESSION AL459951
VERSION AL459951.1 GI:11860276
KEYWORDS GSS
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE

AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

TITLE

JOURNAL Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

Location/Qualifiers
1..46
source
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="82d01"

ORIGIN

Query Match 38.2%; Score 12.6; DB 9; Length 46;
Best Local Similarity 66.7%; Pred. No. 8.8e+05;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CGGTGTACTACCGTTCGACAC 27
|||||
Db 30 CGTTTCATTCACTGCACCGCAGCGC 4

RESULT 38

```

R18118
LOCUS       R18118               49 bp    mRNA    linear    EST 14-APR-1995
DEFINITION  ve90c12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
            IMAGE:125014 5' similar to SP:S02141 S02141 INTER-ALPHA-TRYPSIN
            INHIBITOR HEAVY CHAIN H3 - HUMAN ;, mRNA sequence.

ACCESSION   R18118
VERSION     R18118.1  GI:771728
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 49)
            Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
            Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
            Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
            Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
            Wilson, R.
            The WashU-Merck EST Project
            Unpublished (1995)
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 2101
            High quality sequence starts: 1 High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL This clone is available royalty-free
            through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
            for further information. Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Insert Length: 2101 Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 1.

FEATURES             source
     source
     1..49
         /organism="Homo sapiens"
         /mol_type="mRNA"
         /db_xref="GDB:477559"
         /db_xref="taxon:9606"
         /clone="IMAGE:125014"
         /sex="male"
         /dev_stage="20 week-post conception fetus"
         /lab_host="DH10B (ampicillin resistant)"
         /clone_lib="Soares fetal liver spleen INFLS"
         /note="Organ: Liver and Spleen; Vector: p773D (Pharmacia)
         with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
         1st strand cDNA was primed with a Pac I - oligo(dT) primer
         [5' AACTCGAAGATTAAAGATCTTTTTTTTTTTTTTTT 3'],
         double-stranded cDNA was ligated to Eco RI adaptors
         (Pharmacia), digested with Pac I and cloned into the Pac I
         and Eco RI sites of the modified p773 vector. Library
         went through one round of normalization. Library
         constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN
Query Match      38.2%; Score 12.6; DB 7; Length 49;
Best Local Similarity 66.7%; Pred. No. 8.9e+05;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      6  TACTACCGTTCGGACACCTATG 32
      |||||
Db      21  TGCTACCGATGGCGACCCACTGTGG 47

RESULT 39
AU102859
LOCUS       AU102859             50 bp    mRNA    linear    EST 28-JAN-2004
DEFINITION  Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            COL01421, mRNA sequence.

ACCESSION   AU102859
VERSION     AU102859.1  GI:13552380
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

```

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES             source
     source
     1..50
         /organism="Homo sapiens"
         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /clone="COL01421"
         /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      38.2%; Score 12.6; DB 1; Length 50;
Best Local Similarity 78.9%; Pred. No. 8.9e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  CGGTGTACTACCGTTCG 19
      |||||
Db      10  CGGTGCGCTCGCGCTTCG 28

RESULT 40
AZ482042/c
LOCUS       AZ482042             32 bp    DNA    linear    GSS 04-OCT-2000
DEFINITION  IM0306C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0306C20 R, genomic survey sequence.

ACCESSION   AZ482042
VERSION     AZ482042.1  GI:10643107
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 32)
            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, R., Stokes, R., Tingey, A., von
            Niederhausen, A. and Wright, D., Weiss, R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0306 row: C column: 20
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High quality sequence stop: 32.

FEATURES
source

Location/Qualifiers

1. .32

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="JUGC1M0306C20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 37.6%; Score 12.4; DB 8; Length 32;
Best Local Similarity 92.9%; Pred. No. 1e+06;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CAGACCACTATGGC 33
Db 14 CAGACCACTATGGC 1

Search completed: November 23, 2004, 22:22:29
Job time : 1617.15 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 540.225 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631b-4
Perfect score: 30
Sequence: 1 tggactagctcttggtcatcacccttct 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_ats.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	30	100.0	30	6	AX802290 Sequence
2	19	63.3	31	6	BD181365 A method
3	19	63.3	31	6	AX147028 Sequence
4	19	63.3	31	6	AX523945 Sequence
5	19	63.3	31	6	AX524843 Sequence
6	19	63.3	33	6	I17523 Sequence 13
7	19	63.3	33	6	I28348 Sequence 1
8	17.6	58.7	48	6	AX777198 Sequence
9	16.4	54.7	46	6	AX793994 Sequence
10	16.2	54.0	39	6	AX804053 Sequence
11	15.8	52.7	26	6	AX800237 Sequence
12	15.6	52.0	49	9	U11510 Human RET p
13	15.2	50.7	22	6	AX420204 Sequence
14	15.2	50.7	22	6	AX528208 Sequence
15	15.2	50.7	22	6	AX528214 Sequence
16	15.2	50.7	22	6	AX554648 Sequence
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30	6	CO801293	49.3	14.8	C	25	CO801293 Sequence
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41	6	AX520300	49.3	14.8	C	27	AX520300 Sequence
46	6	AR379395	49.3	14.8	C	28	AR379395 Sequence
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46	6	AR379397	49.3	14.8	C	30	AR379397 Sequence
47	6	AR290158	49.3	14.8	C	31	AR290158 Sequence
36	6	BD262074	48.7	14.6	C	32	BD262074 Antineopl
36	6	AR303048	48.7	14.6	C	33	AR303048 Sequence
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34	6	CO817634	47.3	14.2	C	53	CO817634 Sequence
34	6	CO817635	47.3	14.2	C	54	CO817635 Sequence
39	6	AR151073	47.3	14.2	C	55	AR151073 Sequence
39	6	E15027	47.3	14.2	C	56	E15027 PCR primer
39	6	AR316472	47.3	14.2	C	57	AR316472 Sequence
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29	6	BD080274	46.0	13.8	C	88	BD080274 Transgeni
29	6	CO760899	46.0	13.8	C	89	CO760899 Sequence
30	11	C75926	46.0	13.8	C	90	C75926 Homo sapien
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c 116	13.4	44.7	17	6	AX500582	AX500582 Sequence	c 189	13	43.3	26	6	AX037969	AX037969 Sequence
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260	12.8	42.7	25	6	AX534594	AX534594 Sequence	c 333	12.6	42.0	25	6	AR459800	AR459800 Sequence
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262	12.8	42.7	26	6	AX921451	AX921451 Sequence	c 335	12.6	42.0	25	6	AR459802	AR459802 Sequence
263	12.8	42.7	27	6	AR040190	AR040190 Sequence	c 336	12.6	42.0	25	6	AR459803	AR459803 Sequence
264	12.8	42.7	27	6	AR184883	AR184883 Sequence	c 337	12.6	42.0	25	6	AR459804	AR459804 Sequence
265	12.8	42.7	27	6	AX702380	AX702380 Sequence	c 338	12.6	42.0	25	6	AR459805	AR459805 Sequence
266	12.8	42.7	29	6	BD174845	BD174845 Antibody-	339	12.6	42.0	25	6	AR470477	AR470477 Sequence
267	12.8	42.7	29	6	BD260456	BD260456 Sequence	340	12.6	42.0	25	6	AR470478	AR470478 Sequence
268	12.8	42.7	29	6	AX233420	AX233420 Sequence	341	12.6	42.0	25	6	AR470479	AR470479 Sequence
269	12.8	42.7	30	6	AX611265	AX611265 Sequence	342	12.6	42.0	25	6	AR470480	AR470480 Sequence
270	12.8	42.7	30	6	BD143278	BD143278 Oligonuc1	343	12.6	42.0	25	6	AR470481	AR470481 Sequence
271	12.8	42.7	31	6	AX248526	AX248526 Sequence	344	12.6	42.0	25	6	AR470482	AR470482 Sequence
272	12.8	42.7	34	6	I06237	I06237 Sequence 8	345	12.6	42.0	25	6	AR470483	AR470483 Sequence
273	12.8	42.7	34	6	I07307	I07307 Sequence 19	c 346	12.6	42.0	25	6	AX609669	AX609669 Sequence
274	12.8	42.7	34	6	BD013914	BD013914 Vermin da	347	12.6	42.0	26	6	AR349077	AR349077 Sequence
275	12.8	42.7	38	6	I05542	I05542 Sequence 8	c 348	12.6	42.0	26	6	AR349078	AR349078 Sequence
276	12.8	42.7	38	6	AR182117	AR182117 Sequence	349	12.6	42.0	26	6	AR349079	AR349079 Sequence
277	12.8	42.7	40	6	AR178716	AR178716 Sequence	c 350	12.6	42.0	26	6	AR349080	AR349080 Sequence
278	12.8	42.7	40	6	BD251230	BD251230 Oligonuc1	351	12.6	42.0	29	6	AR429703	AR429703 Sequence
279	12.8	42.7	40	6	AR205421	AR205421 Sequence	352	12.6	42.0	30	6	BD235556	BD235556 Methods a
280	12.8	42.7	40	6	AR220113	AR220113 Sequence	353	12.6	42.0	30	6	BD021856	BD021856 Method fo
281	12.8	42.7	40	6	AR221502	AR221502 Sequence	354	12.6	42.0	31	6	AX248913	AX248913 Sequence
282	12.8	42.7	40	6	AR254204	AR254204 Sequence	355	12.6	42.0	32	6	AX349884	AX349884 Sequence
283	12.8	42.7	40	6	AR282410	AR282410 Sequence	356	12.6	42.0	32	6	BD006910	BD006910 Inhibitio
284	12.8	42.7	40	6	AR368317	AR368317 Sequence	357	12.6	42.0	33	6	A45513	A45513 Sequence 42
285	12.8	42.7	41	6	AX515147	AX515147 Sequence	c 358	12.6	42.0	33	6	I08861	I08861 Sequence 1
286	12.8	42.7	41	6	AX515825	AX515825 Sequence	359	12.6	42.0	33	6	AR267694	AR267694 Sequence
287	12.8	42.7	41	6	AX517941	AX517941 Sequence	c 360	12.6	42.0	34	6	I06978	I06978 Sequence 2
288	12.8	42.7	41	6	AX521082	AX521082 Sequence	c 361	12.6	42.0	34	6	I07047	I07047 Sequence 2
289	12.8	42.7	43	6	A70338	A70338 Sequence 5	362	12.6	42.0	35	6	AX643576	AX643576 Sequence
290	12.8	42.7	43	6	AR117155	AR117155 Sequence	c 363	12.6	42.0	36	6	AX573339	AX573339 Sequence
291	12.8	42.7	43	6	CQ828067	CQ828067 Sequence	364	12.6	42.0	37	6	BD229946	BD229946 Novel DKR
292	12.8	42.7	43	6	CQ828097	CQ828097 Sequence	c 365	12.6	42.0	38	6	CQ784399	CQ784399 Sequence
293	12.8	42.7	43	6	AX404947	AX404947 Sequence	366	12.6	42.0	40	6	AX052779	AX052779 Sequence
294	12.8	42.7	47	6	AR284682	AR284682 Sequence	367	12.6	42.0	40	6	AX767221	AX767221 Sequence
295	12.8	42.7	47	6	AR289787	AR289787 Sequence	368	12.6	42.0	40	9	S08019	S08019 gamma delta
296	12.8	42.7	47	6	AR290601	AR290601 Sequence	c 369	12.6	42.0	41	6	AR020669	AR020669 Sequence
297	12.8	42.7	47	6	AX097534	AX097534 Sequence	c 370	12.6	42.0	41	6	AR121179	AR121179 Sequence
298	12.8	42.7	47	6	AX378326	AX378326 Sequence	c 371	12.6	42.0	41	6	AR160307	AR160307 Sequence
299	12.8	42.7	47	10	MMLOXL02	U65660 Mus musculu	372	12.6	42.0	41	6	AX515367	AX515367 Sequence
300	12.8	42.7	50	6	CQ004805	CQ004805 Sequence	c 373	12.6	42.0	41	6	AX517862	AX517862 Sequence
301	12.8	42.7	50	6	AX538789	AX538789 Sequence	374	12.6	42.0	41	6	AX520898	AX520898 Sequence
302	12.6	42.0	20	6	BD221956	BD221956 Nucleic a	c 375	12.6	42.0	41	6	BD003594	BD003594 Methods a
303	12.6	42.0	20	6	I80914	I80914 Sequence 31	376	12.6	42.0	41	9	HSZ74594	HSZ74594 H eaplens j
304	12.6	42.0	20	6	AR211886	AR211886 Sequence	377	12.6	42.0	42	6	I32723	I32723 Sequence 50
305	12.6	42.0	20	6	AR230540	AR230540 Sequence	c 378	12.6	42.0	42	6	AX612115	AX612115 Sequence
306	12.6	42.0	20	6	AR310235	AR310235 Sequence	c 379	12.6	42.0	42	6	AX612117	AX612117 Sequence
307	12.6	42.0	20	6	AR350647	AR350647 Sequence	c 380	12.6	42.0	45	6	AX612113	AX612113 Sequence
308	12.6	42.0	20	6	AR494381	AR494381 Sequence	c 381	12.6	42.0	47	6	A40450	A40450 Sequence 77
309	12.6	42.0	23	6	I23635	I23635 Sequence 57	c 382	12.6	42.0	47	6	BD196577	BD196577 Prostatic
310	12.6	42.0	23	6	I23636	I23636 Sequence 58	c 383	12.6	42.0	47	6	BD196578	BD196578 Prostatic
311	12.6	42.0	23	6	I23637	I23637 Sequence 59	384	12.6	42.0	47	6	AR289463	AR289463 Sequence

385	12.6	42.0	47	6	AR289812	Sequence	458	12.4	41.3	41	6	AX519738	Sequence
386	12.6	42.0	47	6	AR291072	Sequence	459	12.4	41.3	41	6	AX521019	Sequence
C 387	12.6	42.0	47	6	AR292017	Sequence	460	12.4	41.3	42	6	A71375	Sequence 5
C 388	12.6	42.0	48	6	I68898	Sequence 16	461	12.4	41.3	42	6	A78975	Sequence 5
C 389	12.6	42.0	48	6	I68902	Sequence 17	462	12.4	41.3	42	6	BD003429	Sequence 5
C 390	12.6	42.0	48	6	AR253496	Sequence	463	12.4	41.3	42	6	BD003429	Sequence 5
C 391	12.6	42.0	48	6	AR253500	Sequence	464	12.4	41.3	46	6	AR392731	Sequence
C 392	12.6	42.0	48	6	AX696549	Sequence	C 464	12.4	41.3	47	6	BD221906	Sequence
C 393	12.6	42.0	48	6	AX696553	Sequence	C 465	12.4	41.3	47	6	AR211836	Nucleic a
C 394	12.6	42.0	49	6	CQ816324	Sequence	C 466	12.4	41.3	47	6	AR290041	Sequence
C 395	12.6	42.0	49	6	CQ818919	Sequence	C 467	12.4	41.3	47	6	AR290253	Sequence
C 396	12.6	42.0	50	6	AR112327	Sequence	C 468	12.4	41.3	47	6	AX194739	Sequence
C 397	12.6	42.0	50	6	CQ008442	Sequence	469	12.4	41.3	48	6	I14419	Sequence 46
C 398	12.6	42.0	50	6	E33637	Sequence	470	12.4	41.3	48	10	PMU33863	Sequence
C 399	12.6	42.0	50	6	E33637	Detection o	471	12.4	41.3	48	10	S77042	T-cell rece
C 400	12.4	41.3	17	6	AX500580	Sequence	472	12.4	41.3	49	6	AX101291	Sequence
C 401	12.4	41.3	17	6	AX500584	Sequence	C 473	12.4	41.3	50	6	CQ816944	Sequence
C 402	12.4	41.3	20	6	AX732796	Sequence	C 474	12.4	41.3	50	6	AX068182	Sequence
C 403	12.4	41.3	20	6	BD228528	Sequence	C 475	12.4	41.3	50	6	AX164945	Sequence
C 404	12.4	41.3	20	6	AR314211	Sequence	C 476	12.4	41.3	50	6	AX495663	Sequence
C 405	12.4	41.3	21	6	AR359753	Sequence	C 477	12.4	41.3	50	6	AX495663	Sequence
C 406	12.4	41.3	21	6	AX095276	Sequence	C 478	12.2	40.7	17	6	BD202860	Method an
C 407	12.4	41.3	21	6	AX095792	Sequence	C 479	12.2	40.7	17	6	BD241162	Methods a
C 408	12.4	41.3	22	6	AX686739	Sequence	480	12.2	40.7	17	6	CQ515807	Sequence
C 409	12.4	41.3	23	6	BD266813	Sequence	481	12.2	40.7	17	6	I37572	Sequence 58
C 410	12.4	41.3	23	6	CQ753578	Methods f	C 482	12.2	40.7	17	6	I94422	Sequence 58
C 411	12.4	41.3	23	6	E09974	Primer for	C 483	12.2	40.7	17	6	AR456870	Sequence
C 412	12.4	41.3	23	6	E10118	PCR primer	C 484	12.2	40.7	17	6	AR482663	Sequence
C 413	12.4	41.3	25	6	AR381729	Sequence	C 485	12.2	40.7	17	6	AX266135	Sequence
C 414	12.4	41.3	25	6	AX502577	Sequence	C 486	12.2	40.7	17	6	AX266136	Sequence
C 415	12.4	41.3	25	6	AX502589	Sequence	C 487	12.2	40.7	17	6	AX266143	Sequence
C 416	12.4	41.3	25	6	AX534592	Sequence	C 488	12.2	40.7	17	6	AX266144	Sequence
C 417	12.4	41.3	25	6	AX534593	Sequence	C 489	12.2	40.7	17	6	AX725150	Sequence
C 418	12.4	41.3	25	6	AX609787	Sequence	C 490	12.2	40.7	18	6	AR066856	Sequence
C 419	12.4	41.3	25	6	AX692209	Sequence	491	12.2	40.7	19	6	AX129585	Sequence
C 420	12.4	41.3	25	6	AX692210	Sequence	492	12.2	40.7	20	6	AR100060	Sequence
C 421	12.4	41.3	25	6	AX692211	Sequence	493	12.2	40.7	20	6	AR100061	Sequence
C 422	12.4	41.3	26	6	I12122	Sequence	494	12.2	40.7	20	6	AR136427	Sequence
C 423	12.4	41.3	26	6	I12122	Sequence 27	C 495	12.2	40.7	20	6	AR275085	Sequence
C 424	12.4	41.3	26	6	I12122	Sequence 27	C 496	12.2	40.7	20	6	AR363587	Sequence
C 425	12.4	41.3	27	6	AR191412	Sequence	C 497	12.2	40.7	20	6	AR492097	Sequence
C 426	12.4	41.3	27	6	AR191412	Sequence	C 498	12.2	40.7	20	6	AR492098	Sequence
C 427	12.4	41.3	28	6	AR207923	Sequence	C 499	12.2	40.7	20	6	AX451710	Sequence
C 428	12.4	41.3	29	6	AR044258	Sequence	C 500	12.2	40.7	20	6	AX467189	Sequence
C 429	12.4	41.3	29	6	AR044258	Sequence	C 501	12.2	40.7	20	6	BD168964	Sequence
C 430	12.4	41.3	29	6	I18936	Sequence 8	C 502	12.2	40.7	21	6	I23544	Sequence 22
C 431	12.4	41.3	29	6	I24121	Sequence 8	C 503	12.2	40.7	21	6	I23549	Sequence 27
C 432	12.4	41.3	29	6	I35898	Sequence 13	C 504	12.2	40.7	21	6	AX154110	Sequence
C 433	12.4	41.3	29	6	I36086	Sequence 40	C 505	12.2	40.7	23	6	AR177338	Sequence
C 434	12.4	41.3	29	6	I68869	Sequence 13	C 506	12.2	40.7	23	6	BD203807	Sequence
C 435	12.4	41.3	29	6	AR223530	Sequence	C 507	12.2	40.7	23	6	BD247961	5' EST and
C 436	12.4	41.3	29	6	AR223718	Sequence	C 508	12.2	40.7	23	6	CQ771924	Sequence
C 437	12.4	41.3	29	6	AR234845	Sequence	C 509	12.2	40.7	23	6	AR306539	Sequence
C 438	12.4	41.3	29	6	AR235033	Sequence	C 510	12.2	40.7	23	6	AR340705	Sequence
C 439	12.4	41.3	29	6	AR253467	Sequence	C 511	12.2	40.7	23	6	AR412381	Sequence
C 440	12.4	41.3	29	6	AX611609	Sequence	C 512	12.2	40.7	23	6	AX061613	Sequence
C 441	12.4	41.3	29	6	AX696516	Sequence	C 513	12.2	40.7	23	6	AX884155	Sequence
C 442	12.4	41.3	29	6	AX935736	Sequence	C 514	12.2	40.7	23	6	AX939013	Sequence
C 443	12.4	41.3	29	6	AX936003	Sequence	C 515	12.2	40.7	23	6	AX968604	Sequence
C 444	12.4	41.3	30	6	AX146896	Sequence	C 516	12.2	40.7	23	6	AX969215	Sequence
C 445	12.4	41.3	30	6	AX659567	Sequence	C 517	12.2	40.7	23	6	BD023765	Sequence
C 446	12.4	41.3	31	6	AX105077	Sequence	C 518	12.2	40.7	23	6	BD073622	5' EST of
C 447	12.4	41.3	31	6	AX248327	Sequence	C 519	12.2	40.7	23	6	BD075900	5' EST of
C 448	12.4	41.3	32	6	AX349880	Sequence	C 520	12.2	40.7	23	6	BD076078	5' EST of
C 449	12.4	41.3	33	6	BD237687	Therapeut	C 521	12.2	40.7	23	6	BD076779	5' EST of
C 450	12.4	41.3	33	6	AR473403	Sequence	C 522	12.2	40.7	23	6	BD077440	5' EST of
C 451	12.4	41.3	33	6	BD138039	Expressio	C 523	12.2	40.7	23	6	BD077741	5' EST of
C 452	12.4	41.3	35	6	BD224795	Novel pla	C 524	12.2	40.7	23	6	BD085884	Elongatio
C 453	12.4	41.3	35	6	E10705	Primer. 9/1	C 525	12.2	40.7	23	6	BD107934	EST and e
C 454	12.4	41.3	35	6	AX513816	Sequence	C 526	12.2	40.7	23	6	BD131412	CDNA enco
C 455	12.4	41.3	41	6	AX515471	Sequence	C 527	12.2	40.7	23	6	BD139274	Extended
C 456	12.4	41.3	41	6	AX515544	Sequence	C 528	12.2	40.7	25	6	CQ618743	Sequence
C 457	12.4	41.3	41	6	AX517691	Sequence	C 530	12.2	40.7	25	6	CQ797993	Sequence

C 531	12.2	40.7	25	6	CQ797994	Sequence	604	12.2	40.7	41	6	AX514811	Sequence
C 532	12.2	40.7	25	6	AR459806	Sequence	605	12.2	40.7	41	6	AX517169	Sequence
C 533	12.2	40.7	25	6	AR459807	Sequence	606	12.2	40.7	41	6	AX519123	Sequence
C 534	12.2	40.7	25	6	AX566001	Sequence	607	12.2	40.7	46	6	AR148825	Sequence
C 535	12.2	40.7	25	6	AX566002	Sequence	608	12.2	40.7	46	10	MUSENV1	Mouse env m
C 536	12.2	40.7	25	6	AX766006	Sequence	609	12.2	40.7	47	6	E39260	Method for
C 537	12.2	40.7	25	6	AX766007	Sequence	610	12.2	40.7	47	6	E39260	Method for
C 538	12.2	40.7	26	6	AR026160	Sequence	611	12.2	40.7	47	6	AR288370	Sequence
C 539	12.2	40.7	26	6	AR026212	Sequence	612	12.2	40.7	47	6	AR289307	Sequence
C 540	12.2	40.7	26	6	AR026226	Sequence	613	12.2	40.7	47	6	AR289724	Sequence
C 541	12.2	40.7	26	6	AR026240	Sequence	614	12.2	40.7	48	6	A50035	Sequence 1
C 542	12.2	40.7	26	6	AR089196	Sequence	615	12.2	40.7	48	6	AR031654	Sequence
C 543	12.2	40.7	26	6	AR123651	Sequence	616	12.2	40.7	48	6	AR036479	Sequence
C 544	12.2	40.7	26	6	CG12851	Sequence	617	12.2	40.7	48	6	AR069438	Sequence
C 545	12.2	40.7	26	6	E61336	Probe for d	618	12.2	40.7	48	6	AR122695	Sequence
C 546	12.2	40.7	26	6	I82902	Sequence 4	619	12.2	40.7	48	6	AR122696	Sequence
C 547	12.2	40.7	26	6	I82954	Sequence 56	620	12.2	40.7	48	6	I73460	Sequence 12
C 548	12.2	40.7	26	6	I82968	Sequence 70	621	12.2	40.7	48	6	I90272	Sequence 13
C 549	12.2	40.7	26	6	I82982	Sequence 84	622	12.2	40.7	49	6	AR032506	Sequence
C 550	12.2	40.7	26	6	AR352022	Sequence	623	12.2	40.7	49	6	AR032506	Sequence
C 551	12.2	40.7	26	6	AR431088	Sequence	624	12.2	40.7	49	6	I29246	Sequence 11
C 552	12.2	40.7	26	6	AR431140	Sequence	625	12.2	40.7	49	6	I90920	Sequence 11
C 553	12.2	40.7	26	6	AR431154	Sequence	626	12.2	40.7	49	6	AR209170	Sequence
C 554	12.2	40.7	26	6	AR431168	Sequence	627	12.2	40.7	50	6	CQ813874	Sequence
C 555	12.2	40.7	26	6	AR431168	Sequence	628	12.2	40.7	50	10	MMU41922	Sequence
C 556	12.2	40.7	26	6	AR828881	Sequence	629	12.2	40.7	50	10	MMU41988	Mus musculus
C 557	12.2	40.7	26	6	AR828933	Sequence	630	12.2	40.7	17	6	AX423530	Sequence
C 558	12.2	40.7	26	6	AR828947	Sequence	631	12.2	40.0	18	6	AR083094	Sequence
C 559	12.2	40.7	27	6	AR828961	Sequence	632	12.2	40.0	18	6	AR174871	Sequence
C 560	12.2	40.7	27	6	AR191128	Sequence	633	12.2	40.0	20	6	AR106431	Sequence
C 561	12.2	40.7	28	6	E30857	Process for	634	12.2	40.0	20	6	AR312440	Sequence
C 562	12.2	40.7	28	6	AR390869	Sequence	635	12.2	40.0	20	6	AX296090	Sequence
C 563	12.2	40.7	29	6	A56906	Sequence 2	636	12.2	40.0	20	6	AX683627	Sequence
C 564	12.2	40.7	29	6	AR139092	Sequence	637	12.2	40.0	21	11	DOGIL1A1A	Canis fami
C 565	12.2	40.7	29	6	I64493	Sequence 7	638	12.2	40.0	22	6	AX241236	Sequence
C 566	12.2	40.7	30	6	AR137123	Sequence	639	12.2	40.0	22	6	AX487704	Sequence
C 567	12.2	40.7	30	6	BD271962	Cell surf	640	12.2	40.0	24	6	AR098104	Sequence
C 568	12.2	40.7	30	6	AR275195	Sequence	641	12.2	40.0	24	6	AR216929	Sequence
C 569	12.2	40.7	30	6	AX133703	Sequence	642	12.2	40.0	24	6	AX067818	Sequence
C 570	12.2	40.7	30	6	AX770023	Sequence	643	12.2	40.0	24	6	AX283064	Sequence
C 571	12.2	40.7	31	6	I12445	Sequence 15	644	12.2	40.0	24	6	AX447390	Sequence
C 572	12.2	40.7	31	6	I14507	Sequence 15	645	12.2	40.0	24	6	AX487514	Sequence
C 573	12.2	40.7	31	6	AX248925	Sequence	646	12.2	40.0	24	6	AX487579	Sequence
C 574	12.2	40.7	32	6	E10684	Primer. 9/1	647	12.2	40.0	24	6	BD084848	Modified
C 575	12.2	40.7	33	6	AR014460	Sequence	648	12.2	40.0	24	6	BD086399	KCNQ2 and
C 576	12.2	40.7	33	6	AR077823	Sequence	649	12.2	40.0	25	6	AR146789	Sequence
C 577	12.2	40.7	33	6	AR151063	Sequence	650	12.2	40.0	25	6	AR183844	Sequence
C 578	12.2	40.7	33	6	E15019	PCR primer	651	12.2	40.0	25	6	AX532892	Sequence
C 579	12.2	40.7	33	6	AR316462	Sequence	652	12.2	40.0	25	6	AX532898	Sequence
C 580	12.2	40.7	33	6	BD014655	Process f	653	12.2	40.0	27	6	AR167468	Sequence
C 581	12.2	40.7	34	6	BD188206	bHLH-PAS	654	12.2	40.0	27	6	BD218432	SSX gene,
C 582	12.2	40.7	34	6	BD225447	LYST prot	655	12.2	40.0	27	6	AR189239	Sequence
C 583	12.2	40.7	34	6	I02499	Sequence 3	656	12.2	40.0	27	6	AR305683	Sequence
C 584	12.2	40.7	34	6	AR362750	Sequence	657	12.2	40.0	27	6	AR402532	Sequence
C 585	12.2	40.7	34	6	AR373162	Sequence	658	12.2	40.0	27	6	AR402561	Sequence
C 586	12.2	40.7	34	6	BD169146	bHLH-PAS	659	12.2	40.0	27	6	AR447192	Sequence
C 587	12.2	40.7	35	6	BD272577	PRRSV vac	660	12.2	40.0	27	6	AX093478	Sequence
C 588	12.2	40.7	35	11	C75875	Homo sapien	661	12.2	40.0	27	6	AX107147	Sequence
C 589	12.2	40.7	36	6	AR146013	Sequence	662	12.2	40.0	27	6	AX118436	Sequence
C 590	12.2	40.7	36	6	E02844	DNA encodin	663	12.2	40.0	27	6	BD068032	Enzymatic
C 591	12.2	40.7	36	6	AR180904	Sequence	664	12.2	40.0	27	6	BD068061	Enzymatic
C 592	12.2	40.7	39	6	A67622	Sequence 42	665	12.2	40.0	28	6	AX234358	Sequence
C 593	12.2	40.7	39	6	A67626	Sequence 46	666	12.2	40.0	28	6	AX597999	Sequence
C 594	12.2	40.7	39	6	AR089760	Sequence	667	12.2	40.0	30	6	A49578	Sequence 19
C 595	12.2	40.7	39	6	AR089764	Sequence	668	12.2	40.0	30	6	AR106272	Sequence
C 596	12.2	40.7	39	6	AR148717	Sequence	669	12.2	40.0	30	6	BD008840	Uses of a
C 597	12.2	40.7	39	6	AR151067	Sequence	670	12.2	40.0	30	6	BD097519	Methods f
C 598	12.2	40.7	39	6	E15023	PCR primer	671	12.2	40.0	31	6	BD002906	Gene comp
C 599	12.2	40.7	39	6	AR316466	Sequence	672	12.2	40.0	32	6	AX183759	Sequence
C 600	12.2	40.7	39	6	AX612039	Sequence	673	12.2	40.0	32	6	AX557074	Sequence
C 601	12.2	40.7	39	6	BD014659	Process f	674	12.2	40.0	33	6	AR038154	Sequence
C 602	12.2	40.7	40	6	E12972	Hybrid DNA/	675	12.2	40.0	33	6	AR094117	Sequence
C 603	12.2	40.7	40	6	AX802723	Sequence	676	12.2	40.0	33	6	AX184037	Sequence
C 604	12.2	40.7	40	6	AX803078	Sequence	677	12.2	40.0	33	6	AX589695	Sequence

677	12	40.0	33	6	BD106830	Methods o	750	12	40.0	47	6	AX537339	Sequence
c 678	12	40.0	34	6	AX283065	Sequence	751	12	40.0	47	6	AX741679	Sequence
679	12	40.0	35	6	BD190131	Novel hum	752	12	40.0	47	6	AX776501	Sequence
680	12	40.0	35	6	AX192030	Sequence	753	12	40.0	47	6	BD063524	Streptoco
681	12	40.0	37	6	AR193403	Sequence	754	12	40.0	48	6	AX274412	Sequence
682	12	40.0	37	6	AR491403	Sequence	755	12	40.0	48	6	AX274568	Sequence
683	12	40.0	37	6	AX234367	Sequence	756	12	40.0	48	6	AX583479	Sequence
684	12	40.0	38	6	CQ817646	Sequence	c 757	12	40.0	49	6	AX1174	Sequence 8
c 685	12	40.0	38	6	CQ817647	Sequence	c 758	12	40.0	49	6	AR117404	Sequence
c 686	12	40.0	39	6	AX34187	Synthetic h	c 759	12	40.0	49	6	AR309043	Sequence
c 687	12	40.0	39	6	AR128129	Sequence	c 760	12	40.0	49	6	AX147410	Sequence
c 688	12	40.0	39	6	BD265531	Plastid t	761	12	40.0	49	6	AX662179	Sequence
c 689	12	40.0	39	6	AR237493	Sequence	762	12	40.0	50	6	AR444575	Sequence
c 690	12	40.0	39	6	AX280672	Sequence	763	12	40.0	50	6	AR444577	Sequence
c 691	12	40.0	40	6	AR148734	Sequence	c 764	12	40.0	50	6	AX160068	Sequence
c 692	12	40.0	41	6	AX280671	Sequence	765	12	40.0	50	6	AX694692	Sequence
c 693	12	40.0	41	6	AX514233	Sequence	766	12	40.0	50	9	HUMKREP8	L00204 Human K6b (
c 694	12	40.0	41	6	AX516287	Sequence	c 767	11.8	39.3	17	6	AR072951	Sequence
695	12	40.0	41	6	AX516352	Sequence	768	11.8	39.3	17	6	BD202859	Method an
696	12	40.0	41	6	AX516859	Sequence	c 769	11.8	39.3	17	6	AR220084	Sequence
c 697	12	40.0	41	6	AX519072	Sequence	770	11.8	39.3	17	6	AX734694	Sequence
698	12	40.0	41	6	AX519369	Sequence	c 771	11.8	39.3	17	6	BD002277	Cellulase
699	12	40.0	41	6	AX520386	Sequence	c 772	11.8	39.3	17	6	BD010881	Cellulase
c 700	12	40.0	41	6	AX520415	Sequence	c 773	11.8	39.3	19	6	AR439937	Sequence
c 701	12	40.0	42	6	A36516	Sequence 57	c 774	11.8	39.3	20	6	CQ819708	Sequence
c 702	12	40.0	42	6	AR080149	Sequence	775	11.8	39.3	20	6	I71526	Sequence 67
c 703	12	40.0	42	6	BD266719	Generatio	776	11.8	39.3	20	6	AR241092	Sequence
c 704	12	40.0	42	6	E50930	DNA and uti	777	11.8	39.3	20	6	AX429373	Sequence
c 705	12	40.0	42	6	AR238803	Sequence	778	11.8	39.3	20	6	AX487019	Sequence
c 706	12	40.0	42	6	AR363814	Sequence	779	11.8	39.3	21	6	CQ815012	Sequence
c 707	12	40.0	42	6	AX079214	Sequence	c 780	11.8	39.3	21	6	AX095302	Sequence
708	12	40.0	42	6	AX080047	Sequence	781	11.8	39.3	21	6	AX133261	Sequence
709	12	40.0	42	6	AX080057	Sequence	782	11.8	39.3	21	6	AX956310	Sequence
710	12	40.0	42	6	AX338459	Sequence	783	11.8	39.3	21	6	AX958200	Sequence
711	12	40.0	43	6	BD1822384	Sequence	784	11.8	39.3	21	6	BD091025	ADAMTS po
712	12	40.0	43	6	E23312	Antibody ag	785	11.8	39.3	22	6	AR361979	Sequence
713	12	40.0	43	6	E27081	Remedy for	c 786	11.8	39.3	22	6	AR361980	Sequence
714	12	40.0	43	6	BD011912	Ameliorat	787	11.8	39.3	22	6	AX192297	Sequence
715	12	40.0	43	6	BD011968	Therapeut	c 788	11.8	39.3	22	6	AX192298	Sequence
716	12	40.0	43	6	BD012029	Therapeut	c 789	11.8	39.3	22	6	AX278540	Sequence
717	12	40.0	43	6	BD012916	Inhibitin	c 790	11.8	39.3	22	6	AX513097	Sequence
718	12	40.0	43	6	BD095486	Remedies	791	11.8	39.3	22	6	BD016730	Promoter
719	12	40.0	43	6	BD095647	Stable an	c 792	11.8	39.3	22	6	BD088534	A method
720	12	40.0	43	6	BD140972	An agent	c 793	11.8	39.3	22	6	BD171664	Identific
c 721	12	40.0	44	6	AR058443	Sequence 13	794	11.8	39.3	22	12	AB069511	Synthetic
c 722	12	40.0	45	6	A95463	Sequence	795	11.8	39.3	23	6	BD230495	Total gen
723	12	40.0	45	6	AR135328	Sequence	796	11.8	39.3	23	6	CQ799765	Sequence
724	12	40.0	45	6	AR141103	Sequence	c 797	11.8	39.3	23	6	AR267668	Sequence
725	12	40.0	45	6	AR152395	Sequence	c 798	11.8	39.3	23	6	AR345132	Sequence
726	12	40.0	45	6	AR177526	Sequence	799	11.8	39.3	23	6	AX428096	Sequence
727	12	40.0	45	6	AR221749	Sequence	c 800	11.8	39.3	23	6	AX709071	Sequence
728	12	40.0	45	6	AR222529	Sequence	c 801	11.8	39.3	23	6	BD103832	A method
729	12	40.0	45	6	AR349242	Sequence	c 802	11.8	39.3	24	6	BD230208	Total gen
730	12	40.0	45	6	AX048221	Sequence	c 803	11.8	39.3	24	6	BD230209	Total gen
731	12	40.0	45	6	AX049382	Sequence	c 804	11.8	39.3	24	6	E31368	Histidine k
732	12	40.0	45	6	AX052722	Sequence	c 805	11.8	39.3	24	6	AR494807	Sequence
733	12	40.0	45	6	AX053163	Sequence	c 806	11.8	39.3	24	6	AX181781	Sequence
734	12	40.0	45	6	AX268059	Sequence	c 807	11.8	39.3	24	6	AX289759	Sequence
c 735	12	40.0	46	6	BD237816	Optical s	c 808	11.8	39.3	24	6	AX663757	Sequence
c 736	12	40.0	46	6	AX026757	Sequence	c 809	11.8	39.3	24	6	AX922586	Sequence
c 737	12	40.0	47	6	AR032403	Sequence	c 810	11.8	39.3	24	6	AX922588	Sequence
738	12	40.0	47	6	AR120515	Sequence	c 811	11.8	39.3	24	6	BD077184	Method an
c 739	12	40.0	47	6	I29143	Sequence 15	c 812	11.8	39.3	25	6	AR150687	Sequence
c 740	12	40.0	47	6	I90817	Sequence 15	c 813	11.8	39.3	25	6	BD183221	A method
c 741	12	40.0	47	6	AR209067	Sequence	c 814	11.8	39.3	25	6	CQ620230	Sequence
742	12	40.0	47	6	AR288840	Sequence	c 815	11.8	39.3	25	6	CQ620231	Sequence
743	12	40.0	47	6	AR289508	Sequence	c 816	11.8	39.3	25	6	CQ620232	Sequence
c 744	12	40.0	47	6	AR290402	Sequence	c 817	11.8	39.3	25	6	E16236	Primer 7/1
c 745	12	40.0	47	6	AR290689	Sequence	c 818	11.8	39.3	25	6	E28320	Utilization
746	12	40.0	47	6	AR341206	Sequence	c 819	11.8	39.3	25	6	AR461293	Sequence
747	12	40.0	47	6	AX114382	Sequence	c 820	11.8	39.3	25	6	AR461294	Sequence
c 748	12	40.0	47	6	AX378316	Sequence	c 821	11.8	39.3	25	6	AR461295	Sequence
749	12	40.0	47	6	AX537303	Sequence	c 822	11.8	39.3	25	6	AX513120	Sequence

823	11.8	39.3	25	6	AX534596 Sequence	AX534596 Sequence	896	11.8	39.3	37	6	A07707	A07707 Oligonucleo
824	11.8	39.3	25	6	AX610451 Sequence	AX610451 Sequence	897	11.8	39.3	37	6	Al0006	Al0006 Nucleotide
825	11.8	39.3	26	6	AR090658 Sequence	AR090658 Sequence	898	11.8	39.3	37	6	AX482472	AX482472 Sequence
826	11.8	39.3	26	6	AR197693 Sequence	AR197693 Sequence	c 899	11.8	39.3	38	6	AR286892	AR286892 Sequence
827	11.8	39.3	26	6	AR259847 Sequence	AR259847 Sequence	c 900	11.8	39.3	38	6	AR398882	AR398882 Sequence
828	11.8	39.3	26	6	AR432289 Sequence	AR432289 Sequence	c 901	11.8	39.3	38	6	AX220254	AX220254 Sequence
829	11.8	39.3	27	6	A15621 pCT 70 sequ	A15621 pCT 70 sequ	c 902	11.8	39.3	38	6	AX806454	AX806454 Sequence
830	11.8	39.3	27	6	AR184734 Sequence	AR184734 Sequence	c 903	11.8	39.3	39	5	HPIC28V	X15168 Horned shar
831	11.8	39.3	27	6	AR184947 Sequence	AR184947 Sequence	c 904	11.8	39.3	39	6	A67632	A67632 Sequence 52
832	11.8	39.3	27	6	AR189149 Sequence	AR189149 Sequence	c 905	11.8	39.3	39	6	AR089770	AR089770 Sequence
833	11.8	39.3	27	6	AR190796 Sequence	AR190796 Sequence	c 906	11.8	39.3	39	6	BD266465	BD266465 Univergal
834	11.8	39.3	27	6	AR190813 Sequence	AR190813 Sequence	c 907	11.8	39.3	39	6	AR408891	AR408891 Sequence
835	11.8	39.3	27	6	AR196443 Sequence	AR196443 Sequence	c 908	11.8	39.3	39	9	HSCD85706	Z50819 H. sapiens m
836	11.8	39.3	27	6	AR402771 Sequence	AR402771 Sequence	c 909	11.8	39.3	40	6	AR032554	AR032554 Sequence
837	11.8	39.3	27	6	AR403056 Sequence	AR403056 Sequence	c 910	11.8	39.3	40	6	BD180802	BD180802 Array of
838	11.8	39.3	27	6	AX537620 Sequence	AX537620 Sequence	c 911	11.8	39.3	40	6	I29294	I29294 Sequence 16
839	11.8	39.3	27	6	BD068271 Enzymatic	BD068271 Enzymatic	c 912	11.8	39.3	40	6	190968	190968 Sequence 16
840	11.8	39.3	27	6	BD068556 Enzymatic	BD068556 Enzymatic	c 913	11.8	39.3	40	6	AR209218	AR209218 Sequence
841	11.8	39.3	28	6	CO771743 Sequence	CO771743 Sequence	c 914	11.8	39.3	40	6	AR252386	AR252386 Sequence
842	11.8	39.3	28	6	E38063 Novel alpha	E38063 Novel alpha	c 915	11.8	39.3	40	6	AX403138	AX403138 Sequence
843	11.8	39.3	28	6	AR182351 Sequence	AR182351 Sequence	c 916	11.8	39.3	41	6	AX214509	AX214509 Sequence
844	11.8	39.3	28	6	AR236222 Sequence	AR236222 Sequence	c 917	11.8	39.3	41	6	AX514730	AX514730 Sequence
845	11.8	39.3	28	6	AR243544 Sequence	AR243544 Sequence	c 918	11.8	39.3	41	6	AX516036	AX516036 Sequence
846	11.8	39.3	28	6	AR254416 Sequence	AR254416 Sequence	c 919	11.8	39.3	41	6	AX516288	AX516288 Sequence
847	11.8	39.3	28	6	AR321739 Sequence	AR321739 Sequence	c 920	11.8	39.3	41	6	AX517443	AX517443 Sequence
848	11.8	39.3	28	6	AR411425 Sequence	AR411425 Sequence	c 921	11.8	39.3	41	6	AX518620	AX518620 Sequence
849	11.8	39.3	28	6	AR432995 Sequence	AR432995 Sequence	c 922	11.8	39.3	41	6	AX520738	AX520738 Sequence
850	11.8	39.3	28	6	AX417775 Sequence	AX417775 Sequence	c 923	11.8	39.3	42	6	AR106162	AR106162 Sequence
851	11.8	39.3	28	6	AX449105 Sequence	AX449105 Sequence	c 924	11.8	39.3	42	6	AX456424	AX456424 Sequence
852	11.8	39.3	28	6	AX449107 Sequence	AX449107 Sequence	c 925	11.8	39.3	42	6	AX612024	AX612024 Sequence
853	11.8	39.3	28	6	AX743970 Sequence	AX743970 Sequence	c 926	11.8	39.3	43	6	BD222036	BD222036 Pathogen-
854	11.8	39.3	28	6	BD012534 Inhibitor	BD012534 Inhibitor	c 927	11.8	39.3	43	6	AR237786	AR237786 Sequence
855	11.8	39.3	29	6	AR072422 Sequence	AR072422 Sequence	c 928	11.8	39.3	43	6	AX015670	AX015670 Sequence
856	11.8	39.3	29	6	I26533 Sequence 22	I26533 Sequence 22	c 929	11.8	39.3	43	6	AX601639	AX601639 Sequence
857	11.8	39.3	30	6	A28184 oligonucleo	A28184 oligonucleo	c 930	11.8	39.3	45	6	AR408890	AR408890 Sequence
858	11.8	39.3	30	6	A28184	A28184	c 931	11.8	39.3	45	6	AX776695	AX776695 Sequence
859	11.8	39.3	30	6	A20277 Sequence 9	A20277 Sequence 9	c 932	11.8	39.3	46	6	BD007255	BD007255 Novel fit
860	11.8	39.3	30	6	A92063 Sequence 4	A92063 Sequence 4	c 933	11.8	39.3	46	6	BD022529	BD022529 Multi-fun
861	11.8	39.3	30	6	A98799 Sequence 32	A98799 Sequence 32	c 934	11.8	39.3	47	6	AR289352	AR289352 Sequence
862	11.8	39.3	30	6	AR031959 Sequence	AR031959 Sequence	c 935	11.8	39.3	47	6	AR289469	AR289469 Sequence
863	11.8	39.3	30	6	AR090221 Sequence	AR090221 Sequence	c 936	11.8	39.3	47	6	AR291317	AR291317 Sequence
864	11.8	39.3	30	6	BD177383 A monoclo	BD177383 A monoclo	c 937	11.8	39.3	47	6	AR292129	AR292129 Sequence
865	11.8	39.3	30	6	AR197256 Sequence	AR197256 Sequence	c 938	11.8	39.3	47	6	AR292166	AR292166 Sequence
866	11.8	39.3	30	6	AR243227 Sequence	AR243227 Sequence	c 939	11.8	39.3	48	6	BD007248	BD007248 Novel fit
867	11.8	39.3	30	6	AR259410 Sequence	AR259410 Sequence	c 940	11.8	39.3	48	6	BD022522	BD022522 Multi-fun
868	11.8	39.3	30	6	AR365149 Sequence	AR365149 Sequence	c 941	11.8	39.3	49	4	CTRO5	M60102 Avian neovi
869	11.8	39.3	30	6	AR428169 Sequence	AR428169 Sequence	c 942	11.8	39.3	49	6	CO818796	CO818796 Rabbit trop
870	11.8	39.3	30	6	AX128538 Sequence	AX128538 Sequence	c 943	11.8	39.3	49	6	E62959	E62959 Novel poly
871	11.8	39.3	31	6	BD007526 Novel con	BD007526 Novel con	c 944	11.8	39.3	49	6	AX930379	AX930379 Sequence
872	11.8	39.3	31	6	E41688 Process for	E41688 Process for	c 945	11.8	39.3	49	6	AX930380	AX930380 Sequence
873	11.8	39.3	31	6	AX248718 Sequence	AX248718 Sequence	c 946	11.8	39.3	50	6	BD183724	BD183724 Identific
874	11.8	39.3	32	6	AX256318 Sequence	AX256318 Sequence	c 947	11.8	39.3	50	6	CO002957	CO002957 Sequence
875	11.8	39.3	32	6	E10683 Primer. 9/1	E10683 Primer. 9/1	c 948	11.8	39.3	50	6	CO003050	CO003050 Sequence
876	11.8	39.3	32	6	E31942 Seven-pass	E31942 Seven-pass	c 949	11.8	39.3	50	6	CO003364	CO003364 Sequence
877	11.8	39.3	33	6	AR054981 Sequence	AR054981 Sequence	c 950	11.8	39.3	50	6	CO003683	CO003683 Sequence
878	11.8	39.3	33	6	CO742975 Sequence	CO742975 Sequence	c 951	11.8	39.3	50	6	CO004459	CO004459 Sequence
879	11.8	39.3	33	6	AR410397 Sequence	AR410397 Sequence	c 952	11.8	39.3	50	6	CO005001	CO005001 Sequence
880	11.8	39.3	34	6	AX317243 Sequence 15	AX317243 Sequence 15	c 953	11.8	39.3	50	6	I21263	I21263 Sequence 27
881	11.8	39.3	34	6	AR067668 Sequence	AR067668 Sequence	c 954	11.8	39.3	50	6	AX204543	AX204543 Sequence
882	11.8	39.3	34	6	AR169813 Sequence	AR169813 Sequence	c 955	11.8	39.3	50	6	AX391760	AX391760 Sequence
883	11.8	39.3	34	6	AX477017 Sequence	AX477017 Sequence	c 956	11.8	39.3	50	6	AX394237	AX394237 Sequence
884	11.8	39.3	34	6	AX526393 Sequence	AX526393 Sequence	c 957	11.8	39.3	50	6	A70804	A70804 Sequence 12
885	11.8	39.3	34	6	BD140841 Novel G p	BD140841 Novel G p	c 958	11.8	39.3	50	6	A79288	A79288 Sequence 12
886	11.8	39.3	35	6	A40449 Sequence 76	A40449 Sequence 76	c 959	11.8	39.3	50	6	I38118	I38118 Sequence 11
887	11.8	39.3	35	6	E15078 Primer. 7/1	E15078 Primer. 7/1	c 960	11.8	39.3	50	6	AX968	AX968 Sequence 11
888	11.8	39.3	35	6	E15094 Primer. 7/1	E15094 Primer. 7/1	c 961	11.8	39.3	50	6	AX659502	AX659502 Sequence
889	11.8	39.3	35	6	AX794650 Sequence	AX794650 Sequence	c 962	11.8	39.3	50	6	BD003518	BD003518 A gene re
890	11.8	39.3	36	6	A08122 Synthetic D	A08122 Synthetic D	c 963	11.8	39.3	50	6	BD124158	BD124158 Treatment
891	11.8	39.3	36	6	A13212 oligonucleo	A13212 oligonucleo	c 964	11.8	39.3	50	6	BD088795	BD088795 A method
892	11.8	39.3	36	6	AR034012 Sequence	AR034012 Sequence	c 965	11.8	39.3	50	6	AB068606	AB068606 Synthetic
893	11.8	39.3	36	6	AR124021 Sequence	AR124021 Sequence	c 966	11.8	39.3	50	6	BD229138	BD229138 Genotype
894	11.8	39.3	36	6	AR408671 Sequence	AR408671 Sequence	c 967	11.8	39.3	50	6	CO764732	CO764732 Sequence
895	11.8	39.3	36	6	AX806441 Sequence	AX806441 Sequence	c 968	11.8	39.3	50	6		

969 11.6 38.7 20 6 CQ764740 Sequence
970 11.6 38.7 20 6 CQ764750 Sequence
C 971 11.6 38.7 20 6 E05264 Probe for g
C 972 11.6 38.7 20 6 AR228978 Sequence
C 973 11.6 38.7 20 6 AR242478 Sequence
C 974 11.6 38.7 20 6 AR298321 Sequence
C 975 11.6 38.7 20 6 AR303809 Sequence
C 976 11.6 38.7 20 6 AR315539 Sequence
C 977 11.6 38.7 20 6 AR349390 Sequence
C 978 11.6 38.7 20 6 AX482148 Sequence
C 979 11.6 38.7 20 6 AX487539 Sequence
C 980 11.6 38.7 20 6 AX511387 Sequence
C 981 11.6 38.7 20 6 AX721748 Sequence
C 982 11.6 38.7 20 6 AX801911 Sequence
C 983 11.6 38.7 21 6 AX145501 Sequence
C 984 11.6 38.7 21 6 CQ801098 Sequence
C 985 11.6 38.7 21 6 AR257361 Sequence
C 986 11.6 38.7 21 6 AR474501 Sequence
C 987 11.6 38.7 21 6 AX096404 Sequence
C 988 11.6 38.7 21 6 AX153925 Sequence
C 989 11.6 38.7 21 6 AX259939 Sequence
C 990 11.6 38.7 21 6 AX260017 Sequence
C 991 11.6 38.7 21 6 AX262378 Sequence
C 992 11.6 38.7 22 6 AR285032 Sequence
C 993 11.6 38.7 22 6 AX107102 Sequence
C 994 11.6 38.7 22 6 BD170102 Method of
C 995 11.6 38.7 22 6 BD170164 Method of
C 996 11.6 38.7 23 6 AR267711 Sequence
C 997 11.6 38.7 24 6 AX027831 Sequence
C 998 11.6 38.7 24 6 AX493977 Sequence
C 999 11.6 38.7 24 6 AX539177 Sequence
1000 11.6 38.7 24 6 AX657567 Sequence

ALIGNMENTS

RESULT 1
AX802290 30 bp DNA linear PAT 24-NOV-2003
LOCUS
DEFINITION Sequence 2 from Patent WO03057910.
ACCESSION AX802290
VERSION AX802290.1 GI:38501181
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Pinel-Ober,J., Wenzig,P., Weindel,K., Bartl,K., Schoenbrunner,R.,
Malhotra,K., O'Donnell,P. and Kyger,E.
TITLE Use of silica material in an amplification reaction
JOURNAL Patent: WO 03057910-A 2 17-JUL-2003;
Roche Diagnostics GmbH (DE)
FEATURES
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1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Internal Control Specific Probes"

ORIGIN
Query Match 100.0%; Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGGACTCAGTCTTGGTCATCTCACCTTCT 30
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DB 1 TGGACTCAGTCTTGGTCATCTCACCTTCT 30

RESULT 2
BD181365 31 bp DNA linear PAT 15-MAY-2003
LOCUS

DEFINITION A method for determination of a nucleic acid using a control.
ACCESSION BD181365
VERSION BD181365.1 GI:30792283
KEYWORDS JP 2002335981-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 31)
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: JP 2002335981-A 4 26-NOV-2002;
F HOFFMANN LA ROCHE AG
COMMENT OS Artificial Sequence
PN JP 2002335981-A/4
PD 26-NOV-2002
PF 04-MAR-2002 JP 2002057515
PR 02-MAR-2001 EP 01105172.9
PI STEPHAN JAEGER
PC C12N15/09,C12Q1/68,G01N33/50,G01N33/53,G01N33/566,G01N33/58,
PC C12N15/00
CC Description of Artificial Sequence: ST2535 probe sequence CC
n represents an abasic linker (2-amino-cyclohexyl-) propan-1,3-
diol)
FH Key Location/Qualifiers
FT N region Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 63.3%; Score 19; DB 6; Length 31;
Best Local Similarity 96.8%; Pred. No. 6.2e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TGGACTCAGTCTTGGTCATCTCACCTTCT 30
|||||
DB 1 TGGACTCAGTCTTGGTCATCTCACCTTCT 31
AX147028 31 bp DNA linear PAT 08-JUN-2001
Sequence 22 from Patent WO0137291.
ACCESSION AX147028
VERSION AX147028.1 GI:14346299
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Weindel,K., Riedling,M. and Geiger,A.
TITLE Magnetic glass particles, method for their preparation and uses
JOURNAL Patent: WO 0137291-A 22 25-MAY-2001;
Roche Diagnostics GmbH (DE)
FEATURES
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1. .31
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

misc_feature 1
/note="derivatisation with a
Pentamethine-di-indocarbocyanine via a
alkylphosphatidyl-linker (Pharmacia Biotech
Cy5-N-ethyl-phosphoramidite)"
misc_feature 14
/note="N represents a
2-(amino-cyclohexyl-)propane-1,3-diol-linker derivatised
with hexachloro-6-carboxy-fluorescein (Biogenex
CX-HEX-phosphoramidite)"

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misc_feature 30
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Best Local Similarity 96.8%; Pred. No. 6.2e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
Db 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 31
RESULT 4
LOCUS AX523945 31 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 4 from Patent EP1236804.
ACCESSION AX523945
VERSION AX523945.1 GI:25168876
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: EP 1236804-A 4 04-SEP-2002;
Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
FEATURES
Location/Qualifiers
source 1..31
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="GT2535 probe sequence"
misc_feature 15
/note="n represents an abasic linker
(2-amino-cyclohexyl-1-propan-1,3-diol)"
ORIGIN
Query Match 63.3%; Score 19; DB 6; Length 31;
Best Local Similarity 96.8%; Pred. No. 6.2e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
Db 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 31
RESULT 5
LOCUS AX524843 31 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 4 from Patent EP1236805.
ACCESSION AX524843
VERSION AX524843.1 GI:25169937
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaeger,S.
TITLE A method for the determination of a nucleic acid using a control
JOURNAL Patent: EP 1236805-A 4 04-SEP-2002;
Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
FEATURES
Location/Qualifiers
source 1..31
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="GT2535 probe sequence"
misc_feature 15
/note="n represents an abasic linker
(2-amino-cyclohexyl-1-propan-1,3-diol)"
ORIGIN
Query Match 63.3%; Score 19; DB 6; Length 31;
Best Local Similarity 96.8%; Pred. No. 6.2e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
Db 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 31
RESULT 6
LOCUS I17523 33 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 13 from patent US 5491063.
ACCESSION I17523
VERSION I17523.1 GI:1597878
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Fisher,M.E. and Watson,R.M.
TITLE Methods for in-solution quenching of fluorescently labeled
oligonucleotide probes
JOURNAL Patent: US 5491063-A 13 13-FEB-1996;
Location/Qualifiers
source 1..33
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 63.3%; Score 19; DB 6; Length 33;
Best Local Similarity 96.8%; Pred. No. 6.2e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
Db 31 TGGACTCAGTCCTCTGGTCATCTCACCTTCT 1
RESULT 7
LOCUS I28348 33 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5571673.
ACCESSION I28348
VERSION I28348.1 GI:1819124
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Picone,T.K.H.
TITLE Methods for in-solution quenching of fluorescently labeled
oligonucleotide probes
JOURNAL Patent: US 5571673-A 1 05-NOV-1996;
Location/Qualifiers
source 1..33
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 63.3%; Score 19; DB 6; Length 33;
Best Local Similarity 96.8%; Pred. No. 6.2e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
Db 31 TGGACTCAGTCCTCTGGTCATCTCACCTTCT 1
RESULT 8
LOCUS AX777198 48 bp DNA linear PAT 14-JUL-2003
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DEFINITION	Sequence 52 from Patent WO03040301.
ACCESSION	AX777198
VERSION	AX777198.1 GI:32694346
KEYWORDS	
SOURCE	synthetic construct artificial sequences.
ORGANISM	
REFERENCE	Deak,P., Frenz,L., Glover,D. and Midgley,C. Cell cycle progression proteins Patent: WO 03040301-A 52 15-MAY-2003; Cyclacel Limited (GB)
TITLE	
JOURNAL	
FEATURES	Location/Qualifiers
source	1..48 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Primer"
ORIGIN	
Query Match	58.7%; Score 17.6; DB 6; Length 48;
Best Local Similarity	83.3%; Pred.No. 2.9e+03;
Matches	20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	2 GGACTGAGTCCTGGTGCATCTCAC 25
DB	41 GGCGTTGGTCCTGGTGCATCTCCC 18
RESULT 9	
AR379394/c	
LOCUS	AR379394 46 bp DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 52 from patent US 6607878.
ACCESSION	AR379394
VERSION	AR379394.1 GI:40087028
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	Sorge,J.A.
TITLE	Collections of uniquely tagged molecules
JOURNAL	Patent: US 6607878-A 52 19-AUG-2003;
FEATURES	Location/Qualifiers
source	1..46 /organism="unknown" /mol_type="genomic DNA"
ORIGIN	
Query Match	54.7%; Score 16.4; DB 6; Length 46;
Best Local Similarity	76.9%; Pred.No. 1.1e+04;
Matches	20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY	3 GACTCAGTCCTGGTGCATCTCACCTT 28
DB	41 GACTCAGACTTGTCGATCTGACGT 16
RESULT 10	
AX804053/c	
LOCUS	AX804053 39 bp DNA linear PAT 25-NOV-2003
DEFINITION	Sequence 221 from Patent WO03060160.
ACCESSION	AX804053
VERSION	AX804053.1 GI:385221188
KEYWORDS	
SOURCE	Oreochromis niloticus (Nile tilapia)
ORGANISM	Oreochromis niloticus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Labroidae; Cichlidae; Oreochromis.
REFERENCE	Lie,Y., Slettan,A., Hoeyum,M. and Lingaaas,F.
AUTHORS	
TITLE	
JOURNAL	
MEDLINE	
PUBMED	
REFERENCE	2 (bases 1 to 49)

TITLE	Verification of food origin based on nucleic acid pattern
recognition	
Genomax ASA (NO)	
Genomax ASA (NO)	
LOCATION/Qualifiers	
1..39	/organism="Oreochromis niloticus" /mol_type="unassigned DNA" /db_xref="taxon:8128"
ORIGIN	
Query Match	54.0%; Score 16.2; DB 6; Length 39;
Best Local Similarity	72.4%; Pred.No. 1.4e+04;
Matches	21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY	1 TGGACTCAGTCCTGGTGCATCTCACCTTC 29
DB	32 TGCATTCTGCTCTGGTGCATAGCTGTTTC 4
RESULT 11	
AX800237/c	
LOCUS	AX800237 26 bp DNA linear PAT 13-OCT-2003
DEFINITION	Sequence 56 from Patent EP1327691.
ACCESSION	AX800237
VERSION	AX800237.1 GI:37653480
KEYWORDS	
SOURCE	synthetic construct artificial sequences.
ORGANISM	
REFERENCE	Bai,Y.L. and Terng,H.J.
AUTHORS	Detection of respiratory viruses
TITLE	Patent: EP 1327691-A 56 16-JUL-2003;
JOURNAL	Dr. Chip Biotechnology Incorporation (TW)
FEATURES	Location/Qualifiers
source	1..26 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="ADV probe"
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Query Match	52.7%; Score 15.8; DB 6; Length 26;
Best Local Similarity	81.0%; Pred.No. 2.2e+04;
Matches	17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY	2 GGACTCAGTCCTGGTGCATCT 22
DB	22 GGAAACCAGTCYTGGTCAITG 2
RESULT 12	
HSRETINT32	
LOCUS	Human RET proto-oncogene, intron 16, 3' end.
DEFINITION	
ACCESSION	U11510
VERSION	U11510.1 GI:558792
KEYWORDS	
SEGMENT	32 of 38
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 49)
AUTHORS	Ceccherini,I., Boccardi,R., Luo,Y., Pasini,B., Hofstra,R., Takahashi,M. and Romeo,G.
TITLE	Exon structure and flanking intronic sequences of the human RET
JOURNAL	Proto-oncogene
MEDLINE	Biocem. Biophys. Res. Commun. 196 (3), 1288-1295 (1993)
PUBMED	94071887
REFERENCE	2 (bases 1 to 49)

AUTHORS Ceccherini, I., Hofstra, R., Yin, L., Stulp, R., Barone, V., Stelwagen, T., Boccia, R., Nijveen, H., Bolino, A., Seri, M., Ronchetto, P., Pasini, B., Bozzano, M., Buys, C. and Romeo, G.
TITLE DNA polymorphisms and conditions for SSCP analysis of the 20 exons of the ret proto-oncogene
JOURNAL Oncogene 9 (10), 3025-3029 (1994)
PUBMED 94366753
REFERENCE 8084609
AUTHORS Ceccherini, I.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-1994) Isabella Ceccherini, Laboratorio di Genetica Molecolare, Istituto Giannina Gaslini, Largo G. Gaslini, 5, Genova, 16148, Italy
FEATURES
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 1..49
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="10"
 /map="10q11.2"
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 /evidence=experimental
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 Query Match 52.0%; Score 15.6; DB 9; Length 49;
 Best Local Similarity 70.0%; Pred. No. 2.7e+04;
 Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCTTGTCATCTCACCTTC 30
Db 16 TGGAGCCACTACTGGTCTTTCATCTCT 45

RESULT 13
LOCUS AX420204 22 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 93 from Patent WO0208289.
ACCESSION AX420204
VERSION AX420204.1 GI:21524455
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
 artificial sequences.
REFERENCE 1
AUTHORS Padigaru, M., Mezes, P., Mishra, V., Burgess, C., Casman, S. and Smithson, G.
TITLE G-protein coupled receptors and nucleic acids encoding same
JOURNAL Patent: WO 0208289-A 93 31-JAN-2002;
FEATURES
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 1..22
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 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Ag1279/Ag2590 PCR Primer Sequence"
ORIGIN
 Query Match 50.7%; Score 15.2; DB 6; Length 22;
 Best Local Similarity 85.0%; Pred. No. 4.2e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TCCTTGGTCATCTCACCTTC 29
Db 21 TCCTTTCATCTCTCCTTC 2

RESULT 14
LOCUS AX528208 22 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 76 from Patent WO0226985.
ACCESSION AX528208
VERSION AX528208.1 GI:25172515
KEYWORDS synthetic construct
SOURCE synthetic construct
 artificial sequences.

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
 artificial sequences.
REFERENCE 1
AUTHORS Spytek, K.A., Casman, S., Padigaru, M., Dickson, K., Vernet, C., Spaderna, S.K., Shenoy, S., Gerlach, V., Ellerman, K., Edinger, S., Macdougall, J.R., Smithson, G., Li, L., Malyankar, U.M., Taylor, S., Gunther, E. and Tchernev, V.T.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0226985-A 76 04-APR-2002;
FEATURES
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 1..22
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
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 Best Local Similarity 85.0%; Pred. No. 4.2e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TCCTTGGTCATCTCACCTTC 29
Db 21 TCCTTTCATCTCTCCTTC 2

RESULT 15
LOCUS AX528214 22 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 82 from Patent WO0226985.
ACCESSION AX528214
VERSION AX528214.1 GI:25172521
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
 artificial sequences.
REFERENCE 1
AUTHORS Spytek, K.A., Casman, S., Padigaru, M., Dickson, K., Vernet, C., Spaderna, S.K., Shenoy, S., Gerlach, V., Ellerman, K., Edinger, S., Macdougall, J.R., Smithson, G., Li, L., Malyankar, U.M., Taylor, S., Gunther, E. and Tchernev, V.T.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0226985-A 82 04-APR-2002;
FEATURES
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="PCR Primer Sequence"
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 Query Match 50.7%; Score 15.2; DB 6; Length 22;
 Best Local Similarity 85.0%; Pred. No. 4.2e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TCCTTGGTCATCTCACCTTC 29
Db 21 TCCTTTCATCTCTCCTTC 2

RESULT 16
LOCUS AX554648 22 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 202 from Patent WO0246229.
ACCESSION AX554648
VERSION AX554648.1 GI:25898315
KEYWORDS synthetic construct
SOURCE synthetic construct
 artificial sequences.

artificial sequences.

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1
REFERENCE
AUTHORS      Casman,S.J., Padigaru,M., Burgess,C.E., Shinkets,R.A., Spytek,K.A.,
              Gilbert,J.A., Mayotte,J.E., Baumgartner,J.C., Mishra,V.,
              Vernet,C.A., Dickinson,K.S., Ballinger,R.A. and Wolenc,A.R.
TITLE        Novel proteins and nucleic acids encoding same
JOURNAL      Patent: WO 0246229-A 202 13-JUN-2002;
              Curagen Corporation (US)
FEATURES     Location/Qualifiers
source       1..22
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="PCR Primer Sequence"
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Query Match      50.7%; Score 15.2; DB 6; Length 22;
Best Local Similarity 85.0%; Pred. No. 4.2e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      10 TCCTTGGTCATCTCACCTTC 29
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Db       21 TCCTTTCATCTCTCCTTC 2
          ||||| ||||| ||||| |||||
RESULT 17
AR230098/c
LOCUS      AR230098
DEFINITION Sequence 7 from patent US 6451557.
ACCESSION  AR230098
VERSION     AR230098.1 GI:27270082
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 24)
AUTHORS    Vaughan,P.R., Galanis,M., Ramshaw,J.A.M. and Werkmeister,J.A.
TITLE      Method for producing, in yeast, a hydroxylated triple helical
           protein, and yeast host cells useful in said method
JOURNAL    Patent: US 6451557-A 7 17-SEP-2002;
           Location/Qualifiers
FEATURES   source
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           /organism="unknown"
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ORIGIN
Query Match      50.7%; Score 15.2; DB 6; Length 24;
Best Local Similarity 85.0%; Pred. No. 4.2e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      10 TCCTTGGTCATCTCACCTTC 29
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Db       20 TCCTTGGTGACCTCCCTTC 1
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RESULT 18
AX022200/c
LOCUS      AX022200
DEFINITION Sequence 7 from Patent EP0950098.
ACCESSION  AX022200
VERSION     AX022200.1 GI:10045866
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1
AUTHORS    Ramshaw,J.A., Galanis,M., Vaughan,P.R. and Werkmeister,J.A.
TITLE      Stable expression of triple helical proteins
JOURNAL    Patent: EP 0950098-A 7 20-OCT-1999;
           COMMW SCIENT IND RES ORG (AU)
FEATURES   Location/Qualifiers
source     1..24
           /organism="unidentified"
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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ORIGIN

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Query Match      50.7%; Score 15.2; DB 6; Length 24;
Best Local Similarity 85.0%; Pred. No. 4.2e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      10 TCCTTGGTCATCTCACCTTC 29
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Db       20 TCCTTGGTGACCTCCCTTC 1
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RESULT 19
AX030726/c
LOCUS      AX030726
DEFINITION Sequence 7 from Patent WO9818918.
ACCESSION  AX030726
VERSION     AX030726.1 GI:10278240
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1
AUTHORS    Ramshaw,J.A., Galanis,M., Vaughan,P.R. and Werkmeister,J.A.
TITLE      Stable expression of triple helical proteins
JOURNAL    Patent: WO 9818918-A 7 07-MAY-1998;
           RAMSHAW JOHN ALAN MAURICE (AU) ; GALANIS MARIA (AU) ; COMMW SCIENT
           IND RES ORG (AU) ; VAUGHAN PAUL RICHARD (AU) ; WERKMEISTER JEROME
           ANTHONY (AU)
FEATURES   Location/Qualifiers
source     1..24
           /organism="unidentified"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32644"
ORIGIN
Query Match      50.7%; Score 15.2; DB 6; Length 24;
Best Local Similarity 85.0%; Pred. No. 4.2e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      10 TCCTTGGTCATCTCACCTTC 29
          ||||| ||||| ||||| |||||
Db       20 TCCTTGGTGACCTCCCTTC 1
          ||||| ||||| ||||| |||||
RESULT 20
BD008647/c
LOCUS      BD008647
DEFINITION Stable expression of the triple helical protein.
ACCESSION  BD008647
VERSION     BD008647.1 GI:18637020
KEYWORDS   JP 2001502548-A/7.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 24)
AUTHORS    Vaughan,P.R., Galanis,M., Ramshaw,J.A.M. and Werkmeister,J.A.
TITLE      Stable expression of the triple helical protein
JOURNAL    Patent: JP 2001502548-A 7 27-FEB-2001;
           COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
           OS
COMMENT     Unidentified
           PN JP 2001502548-A/7
           PD 27-FEB-2001
           PF 29-OCT-1997 JP 1998519817
           PR
           PI PAUL RICHARD VAUGHAN, MARIA GALANIS, JOHN ALAN MAURICE RAMSHAW,
           PJ JEROME ANTHONY WERKMEISTER
           PC C12N15/12,C12N15/81,C12N15/53,C07K14/78,A61K38/39 CC
           Strandedness: Single;
           CC Topology: Linear;
           FH Key
           FT source
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  Best Local Similarity 85.0%; Pred. No. 4.2e+04;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TCCTTGGTCATCTCACCTTC 29
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Db 20 TCCTTGGTGACCTCCCTTC 1

RESULT 21
LOCUS E14084 39 bp DNA linear PAT 28-JUL-1999
DEFINITION Primer.
ACCESSION E14084
VERSION E14084.1 GI:5708767
KEYWORDS JP 1997268200-A/13.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Muramatsu, S. and Zushi, M.
TITLE RAT THROMBOMODULIN
JOURNAL Patent: JP 1997268200-A 13 14-OCT-1997;
        ASahi CHEM IND CO LTD
COMMENT OS None
        OC Artificial sequences.
        PN JP 1997268200-A/13
        PD 14-OCT-1997
        PF 01-APR-1996 JP 1996078494
        PI MURAMATSU SHUJI, ZUSHI MICHITAKA
        PC
C07K14/745,A01K67/027,C07H21/04,C12N15/09,C12P21/02//A61K38/00, PC
(C12P21/02,
PC C12R1:91);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
FH Key
FH Location/Qualifiers
FT source 1..39
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    /db_xref='taxon:32644'
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  Best Local Similarity 85.0%; Pred. No. 4.2e+04;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CAGTCCTTGGTCATCTCACC 26
    ||||| ||||| ||||| |||||
Db 14 CAGTCCTTGGCTAATCTGACC 33

RESULT 22
LOCUS AR284878 47 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 930 from patent US 6528260.
ACCESSION AR284878
VERSION AR284878.1 GI:29721782
KEYWORDS
SOURCE Unknown.

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        /db_xref='taxon:32644'
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  Best Local Similarity 85.0%; Pred. No. 4.2e+04;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TCCTTGGTCATCTCACCTTC 29
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Db 20 TCCTTGGTGACCTCCCTTC 1

RESULT 23
LOCUS AX249405/c 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 1484 from Patent WO0166800.
ACCESSION AX249405
VERSION AX249405.1 GI:15864028
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Cargill, M., Ireland, J. S. and Lander, E. S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 1484 13-SEP-2001;
        WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
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    /organism='Homo sapiens'
    /mol_type='unassigned DNA'
    /db_xref='taxon:9606'
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  Query Match      50.0%; Score 15; DB 6; Length 31;
  Best Local Similarity 72.0%; Pred. No. 5.2e+04;
  Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCCTTGGTCATCTCAC 25
    ||||| ||||| ||||| |||||
Db 31 TGGACTAAGCCTTTGKCCATCGCCC 7

RESULT 24
LOCUS AX800208 20 bp DNA linear PAT 13-OCT-2003
DEFINITION Sequence 27 from Patent EP1327691.
ACCESSION AX800208
VERSION AX800208.1 GI:37653451
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bai, Y. L. and Terng, H. J.
TITLE Detection of respiratory viruses
JOURNAL Patent: EP 1327691-A 27 16-JUL-2003;
        Dr. Chip Biotechnology Incorporation (TW)
FEATURES
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    /mol_type='unassigned DNA'
    /db_xref='taxon:32630'
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Query Match          49.3%; Score 14.8; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 6.5e+04;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
/notes="ADV primer"

QY 3 GACTCAGTCCTTGGTCATCT 22
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Db 1 GAACCACTCTTGGTCATGT 20
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RESULT 25
LOCUS      CQ801293          30 bp      DNA          linear      PAT 05-MAY-2004
DEFINITION Sequence 154 from Patent WO2004033689.
ACCESSION  CQ801293
VERSION     CQ801293.1 GI:47058049
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.

REFERENCE  1
AUTHORS   Blondelet-Rouault,M.H., Dominguez,H., Darbon-Rongere,E.,
Gerbaud,C., Gondran,A., Karray,F., Lacroix,P., oestreicher-mermet-
Bouvier,N., Pernodet,J.L. and Tiphile,K.
TITLE     Polypeptides involved in spiramycin biosynthesis, nucleotide
sequences encoding said polypeptides and uses thereof
JOURNAL   Patent: WO 2004033689-A 154 22-APR-2004;
Aventis Pharma S.A. (FR); CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)
FEATURES   source
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            /organism="synthetic construct"
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            /db_xref="taxon:32830"
            /note="Oligonucleotide KF43"

ORIGIN

Query Match          49.3%; Score 14.8; DB 6; Length 30;
Best Local Similarity 88.9%; Pred. No. 6.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 CCTTGTCATCTCACCCTT 28
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Db 13 CCTTGTCATCTGCCTT 30
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RESULT 26
LOCUS      AX514149          41 bp      DNA          linear      PAT 05-OCT-2002
DEFINITION Sequence 347 from Patent WO2052044.
ACCESSION  AX514149
VERSION     AX514149.1 GI:23560508
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE     Detection of genetic polymorphisms
JOURNAL   Patent: WO 02052044-A 347 04-JUL-2002;
Riken (JP)
FEATURES   source
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ORIGIN

Query Match          49.3%; Score 14.8; DB 6; Length 41;
Best Local Similarity 80.0%; Pred. No. 6.5e+04;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTCAATTCVGTGTCATCTGA 32
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Db 13 CTCAATTCVGTGTCATCTGA 32
   |||||:|||||

RESULT 27
LOCUS      AX520300          41 bp      DNA          linear      PAT 05-OCT-2002
DEFINITION Sequence 6498 from Patent WO02052044.
ACCESSION  AX520300
VERSION     AX520300.1 GI:23570842
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE     Detection of genetic polymorphisms
JOURNAL   Patent: WO 02052044-A 6498 04-JUL-2002;
Riken (JP)
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            /db_xref="taxon:9606"

ORIGIN

Query Match          49.3%; Score 14.8; DB 6; Length 41;
Best Local Similarity 80.0%; Pred. No. 6.5e+04;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTCAATTCVGTGTCATCTGA 32
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Db 13 CTCAATTCVGTGTCATCTGA 32
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RESULT 28
LOCUS      AR379395          46 bp      DNA          linear      PAT 18-DEC-2003
DEFINITION Sequence 53 from patent US 6607878.
ACCESSION  AR379395
VERSION     AR379395.1 GI:40087029
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 46)
AUTHORS   Soize,J.A.
TITLE     Collections of uniquely tagged molecules
JOURNAL   Patent: US 6607878-A 53 19-AUG-2003;
Riken (JP)
FEATURES   source
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ORIGIN

Query Match          49.3%; Score 14.8; DB 6; Length 46;
Best Local Similarity 73.1%; Pred. No. 6.5e+04;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGGTCATCTCACCTT 28
   |||||:|||||
Db 41 GACTCAGTCCTTGGTCATCTCACCTT 16
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RESULT 29
LOCUS      AR379396/c
DEFINITION Sequence 54 from patent US 6607878.
ACCESSION  AR379396
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VERSION AR379396.1 GI:40087030
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 46)
AUTHORS Sorge,J.A.
TITLE Collections of uniquely tagged molecules
JOURNAL Patent: US 6607878-A 54 19-AUG-2003;
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Query Match 49.3%; Score 14.8; DB 6; Length 46;
Best Local Similarity 73.1%; Pred. No. 6.5e+04;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 3 GACTCAGTCCTTGGTCATCTCACCTT 28
    ||||| ||||| ||||| |||||
Db 41 GACTCAGACCTTGTGCACTGACGTT 16
    ||||| ||||| ||||| |||||
RESULT 30
LOCUS AR379397/c 46 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 55 from patent US 6607878.
ACCESSION AR379397
VERSION AR379397.1 GI:40087031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 46)
AUTHORS Sorge,J.A.
TITLE Collections of uniquely tagged molecules
JOURNAL Patent: US 6607878-A 55 19-AUG-2003;
FEATURES
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        /mol_type="genomic DNA"
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Query Match 49.3%; Score 14.8; DB 6; Length 46;
Best Local Similarity 73.1%; Pred. No. 6.5e+04;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 3 GACTCAGTCCTTGGTCATCTCACCTT 28
    ||||| ||||| ||||| |||||
Db 41 GACTCAGACCTTGTGCACTGACGTT 16
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RESULT 31
LOCUS AR290158 47 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1893 from patent US 6537751.
ACCESSION AR290158
VERSION AR290158.1 GI:31677442
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 47)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 1893 25-MAR-2003;
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Query Match 49.3%; Score 14.8; DB 6; Length 46;
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Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 3 GACTCAGTCCTTGGTCATCTCACCTT 28
    ||||| ||||| ||||| |||||
Db 41 GACTCAGACCTTGTGCACTGACGTT 16
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RESULT 32
LOCUS BD262074 36 bp DNA linear PAT 17-JUL-2003
DEFINITION Antineoplastic viral agent containing toxin gene under regulation
ACCESSION BD262074.1 GI:33071842
VERSION BD262074.1
KEYWORDS JP 2002539796-A/17.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 36)
AUTHORS Iggo,R. and Brunori,M.
TITLE Antineoplastic viral agent containing toxin gene under regulation
JOURNAL by oncotyte-inducible transcriptional factor
JOURNAL Patent: JP 2002539796-A 17 26-NOV-2002;
COMMENT BTG INTERNATIONAL LTD
OS Artificial Sequence
PN JP 2002539796-A/17
PD 26-NOV-2002
PF 24-MAR-2000 JP 2000606768
PR 24-MAR-1999 GB 9906815.7
PI RICHARD IGGO,MICHELE BRUNORI
PC C12N15/09,A61K35/76,A61K48/00,A61P35/04,C12N7/00,C12N15/00 CC
Description of Artificial Sequence: Primer
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FT Location/Qualifiers
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    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
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Query Match 48.7%; Score 14.6; DB 6; Length 36;
Best Local Similarity 69.0%; Pred. No. 8.2e+04;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 TGGACTCAGTCCTTGGTCATCTCACCTT 29
    ||||| ||||| ||||| |||||
Db 2 TGGCGCCCGCTATTGGTCATCTGAACTTC 30
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RESULT 33
LOCUS AR303048 36 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 20 from patent US 6544507.
ACCESSION AR303048
VERSION AR303048.1 GI:31691672
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Iggo,R. and Brunori,M.A.
TITLE Anti-neoplastic viral agents
JOURNAL Patent: US 6544507-A 20 08-APR-2003;
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        /mol_type="genomic DNA"
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Query Match 48.7%; Score 14.6; DB 6; Length 36;
Best Local Similarity 69.0%; Pred. No. 8.2e+04;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 TGGACTCAGTCCTTGGTCATCTCACCTT 29
    ||||| ||||| ||||| |||||
Db 2 TGGCGCCCGCTATTGGTCATCTGAACTTC 30
    ||||| ||||| ||||| |||||
RESULT 33
LOCUS AR303048 36 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 20 from patent US 6544507.
ACCESSION AR303048
VERSION AR303048.1 GI:31691672
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Iggo,R. and Brunori,M.A.
TITLE Anti-neoplastic viral agents
JOURNAL Patent: US 6544507-A 20 08-APR-2003;
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Query Match 48.7%; Score 14.6; DB 6; Length 36;
 Best Local Similarity 69.0%; Pred. No. 8.2e+04;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGGTCATCTCACCTTC 29
 |||||
 Db 2 TGGGCCCCGCTATTGGTCATCTGAACTTC 30

RESULT 34
 AX036808
 LOCUS
 DEFINITION Sequence 20 from Patent WO0056909.
 ACCESSION AX036808
 VERSION AX036808.1 GI:11226287
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Brunori, M. and Igo, R.
 TITLE Anti-neoplastic viral agents comprising toxin gene under control of
 tumour cell-derived transcription factors
 JOURNAL Patent: WO 0056909-A 20 28-SEP-2000;
 BRUNORI MICHELE (CH); IGO RICHARD (CH); BTG INT LTD (GB)
 FEATURES Location/Qualifiers
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 /note="Primer"

ORIGIN
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 Best Local Similarity 69.0%; Pred. No. 8.2e+04;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGGTCATCTCACCTTC 29
 |||||
 Db 2 TGGGCCCCGCTATTGGTCATCTGAACTTC 30

RESULT 35
 AR443130/c
 LOCUS
 DEFINITION Sequence 28 from patent US 5670453.
 ACCESSION AR443130
 VERSION AR443130.1 GI:42670876
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 42)
 AUTHORS Frenken, L.G., Howell, S., Ledebor, A.M. and van der Logt, C.P.
 TITLE Multivalent antigen-binding proteins
 JOURNAL Patent: US 5670453-A 28 30-DEC-2003;
 FEATURES Location/Qualifiers
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 Best Local Similarity 69.0%; Pred. No. 8.1e+04;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 GGACTCAGTCCTTGGTCATCTCACCTTC 30
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 Db 41 GGAGCCAGGTCACCGTCTCTCACCTTC 13

RESULT 36

AR207700/c
 LOCUS
 DEFINITION Sequence 40 from patent US 6379897.
 ACCESSION AR207700
 VERSION AR207700.1 GI:21507522
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 49)
 AUTHORS Weidenhammer, E.M., Wang, L., Xu, X., Heller, M.J. and Kahl, B.F.
 TITLE Methods for gene expression monitoring on electronic microarrays
 JOURNAL Patent: US 6379897-A 40 30-APR-2002;
 FEATURES Location/Qualifiers
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 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 48.7%; Score 14.6; DB 6; Length 49;
 Best Local Similarity 69.0%; Pred. No. 8.1e+04;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 GGACTCAGTCCTTGGTCATCTCACCTTC 30
 |||||
 Db 43 GCACCTAGCTCTAGGTCTCTCTCCCTAT 15

RESULT 37
 AR265026/c
 LOCUS
 DEFINITION Sequence 40 from patent US 6492122.
 ACCESSION AR265026
 VERSION AR265026.1 GI:29693413
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 49)
 AUTHORS Weidenhammer, E.M., Wang, L., Xu, X., Heller, M.J. and Kahl, B.F.
 TITLE Quantitative analysis methods on active electronic microarrays
 JOURNAL Patent: US 6492122-A 40 10-DEC-2002;
 FEATURES Location/Qualifiers
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ORIGIN
 Query Match 48.7%; Score 14.6; DB 6; Length 49;
 Best Local Similarity 69.0%; Pred. No. 8.1e+04;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 GGACTCAGTCCTTGGTCATCTCACCTTC 30
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 Db 43 GCACCTAGCTCTAGGTCTCTCTCCCTAT 15

RESULT 38
 CQ008348
 LOCUS
 DEFINITION Sequence 6988 from Patent WO0147944.
 ACCESSION CQ008348
 VERSION CQ008348.1 GI:41015046
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Shimkets, R.A. and Leach, M.
 TITLE Nucleic acids containing single nucleotide polymorphisms and
 methods of use thereof
 JOURNAL Patent: WO 0147944-A 6988 05-JUL-2001;

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    Location/Qualifiers
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
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        /note="Nucleotide deleted between bases 25 and 26"
        Accession number cg4016530"
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  Query Match
  Best Local Similarity 48.7%; Score 14.6; DB 6; Length 50;
  Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 10 TCCTTGGTCATCTCACCTTCT 30
Db 3 TCCTTGGTCATCTCATCTGCT 23
RESULT 39
E12700/c
LOCUS E12700 24 bp DNA linear PAT 27-APR-1998
DEFINITION E12700
ACCESSION E12700
VERSION E12700.1 GI:3251532
KEYWORDS JP 1997056380-A/17.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
  1 (bases 1 to 24)
  Tanida,E., Oue,C., Yagi,S., Hasegawa,A., Kiyozawa,K. and Yano,A.
  ASIALOGLYCOPROTEIN RECEPTOR DERIVATIVE AND ITS USE
  Patent: JP 1997056380-A 17 04-MAR-1997;
  TONEN CORP, INTERNATL REAGENTS CORP, KIZOZAWA KENDOU
COMMENT
  OC Artificial sequences.
  PN JP 1997056380-A/17
  PD 04-MAR-1997
  PF 21-AUG-1995 JP 1995212118
  PI TANIDA EMIKO, OUE CHIHARU, YAGI SHINTARO, HASEGAWA AKIRA, PI
  KIZOZAWA KENDOU,
  YANO AKIHIKO
  PC C12N15/09,C07H21/04,C07K14/705,C12N1/21,C12N5/10,C12P21/02, PC
  G01N33/53,
  PC G01N33/566,G01N33/576,(C12N1/21,C12R1:19),(C12N5/10,C12R1:91),
  PC (C12P21/02,
  PC C12R1:19),(C12P21/02,C12R1:91);
  CC strandedness: Single;
  CC topology: Linear;
  CC hypothetical: No;
  CC Key Location/Qualifiers
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  FT source 1..24
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  FT Location/Qualifiers
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Search completed: November 23, 2004, 18:47:10
Job time : 543.225 secs
ORIGIN
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  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 AGTCCTTGGTCATCTC 23
Db 19 AGTCCTTGGTCATCTC 4
RESULT 40
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LOCUS E12696 25 bp DNA linear PAT 27-APR-1998
DEFINITION E12696
ACCESSION E12696
VERSION E12696.1 GI:3251528
KEYWORDS JP 1997056380-A/13.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
  1 (bases 1 to 25)
  Tanida,E., Oue,C., Yagi,S., Hasegawa,A., Kiyozawa,K. and Yano,A.
  ASIALOGLYCOPROTEIN RECEPTOR DERIVATIVE AND ITS USE
  Patent: JP 1997056380-A 13 04-MAR-1997;
  TONEN CORP, INTERNATL REAGENTS CORP, KIZOZAWA KENDOU
COMMENT
  OC Artificial sequences.
  PN JP 1997056380-A/13
  PD 04-MAR-1997
  PF 21-AUG-1995 JP 1995212118
  PI TANIDA EMIKO, OUE CHIHARU, YAGI SHINTARO, HASEGAWA AKIRA, PI
  KIZOZAWA KENDOU,
  YANO AKIHIKO
  PC C12N15/09,C07H21/04,C07K14/705,C12N1/21,C12N5/10,C12P21/02, PC
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  PC G01N33/566,G01N33/576,(C12N1/21,C12R1:19),(C12N5/10,C12R1:91),
  PC (C12P21/02,
  PC C12R1:19),(C12P21/02,C12R1:91);
  CC strandedness: Single;
  CC topology: Linear;
  CC hypothetical: No;
  CC Key Location/Qualifiers
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  FT source 1..25
  FT /organism="Artificial sequences".
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FEATURES
  source
    Query Match
    Best Local Similarity 93.8%; Score 14.4; DB 6; Length 25;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 AGTCCTTGGTCATCTC 23
Db 19 ACTCCTTGGTCATCTC 4
Search completed: November 23, 2004, 18:47:10
Job time : 543.225 secs
ORIGIN
  Query Match
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  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 AGTCCTTGGTCATCTC 23
Db 19 ACTCCTTGGTCATCTC 4
Search completed: November 23, 2004, 18:47:10
Job time : 543.225 secs
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:49:29 ; Search time 161.011 Seconds
(without alignments)
978.085 Million cell updates/sec

Title: US-10-087-631B-4
Perfect score: 30
Sequence: 1 tggactcagtccttggtccatccactct 30

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3992700

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq_23Sep04:*

1: Geneseqn1980s:.*
2: Geneseqn1990s:.*
3: Geneseqn2000s:.*
4: Geneseqn2001as:.*
5: Geneseqn2001bs:.*
6: Geneseqn2002as:.*
7: Geneseqn2002bs:.*
8: Geneseqn2003as:.*
9: Geneseqn2003bs:.*
10: Geneseqn2003cs:.*
11: Geneseqn2003ds:.*
12: Geneseqn2004as:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	30	100.0	30	9	ACF35783 Internal
2	30	100.0	31	6	AAD43286
3	30	100.0	31	6	AAD43738 ST2535 pr
4	19	63.3	31	4	AAD43738 ST2535 pr
5	19	63.3	33	2	AAD43738 Nucleotid
6	17.6	58.7	48	10	AAT32453 Probe, SK
7	16.8	56.0	38	10	ADK11540 RNAi prim
8	16.6	55.3	25	9	ADG78921 Schizophr
9	16.4	54.7	24	2	ACI99856 Human mic
10	16.4	54.7	46	2	AAX35233 ANF detec
11	16.2	54.0	25	9	AAX55829 PCR mutag
12	16.2	54.0	39	10	ACK23341 Human mic
13	16	53.3	25	9	ADK11540 RNAi prim
14	15.8	52.7	26	11	ADG78921 Schizophr
15	15.6	52.0	50	6	ABZ00414 Human leu
16	15.6	52.0	50	6	ABZ04927 Human leu
17	15.6	52.0	50	12	ADP12630 50-mer ol
18	15.4	51.3	25	9	ADK12515 Human mic
19	15.4	51.3	31	4	AAT30996 Human sin
20	15.2	50.7	22	6	AAD29041 Human G-p
21	15.2	50.7	22	6	AAD29038 Human G-p

c	22	15.2	50.7	22	6	ABN89142	ABN89142 Human GPC
c	23	15.2	50.7	22	6	ABN89136	ABN89136 Human GPC
c	24	15.2	50.7	22	6	ABT05749	ABT05749 GPCR rela
c	25	15.2	50.7	23	10	AAV27123	AAV27123 Synthetic
c	26	15.2	50.7	33	2	AAAL56525	AAAL56525 PCR prime
c	27	15.2	50.7	37	2	AAZ32382	AAZ32382 Receptor
c	28	15.2	50.7	39	2	AAZ32382	AAZ32382 Receptor
c	29	15.2	50.7	39	2	AAZ32382	AAZ32382 Receptor
c	30	15	50.0	50	12	ADQ4820	ADQ4820 Generic b
c	31	15	50.0	25	9	ACK06327	ACK06327 Human mic
c	32	15	50.0	25	9	ACK06326	ACK06326 Human mic
c	33	15	50.0	25	9	ACK06326	ACK06326 Human mic
c	34	15	50.0	25	9	ACK06326	ACK06326 Human mic
c	35	14.8	49.3	20	11	ADM28549	ADM28549 Adenoviru
c	36	14.8	49.3	20	11	ADM28549	ADM28549 Adenoviru
c	37	14.8	49.3	30	12	ADN7703	ADN7703 Primer KF
c	38	14.8	49.3	46	2	AAZ55831	AAZ55831 PCR mutag
c	39	14.8	49.3	46	2	AAZ55830	AAZ55830 PCR mutag
c	40	14.8	49.3	46	2	AAZ55832	AAZ55832 PCR mutag
c	41	14.6	48.7	22	4	AAF82365	AAF82365 Human Ad2
c	42	14.6	48.7	25	9	ACK23340	ACK23340 Human mic
c	43	14.6	48.7	25	9	ACK02538	ACK02538 Human mic
c	44	14.6	48.7	26	10	ADE47933	ADE47933 Human NOV
c	45	14.6	48.7	26	12	ADJ79203	ADJ79203 Human NOV
c	46	14.6	48.7	36	3	AAA94146	AAA94146 Adenoviru
c	47	14.6	48.7	36	10	ACA70974	ACA70974 Human ade
c	48	14.6	48.7	38	12	ADL65120	ADL65120 Human sin
c	49	14.6	48.7	38	12	ADL65267	ADL65267 Human sin
c	50	14.6	48.7	40	10	ABS56258	ABS56258 Chimeric
c	51	14.6	48.7	42	3	ADN00367	ADN00367 Anti-hCG
c	52	14.6	48.7	49	6	ABS98699	ABS98699 Human mac
c	53	14.6	48.7	49	6	AAZ39905	AAZ39905 Human PCR
c	54	14.6	48.7	49	8	ABX79014	ABX79014 Electroni
c	55	14.6	48.7	50	4	AAAL33780	AAAL33780 Human SNP
c	56	14.6	48.7	50	6	ABL58887	ABL58887 AMS (CTTC
c	57	14.4	48.0	24	2	AAZ76746	AAZ76746 PCR prime
c	58	14.4	48.0	24	2	AAZ76746	AAZ76746 PCR prime
c	59	14.4	48.0	25	2	AAZ76746	AAZ76746 PCR prime
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c	61	14.4	48.0	25	9	ACK01933	ACK01933 Human mic
c	62	14.4	48.0	27	2	AAV94069	AAV94069 Human IL-
c	63	14.4	48.0	34	2	AAZ62203	AAZ62203 Escherich
c	64	14.4	48.0	41	6	ABZ48082	ABZ48082 Human ATP
c	65	14.4	48.0	41	10	AAAL56519	AAAL56519 Probe 1 r
c	66	14.4	48.0	45	4	AAAL3353	AAAL3353 Mutagenic
c	67	14.4	48.0	47	6	ABK40758	ABK40758 Human obe
c	68	14.2	47.3	19	12	ADE52369	ADE52369 Mouse C5L
c	69	14.2	47.3	24	2	AAV27122	AAV27122 Synthetic
c	70	14.2	47.3	29	10	ADD69745	ADD69745 Cerebral
c	71	14.2	47.3	30	4	AAI65149	AAI65149 Canine IL
c	72	14.2	47.3	30	8	ACD27994	ACD27994 Interleuk
c	73	14.2	47.3	31	2	AAZ38921	AAZ38921 Human gen
c	74	14.2	47.3	34	12	ADQ71671	ADQ71671 3' PCR pr
c	75	14.2	47.3	34	12	ADQ71671	ADQ71671 3' PCR pr
c	76	14.2	47.3	37	6	ABK98999	ABK98999 Canine PC
c	77	14.2	47.3	39	2	AAV13826	AAV13826 Primer fo
c	78	14.2	47.3	39	2	AAZ03164	AAZ03164 PCR prime
c	79	14.2	47.3	39	2	AAZ03164	AAZ03164 PCR prime
c	80	14.2	47.3	39	4	AAI64390	AAI64390 PCR prime
c	81	14.2	47.3	45	5	AAZ93044	AAZ93044 Influenza
c	82	14.2	47.3	45	8	ABX11916	ABX11916 Influenza
c	83	14.2	47.3	45	8	ABX11916	ABX11916 Influenza
c	84	14.2	47.3	45	10	ADB84217	ADB84217 Influenza
c	85	14.2	47.3	45	10	ADA15630	ADA15630 Influenza
c	86	14.2	47.3	47	2	AAZ01112	AAZ01112 Probe for
c	87	14.2	47.3	48	2	AAQ81547	AAQ81547 Primer fo
c	88	14.2	47.3	48	2	AAQ81546	AAQ81546 Primer fo
c	89	14.2	47.3	48	2	AAZ82216	AAZ82216 Influenza
c	90	14.2	47.3	49	4	AAZ25516	AAZ25516 Multiplex
c	91	14	46.7	17	6	ABK18013	ABK18013 Human ERG
c	92	14	46.7	17	6	ABK18012	ABK18012 Human ERG
c	93	14	46.7	17	6	ABK18962	ABK18962 Human ERG
c	94	14	46.7	19	11	ADM28547	ADM28547 Adenoviru

C 95	14	46.7	22	10	ADP87368	Adf87368 Single nu	168	13.6	45.3	39	2	AA53860	Human ade
C 96	14	46.7	23	10	ADP88702	Adf88702 Reverse p	169	13.6	45.3	39	3	AAA3303	Low adeno
C 97	14	46.7	24	2	AAV04689	Aav04689 Connexin	170	13.6	45.3	39	3	AAA03705	Human ade
C 98	14	46.7	24	12	ADJ14729	Adj14729 Debrisoqu	171	13.6	45.3	39	3	AAF19425	Human ade
C 99	14	46.7	24	12	ADJ14498	Adj14498 Debrisoqu	172	13.6	45.3	39	10	ABZ95119	Human ade
100	14	46.7	24	12	ADJ060832	Adj060832 Human deb	173	13.6	45.3	39	11	ABD18990	Human ade
101	14	46.7	24	12	ADJ060987	Adj060987 Human deb	174	13.6	45.3	41	6	ABZ49716	Human sul
102	14	46.7	24	12	ADJ060600	Adj060600 Human deb	175	13.6	45.3	41	6	ABZ43563	Human sul
103	14	46.7	25	9	ACK27601	Ack27601 Human mic	176	13.6	45.3	41	6	ABO84170	Human sul
C 104	14	46.7	25	9	ACK180489	Ack180489 Human mic	177	13.6	45.3	43	12	ADJ45023	Plant CDN
C 105	14	46.7	25	9	ACK113245	Ack113245 Human mic	178	13.6	45.3	47	3	AAZ68174	Human map
C 106	14	46.7	28	6	ABK66582	Abk66582 Human gen	179	13.6	45.3	47	3	AAZ67268	Human map
C 107	14	46.7	44	2	AAAT34581	Aat34581 Forward p	180	13.6	45.3	47	3	AAZ67546	Human map
C 108	14	46.7	44	2	AAO101299	Aao101299 PCR prime	181	13.4	44.7	17	6	ABV80643	Human HTP
C 109	14	46.7	47	3	AAZ68639	Aaz68639 Human map	182	13.4	44.7	17	6	ABV80642	Human HTP
C 110	14	46.7	50	6	ABZ00894	Abz00894 Human leu	183	13.4	44.7	17	6	ABV80644	Human HTP
C 111	13.8	46.0	23	4	ADJ10396	Adj10396 Human APM	184	13.4	44.7	20	6	AAD40896	Human HDA
C 112	13.8	46.0	23	12	ADJ72582	Adj72582 Human APM	185	13.4	44.7	20	6	ADJ45023	Plant CDN
C 113	13.8	46.0	23	12	ADG14741	Adg14741 OBG3 3'UT	186	13.4	44.7	23	10	ADB61411	GPR40 DNA
C 114	13.8	46.0	24	6	ABZ30033	Abz30033 Candida a	187	13.4	44.7	24	6	ABI88834	Capture o
C 115	13.8	46.0	25	9	ACK196204	Ack196204 Human mic	188	13.4	44.7	24	6	ABI88835	Capture o
C 116	13.8	46.0	25	9	ACK12514	Ack12514 Human mic	189	13.4	44.7	25	6	ABV82648	Human HTP
C 117	13.8	46.0	28	2	AAZ24929	Aaz24929 Arabidops	190	13.4	44.7	25	6	ABV82640	Human HTP
C 118	13.8	46.0	28	3	AAA97799	Aaa97799 T. haloph	191	13.4	44.7	25	6	ABV82643	Human HTP
C 119	13.8	46.0	28	3	AAA97800	Aaa97800 T. haloph	192	13.4	44.7	25	6	ABV82645	Human HTP
C 120	13.8	46.0	29	12	ADI28588	Adi28588 Interleuk	193	13.4	44.7	25	6	ABV82639	Human HTP
C 121	13.8	46.0	36	2	AAQ11736	Aaq11736 Sequence	194	13.4	44.7	25	6	ABV82642	Human HTP
C 122	13.8	46.0	36	5	AAK61911	Aak61911 S. cerevi	195	13.4	44.7	25	6	ABV82644	Human HTP
C 123	13.8	46.0	37	12	ADJ67929	Adj67929 A. aeolic	196	13.4	44.7	25	6	ABV82643	Human HTP
C 124	13.8	46.0	37	12	ADJ68141	Adj68141 A. aeolic	197	13.4	44.7	25	6	ABV82649	Human HTP
C 125	13.8	46.0	37	12	ADK01219	Adk01219 DNA polym	198	13.4	44.7	25	6	ABV82643	Human HTP
C 126	13.8	46.0	37	12	ADJ79438	Adj79438 A. aeolic	199	13.4	44.7	25	9	ACI94384	Human mic
C 127	13.8	46.0	37	12	ADJ84878	Adj84878 Bacterial	200	13.4	44.7	25	9	ACH54631	DNA targe
C 128	13.8	46.0	37	12	ADM77566	Adm77566 DNA polym	201	13.4	44.7	25	9	ACH55566	DNA targe
C 129	13.8	46.0	37	12	ADM66333	Adm66333 A. aeolic	202	13.4	44.7	27	10	ADD01570	Human Fc
C 130	13.8	46.0	37	12	ADO04386	Ado04386 A. aeolic	203	13.4	44.7	28	2	AAAT30540	Primer 5'
C 131	13.8	46.0	37	12	ADP82463	Adp82463 Aquifex a	204	13.4	44.7	30	2	AAV57967	Human mve
C 132	13.8	46.0	41	6	ABZ45067	Abz45067 Human ATP	205	13.4	44.7	30	12	ADO12455	Single mu
C 133	13.8	46.0	41	6	ABZ45067	Abz45067 Human ATP	206	13.4	44.7	30	12	ADO12500	Single mu
C 134	13.8	46.0	47	3	AAH88371	Aah88371 CMS disor	207	13.4	44.7	30	12	ADO79909	CENPC1 PC
C 135	13.8	46.0	47	3	AAH88371	Aah88371 CMS disor	208	13.4	44.7	31	4	AAI131261	Human sin
C 136	13.8	46.0	50	5	ABJ001122	Abj001122 Human sil	209	13.4	44.7	32	6	ABL53952	Leukaemia
C 137	13.8	46.0	50	6	ABZ04509	Abz04509 Human leu	210	13.4	44.7	32	10	ADD01391	Human MLL
C 138	13.6	45.3	20	8	ABZ58618	Abz58618 Cytochrom	211	13.4	44.7	32	10	ADD01586	Human Fc
C 139	13.6	45.3	20	8	ACC43102	Acc43102 OProbe us	212	13.4	44.7	33	10	ADE36801	Rhesus ro
C 140	13.6	45.3	20	10	ADH94016	Adh94016 Human glu	213	13.4	44.7	36	4	AAD12894	Bcl-2-Igh
C 141	13.6	45.3	20	12	ADH67343	Adh67343 Human glu	214	13.4	44.7	36	4	AAD12893	Anti-sens
C 142	13.6	45.3	20	12	ADJ24395	Adj24395 Human end	215	13.4	44.7	36	4	AAO06822	5' PCR pr
C 143	13.6	45.3	22	5	AAH27178	Aah27178 PCR prime	216	13.4	44.7	37	3	AAV10819	Human MSH
C 144	13.6	45.3	22	6	ABK65145	Abk65145 PCR prime	217	13.4	44.7	39	12	ADL64388	Human sin
C 145	13.6	45.3	23	6	ABK65145	Abk65145 PCR prime	218	13.4	44.7	40	2	AAAT70652	Fibrin cl
C 146	13.6	45.3	24	6	ABO08721	Abq08721 Oligonuc	219	13.4	44.7	40	12	ADI28600	Woodchuck
C 147	13.6	45.3	24	6	ABO08721	Abq08721 Oligonuc	220	13.4	44.7	41	6	ABZ49250	Human aid
C 148	13.6	45.3	24	6	ABQ08680	Abq08680 Oligonuc	221	13.4	44.7	42	2	AAAT39249	PCR suppl
C 149	13.6	45.3	25	9	ACI13008	Act13008 Human mic	222	13.4	44.7	42	2	AAV26802	PCR suppl
C 150	13.6	45.3	25	9	ACI93221	Act93221 Human mic	223	13.4	44.7	44	5	AAF16775	EPSPS com
C 151	13.6	45.3	25	9	ACI73514	Act73514 Human mic	224	13.4	44.7	44	5	AAF16763	S. typhimu
C 152	13.6	45.3	25	9	ACI42197	Act42197 Human mic	225	13.4	44.7	45	6	AAI18943	Human CIA
C 153	13.6	45.3	25	9	ACI00251	Act00251 Human mic	226	13.4	44.7	49	3	AAZ95271	Linker fo
C 154	13.6	45.3	26	6	ABS59067	Abs59067 Human G-p	227	13.4	44.7	50	2	AAAT23193	Human gen
C 155	13.6	45.3	26	12	ADG47269	Adg47269 LTR U5 se	228	13.4	44.7	50	6	ABZ00529	Human leu
C 156	13.6	45.3	28	4	AAH91201	Aah91201 Human inf	229	13.2	44.0	19	10	ADF75536	Sense siN
C 157	13.6	45.3	28	10	ADJ33323	Adj33323 Probe rT1	230	13.2	44.0	19	10	ADF75536	Sense siN
C 158	13.6	45.3	29	2	AAQ67090	Aaq67090 Human TNF	231	13.2	44.0	20	8	ACC46996	Human pho
C 159	13.6	45.3	29	2	AAQ67211	Aaq67211 Mutant TN	232	13.2	44.0	20	10	ABZ98527	Human ICA
C 160	13.6	45.3	29	6	ABV99429	Abv99429 Human NOV	233	13.2	44.0	20	11	ABD31558	Human ICA
C 161	13.6	45.3	29	6	ADJ17702	Adj17702 Labelled	234	13.2	44.0	20	12	ADJ60377	Oligonuc1
C 162	13.6	45.3	29	12	ADN42790	Adn42790 Human NOV	235	13.2	44.0	20	12	ADJ54516	Human B7-
C 163	13.6	45.3	30	2	AAQ38558	Aaq38558 T cell re	236	13.2	44.0	20	12	ADJ23933	Human end
C 164	13.6	45.3	30	2	AAQ02263	Aaq02263 T cell re	237	13.2	44.0	20	12	ADJ23624	Human end
C 165	13.6	45.3	31	2	AAQ62562	Aaq62562 Granule b	238	13.2	44.0	20	12	ADO45866	Human oli
C 166	13.6	45.3	31	3	AAZ96707	Aaz96707 T cell an	239	13.2	44.0	21	6	ABL44254	Human chr
C 167	13.6	45.3	35	1	AAAN94233	Aaan94233 Sequence	240	13.2	44.0	21	6	ABL44254	Human chr

C 241	13.2	44.0	22	4	AAS14515	Aae14515 Human GST	314	13	43.3	29	12	AD128586	Adi28586 Interleuk
C 242	13.2	44.0	22	6	ABA00040	AbA00040 TREM-1 se	315	13	43.3	30	2	AAV19100	Aav19100 Bacillus
C 243	13.2	44.0	23	6	ABS78800	AbS78800 Human NOV	C 316-	13	43.3	30	2	AAV54150	Aav54150 Primer fo
C 244	13.2	44.0	25	9	ACI29158	ACI29158 Human mic	317	13	43.3	30	2	AAV18004	Aav18004 Primer us
C 245	13.2	44.0	25	9	ACI00355	ACI00355 Human mic	C 318	13	43.3	30	12	ADO56313	Ado56313 Human cyc
C 246	13.2	44.0	25	9	ACK10841	ACK10841 Human mic	319	13	43.3	31	8	ACD43835	ACd43835 Human gen
C 247	13.2	44.0	25	9	ACK129159	ACK129159 Human mic	320	13	43.3	32	2	AAT18048	Aat18048 Sense pri
C 248	13.2	44.0	25	9	ADA01830	AdA01830 Mouse car	321	13	43.3	32	3	AAA51225	Aaa51225 3' primer
C 249	13.2	44.0	25	10	ADP171569	ADp171569 Mouse car	322	13	43.3	32	6	ABK11956	ABk11956 E. coli v
C 250	13.2	44.0	25	12	ADP14216	ADp14216 Renal cel	C 323	13	43.3	32	10	ADF68136	Adf68136 Stabilise
C 251	13.2	44.0	26	2	AAV36894	Aav36894 Nucleotid	324	13	43.3	33	12	ADN97476	Adn97476 Attificia
C 252	13.2	44.0	26	4	AAI66798	Aai66798 Barley HV	325	13	43.3	33	10	ABZ58800	Abz58800 Cinnamyci
C 253	13.2	44.0	27	3	AAH88770	AaH88770 Respirato	326	13	43.3	34	2	AAQ87358	Aaq87358 Human fam
C 254	13.2	44.0	29	2	AAH56371	AaH56371 Streptoco	327	13	43.3	35	2	AAQ92510	Aaq92510 Human imm
C 255	13.2	44.0	30	2	AAV55607	Aav55607 Primer fo	328	13	43.3	35	2	AAV37304	Aav37304 PCR prime
C 256	13.2	44.0	30	3	AAH88769	AaH88769 Respirato	329	13	43.3	35	3	AAAL3316	Aaal3316 PCR prime
C 257	13.2	44.0	30	12	ADO79574	Ado79574 KJAA0783	330	13	43.3	35	6	ABA94788	AbA94788 HCV-AB 68
C 258	13.2	44.0	31	4	AAI30117	Aai30117 Human sin	331	13	43.3	36	6	ABK12310	ABk12310 Marinococ
C 259	13.2	44.0	34	2	AAV83986	Aav83986 PCR prime	C 332	13	43.3	36	8	ABSS8071	AbS8071 Rhodobact
C 260	13.2	44.0	34	3	AAAI4935	AaAI4935 PCR prime	333	13	43.3	36	8	ABS58072	AbS58072 Pea rbcS-
C 261	13.2	44.0	34	5	AAF85602	Aaf85602 Acremoniu	C 334	13	43.3	37	2	AAV99401	Aav99401 Oligonuc1
C 262	13.2	44.0	36	2	AAV27501	Aav27501 Streptoco	C 335	13	43.3	38	10	ADD19574	AdD19574 Oreochrom
C 263	13.2	44.0	36	6	ABQ84969	Abq84969 Streptoco	C 336	13	43.3	38	12	ADO26066	Ado26066 Arabidrops
C 264	13.2	44.0	36	10	ADC45372	Adc45372 S. pneumo	C 337	13	43.3	39	12	ADN12341	Adn12341 hagt-clon
C 265	13.2	44.0	37	12	ADI38942	Adi38942 Phosphorr	338	13	43.3	40	6	AAH48523	AaH48523 Nucleic a
C 266	13.2	44.0	41	6	ABZ45239	Abz45239 Human car	C 339	13	43.3	41	2	AAQ56317	Aaq56317 Probe for
C 267	13.2	44.0	41	6	ABZ47355	Abz47355 Human ATP	340	13	43.3	41	4	AAH74191	AaH74191 s1 RNA bi
C 268	13.2	44.0	41	6	ABZ44561	Abz44561 Human ATP	341	13	43.3	41	4	AAH74190	AaH74190 s1 RNA bi
C 269	13.2	44.0	41	6	ABZ50498	Abz50498 Human car	C 342	13	43.3	41	6	ABS60060	AbS60060 Human DNA
C 270	13.2	44.0	42	3	AAAI2095	AaAI2095 Human ICA	C 343	13	43.3	41	6	ABZ50314	Abz50314 Human cyt
C 271	13.2	44.0	44	10	ADF72048	Adf72048 Human ABC	344	13	43.3	43	2	AAV09726	Aav09726 Adenoviru
C 272	13.2	44.0	46	2	AAH55828	AaH55828 PCR mutag	C 345	13	43.3	43	8	ACC57826	Acc57826 Primer B-
C 273	13.2	44.0	46	2	AAH55834	AaH55834 PCR mutag	346	13	43.3	46	3	AAA75226	Aaa75226 Nucleotid
C 274	13.2	44.0	46	2	AAH55833	AaH55833 PCR mutag	C 347	13	43.3	46	12	ADJ14733	Adj14733 Debrisoqu
C 275	13.2	44.0	46	2	AAH55826	AaH55826 PCR mutag	C 348	13	43.3	46	12	ADJ14502	Adj14502 Debrisoqu
C 276	13.2	44.0	46	2	AAH55827	AaH55827 PCR mutag	C 349	13	43.3	46	12	ADO60836	Ado60836 Human deb
C 277	13.2	44.0	47	2	AAH55827	AaH55827 PCR mutag	C 350	13	43.3	46	12	ADO60991	Ado60991 Human deb
C 278	13.2	44.0	47	3	AAZ67175	Aaz67175 Human map	C 351	13	43.3	47	3	AAZ67200	Aaz67200 Human map
C 279	13.2	44.0	47	3	AAZ67175	Aaz67175 Human map	352	13	43.3	47	3	AAZ67200	Aaz67200 Human map
C 280	13.2	44.0	48	2	AAV13614	Aav13614 Hepatitis	353	13	43.3	47	3	AZ68460	Az68460 Human map
C 281	13.2	44.0	50	4	AAI33779	Aai33779 Human SNP	C 354	13	43.3	47	12	ADJ14732	Adj14732 Debrisoqu
C 282	13.2	44.0	50	6	ABK18525	Abk18525 Human leu	C 355	13	43.3	47	12	ADJ14501	Adj14501 Debrisoqu
C 283	13	43.3	17	6	ABK18566	Abk18566 Human ERG	C 356	13	43.3	47	12	ADO60835	Ado60835 Human deb
C 284	13	43.3	20	2	AAQ76305	Aaq76305 Neomycin-	C 357	13	43.3	47	12	ADO60603	Ado60603 Human deb
C 285	13	43.3	20	2	AAV67146	Aav67146 PCR prime	C 358	13	43.3	47	12	ADO60990	Ado60990 Human deb
C 286	13	43.3	20	8	ABS58165	AbS58165 Streptomy	359	13	43.3	48	2	AAT59754	Aat59754 Target tr
C 287	13	43.3	22	2	AZ41006	Az41006 Human cel	C 360	13	43.3	48	2	AAZ10912	Aaz10912 Probe #4
C 288	13	43.3	22	2	AZ22097	Aaz22097 Human cel	C 361	13	43.3	48	5	AAF57787	Aaf57787 Oligonuc1
C 289	13	43.3	22	8	ABV75134	Abv75134 Human CII	362	13	43.3	48	6	ABK22421	ABk22421 Human ERG
C 290	13	43.3	22	10	AAH60473	AaH60473 Human c-I	C 363	13	43.3	48	10	ADC02709	Adc02709 Ex vivo s
C 291	13	43.3	22	10	ADH76940	Adh76940 Neo F PCR	C 364	13	43.3	48	10	ADC02705	Adc02705 Ex vivo s
C 292	13	43.3	22	10	ADH76944	Adh76944 Neo F PCR	C 365	13	43.3	48	12	ADIS8384	Adi58384 Human int
C 293	13	43.3	22	10	ABV75297	Abv75297 Nucleotid	C 366	13	43.3	48	12	ADIS8380	Adi58380 Human int
C 294	13	43.3	25	3	AZ58162	Az58162 Neomycin	C 367	13	43.3	48	12	ADM28758	Adm28758 Mouse OPG
C 295	13	43.3	25	3	AAH38927	AaH38927 SNP speci	368	13	43.3	49	2	AAZ10913	Aaz10913 Probe #5
C 296	13	43.3	25	6	ABV91693	Abv91693 Human POS	C 369	13	43.3	50	2	AAQ69643	Aaq69643 Human pre
C 297	13	43.3	25	6	ABV91692	Abv91692 Human POS	C 370	13	43.3	50	2	AAT64105	Aat64105 Human pre
C 298	13	43.3	25	6	ABV91689	Abv91689 Human POS	C 371	13	43.3	50	2	AAI17393	Aai17393 Test sequ
C 299	13	43.3	25	6	ABV91691	Abv91691 Human POS	C 372	13	43.3	50	2	AAH52142	Aah52142 Synthetic
C 300	13	43.3	25	6	ABV91690	Abv91690 Human POS	C 373	13	43.3	50	2	AAH52090	Aah52090 Synthetic
C 301	13	43.3	25	9	ACI93081	ACi93081 Human mic	C 374	13	43.3	50	6	ABK82884	ABk82884 DNA bindi
C 302	13	43.3	25	9	ACK17019	ACK17019 Human mic	C 375	13	43.3	50	6	ABK30176	ABk30176 CYP2D6 ge
C 303	13	43.3	25	9	ACI81535	ACi81535 Human mic	376	13	43.3	50	6	ABZ04284	Abz04284 Human leu
C 304	13	43.3	25	9	ACI41824	ACi41824 Human mic	C 377	13	43.3	50	12	ADB80423	AdB80423 Duplex ol
C 305	13	43.3	25	9	ACK02539	ACK02539 Human mic	378	12.8	42.7	17	4	ABA80685	AbA80685 LDLR muta
C 306	13	43.3	25	9	ACI42663	ACi42663 Human mic	C 379	12.8	42.7	17	4	ABA80684	AbA80684 LDLR muta
C 307	13	43.3	25	12	ADJ93541	Adj93541 Mouse Mel	380	12.8	42.7	18	3	AAZ71666	Aaz71666 Human bla
C 308	13	43.3	26	5	AAF17192	Aaf17192 Informati	381	12.8	42.7	19	11	ADO15037	Ado15037 Human PDG
C 309	13	43.3	27	2	AAV15726	Aav15726 Primer AT	C 382	12.8	42.7	19	11	ADO14726	Ado14726 Human PDG
C 310	13	43.3	27	6	ABK18175	ABk18175 Lung spec	383	12.8	42.7	19	12	ADO61553	Ado61553 Anti-ORC1
C 311	13	43.3	29	3	AAK93141	Aak93141 29-mer ol	384	12.8	42.7	20	2	AAH24316	Aah24316 Rat bone
C 312	13	43.3	29	6	ABN81594	Abn81594 Human FGF	385	12.8	42.7	20	3	AAH87720	Aah87720 Rat LIM m
C 313	13	43.3	29	12	ADI28587	Adi28587 Interleuk	C 386	12.8	42.7	20	4	AAF62435	Aaf62435 A thalian

387	12.8	42.7	20	4	AAH45766	Aah45766 Human E2F	460	12.8	42.7	41	6	ABZ50435	Abz50435 Human cyt
388	12.8	42.7	20	8	ABT21294	Abt21294 Multiplex	C 461	12.8	42.7	41	6	ABZ43230	Abz43230 Human ATP
389	12.8	42.7	20	8	ABT43285	Abt43285 Neuroblas	462	12.8	42.7	41	8	ACC42873	Acc42873 Zinc fing
390	12.8	42.7	20	8	ABT32434	Abt32434 Neuroblas	463	12.8	42.7	41	8	ACC42874	Acc42874 Zinc fing
391	12.8	42.7	20	10	ADD68974	Add68974 Human B-c	C 464	12.8	42.7	41	10	AAI56520	Aai56520 Probe 2 r
392	12.8	42.7	20	10	ACC58348	Acc58348 Rat LIM m	465	12.8	42.7	43	2	AAV11896	Aav11896 L. lactis
393	12.8	42.7	21	2	AAX226585	Aax226585 Human pol	466	12.8	42.7	43	12	ADP67587	Adp67587 Gene aada
394	12.8	42.7	21	2	AAX24326	Aax24326 Human bon	C 467	12.8	42.7	45	2	AAT61001	Aat61001 L-galacto
395	12.8	42.7	21	3	AAZ75889	Aaz75889 Human bla	C 468	12.8	42.7	47	2	AAQ14691	Aaq14691 Sclavo pe
396	12.8	42.7	21	3	AAZ75889	Aaz75889 Human bla	C 468	12.8	42.7	47	2	AAQ14691	Aaq14691 Sclavo pe
397	12.8	42.7	21	4	AAZ75889	Aaz75889 Human bla	C 469	12.8	42.7	47	2	AAQ14691	Aaq14691 Sclavo pe
398	12.8	42.7	21	4	AAZ75889	Aaz75889 Human bla	C 470	12.8	42.7	47	3	AAZ67641	Aaz67641 Human map
399	12.8	42.7	22	10	ACC58361	Acc58361 Human LIM	471	12.8	42.7	47	5	AAF80124	Aaf80124 Primer us
400	12.8	42.7	22	4	AAI66687	Aai66687 Human CET	472	12.8	42.7	47	6	ABK40867	Abk40867 Human obe
401	12.8	42.7	23	6	ABA90543	Ab90543 Lactococc	C 473	12.8	42.7	50	4	AAI30237	Aai30237 Human SNP
402	12.8	42.7	24	3	AAH87732	Aah87732 Human LIM	C 474	12.8	42.7	50	6	ABA00181	Ab00181 Primer Sn
403	12.8	42.7	24	5	AAH21789	Aah21789 Mouse GAS	475	12.8	42.7	50	6	AB206619	Ab206619 Human leu
404	12.8	42.7	24	10	ACC58354	Acc58354 Human LIM	C 476	12.8	42.7	50	6	AB207009	Ab207009 Human leu
405	12.8	42.7	25	6	ABV93390	Abv93390 Human POS	477	12.6	42.0	19	8	ACA96045	Aca96045 Flavonoid
406	12.8	42.7	25	6	ABV93391	Abv93391 Human POS	478	12.6	42.0	20	2	AAT76856	Aat76856 Primer fo
407	12.8	42.7	25	9	ACK13150	Ack13150 Human mic	479	12.6	42.0	20	3	AAZ87094	Aaz87094 PCR prime
408	12.8	42.7	25	9	ACK193419	Ack193419 Human mic	480	12.6	42.0	20	3	AAA55485	Aaa55485 Hepatitis
409	12.8	42.7	25	9	ACK25817	Ack25817 Human mic	481	12.6	42.0	20	10	ABZ97933	Abz97933 Human RAN
410	12.8	42.7	25	9	ACT127434	Act127434 Human mic	482	12.6	42.0	20	11	ABD30964	Abd30964 Human RAN
411	12.8	42.7	25	9	ACK22696	Ack22696 Human mic	C 483	12.6	42.0	20	12	ADH67609	Adh67609 Human glu
412	12.8	42.7	25	9	ACK22697	Ack22697 Human mic	C 484	12.6	42.0	20	12	ADH67404	Adh67404 Human glu
413	12.8	42.7	25	9	ACK23762	Ack23762 Human mic	485	12.6	42.0	20	12	ADJ59798	Adj59798 Oligonuc
414	12.8	42.7	25	9	ACK183762	Ack183762 Human mic	486	12.6	42.0	20	12	ADJ24370	Adj24370 Human end
415	12.8	42.7	25	9	ACK138783	Ack138783 Human mic	487	12.6	42.0	20	12	ADO45288	Ado45288 Human oli
416	12.8	42.7	25	9	ACK194909	Ack194909 Human mic	C 488	12.6	42.0	20	12	ADP27693	Adp27693 PCR prime
417	12.8	42.7	25	9	ACK06380	Ack06380 Human mic	489	12.6	42.0	21	2	AAZ09406	Aaz09406 Human bla
418	12.8	42.7	25	9	ACK196843	Ack196843 Human mic	C 490	12.6	42.0	21	4	AAH62307	Aah62307 TAF2E pol
419	12.8	42.7	25	9	ACK25816	Ack25816 Human mic	491	12.6	42.0	21	9	AAZ58233	Aaz58233 CytoKine
420	12.8	42.7	25	9	ACK124444	Ack124444 Human mic	C 492	12.6	42.0	21	12	ADO42740	Ado42740 Human NOV
421	12.8	42.7	25	9	ACK108338	Ack108338 Human mic	493	12.6	42.0	22	2	AAV51534	Aav51534 Zee mays
422	12.8	42.7	25	9	ACK184257	Ack184257 Human mic	C 494	12.6	42.0	22	2	AAV79997	Aav79997 Primer us
423	12.8	42.7	25	9	ACK174163	Ack174163 Human mic	495	12.6	42.0	24	5	AB197683	Ab197683 Endogenou
424	12.8	42.7	25	9	ACK154881	Ack154881 Human mic	496	12.6	42.0	24	6	ABL53420	AbL53420 Pregnancy
425	12.8	42.7	25	9	ACK13151	Ack13151 Human mic	C 497	12.6	42.0	24	6	ABK89541	Abk89541 Synthetic
426	12.8	42.7	26	6	ADH49160	Adh49160 NOV64 pro	C 498	12.6	42.0	24	8	ABX12339	Abx12339 Fluoresce
427	12.8	42.7	26	2	AAZ67621	Aaz67621 Human fit	499	12.6	42.0	25	6	ABN14163	Abn14163 Human GDM
428	12.8	42.7	27	2	AAV94404	Aav94404 Canine il	500	12.6	42.0	25	6	ABN14167	Abn14167 Human GDM
429	12.8	42.7	27	6	ABZ64750	Abz64750 GPCR8 rea	C 501	12.6	42.0	25	6	ABN03487	Abn03487 Human GDM
430	12.8	42.7	28	8	AAI60796	Aai60796 Human CVS	502	12.6	42.0	25	6	ABN03488	Abn03488 Human GDM
431	12.8	42.7	28	10	ADC36293	Adc36293 Weed cont	503	12.6	42.0	25	6	ABN14162	Abn14162 Human GDM
432	12.8	42.7	28	2	AAZ10820	Aaz10820 Probe for	504	12.6	42.0	25	6	ABN14166	Abn14166 Human GDM
433	12.8	42.7	29	4	AAZ59355	Aaz59355 Human sec	505	12.6	42.0	25	6	ABN14168	Abn14168 Human GDM
434	12.8	42.7	29	5	AAZ43564	Aaz43564 Corneodes	C 507	12.6	42.0	25	6	ABN14165	Abn14165 Human GDM
435	12.8	42.7	29	6	ABA91024	Ab91024 Biotinylia	C 508	12.6	42.0	25	6	ABN03489	Abn03489 Human GDM
436	12.8	42.7	29	10	ABT15869	Abt15869 Anti-huma	C 509	12.6	42.0	25	6	ABN03486	Abn03486 Human GDM
437	12.8	42.7	29	12	ADO56421	Ado56421 Human cyc	C 510	12.6	42.0	25	6	ABN03490	Abn03490 Human GDM
438	12.8	42.7	30	6	ABK91859	Abk91859 Mouse mag	C 511	12.6	42.0	25	6	ABN14164	Abn14164 Human GDM
439	12.8	42.7	30	12	ADP08456	Adp08456 PCR prime	C 512	12.6	42.0	25	6	ABN14164	Abn14164 Human GDM
440	12.8	42.7	31	4	AAI229918	Aai229918 Human sin	C 513	12.6	42.0	25	6	AD45008	Ad45008 Peamomys
441	12.8	42.7	33	4	AAH49655	Aah49655 Protein k	C 514	12.6	42.0	25	9	ACK30579	Ack30579 Human mic
442	12.8	42.7	33	4	AAI71910	Aai71910 Human dth	515	12.6	42.0	25	9	ACK30579	Ack30579 Human mic
443	12.8	42.7	33	8	ACC42802	Acc42802 Ribosome	C 516	12.6	42.0	25	9	ACK30578	Ack30578 Human mic
444	12.8	42.7	33	8	ABX12797	Abx12797 PCR prime	517	12.6	42.0	25	9	ACI46006	Act46006 Human mic
445	12.8	42.7	33	10	ADP76129	Adp76129 Mutagenic	C 518	12.6	42.0	25	9	ACI95872	Act95872 Human mic
446	12.8	42.7	33	10	ADP76128	Adp76128 Mutagenic	519	12.6	42.0	25	9	ACI130926	Act130926 Human mic
447	12.8	42.7	38	6	ABZ52901	Abz52901 PCR prime	520	12.6	42.0	25	9	ACI130926	Act130926 Human mic
448	12.8	42.7	38	6	ABZ55063	Abz55063 Protein cho	C 521	12.6	42.0	25	9	ACK183871	Ack183871 Human mic
449	12.8	42.7	40	3	ABA97725	Ab97725 Thymus t	522	12.6	42.0	25	9	ACK05763	Ack05763 Human mic
450	12.8	42.7	40	3	AAA62656	Aaa62656 Beta-lact	523	12.6	42.0	25	9	ACI92565	Act92565 Human mic
451	12.8	42.7	40	10	ADD68840	Add68840 Bridging	C 524	12.6	42.0	25	9	ACI52834	Act52834 Human mic
452	12.8	42.7	41	4	AAH74191	Aah74191 sl RNA bi	C 525	12.6	42.0	25	12	ADP75841	Adp75841 PCR prime
453	12.8	42.7	41	4	AAH74190	Aah74190 sl RNA bi	526	12.6	42.0	26	2	AAT72340	Aat72340 Human Pap
454	12.8	42.7	41	6	ABA01655	Ab01655 Human reg	C 527	12.6	42.0	26	2	AAT72341	Aat72341 Human Pap
455	12.8	42.7	41	6	ABZ55302	Abz55302 Human mit	528	12.6	42.0	26	2	AAT72342	Aat72342 Human Pap
456	12.8	42.7	41	6	ABZ49153	Abz49153 Human ald	529	12.6	42.0	26	2	AAT72343	Aat72343 Human Pap
457	12.8	42.7	41	6	ABZ44958	Abz44958 Human ald	530	12.6	42.0	28	6	ABK98985	Abk98985 Feline PC
458	12.8	42.7	41	6	ABZ47105	Abz47105 Human ATP	531	12.6	42.0	29	8	ABZ68983	Abz68983 PCR prime
459	12.8	42.7	41	6	ABZ44885	Abz44885 Human cyt	532	12.6	42.0	30	2	AAV18700	Aav18700 Homo sapi

533	12.6	42.0	30	3	AAZ50179	Aaz50179 PCR prime	606	12.4	41.3	20	2	AAQ31848	Aeq31848 Primer GG
534	12.6	42.0	30	3	AAA46111	Aaa46111 Human G p	c 607	12.4	41.3	20	2	AAQ31840	Aeq31840 Primer bi
535	12.6	42.0	30	3	AAA46112	Aaa46112 Human G p	608	12.4	41.3	20	2	AAQ31840	Aeq31840 Primer bi
536	12.6	42.0	30	12	ADG86485	Adg86485 Human hCH	c 609	12.4	41.3	20	2	AAQ31840	Aeq31840 Primer bi
537	12.6	42.0	30	12	ADG86484	Adg86484 Human hCH	c 610	12.4	41.3	21	10	ADH72827	Adh72827 Hypoxia r
538	12.6	42.0	30	12	ADP20277	Adp20277 G protein	c 611	12.4	41.3	21	10	ADC26353	Adc26353 NOV prote
539	12.6	42.0	30	12	ADP20278	Adp20278 G protein	c 612	12.4	41.3	22	6	AAAL49024	Aal49024 Murine PA
540	12.6	42.0	31	2	ATAT38854	Atat38854 Primer fo	c 613	12.4	41.3	22	6	ABX97351	Abx97351 Human NOV
541	12.6	42.0	31	4	AAI30504	Aai30504 Human sin	c 614	12.4	41.3	22	8	ABX72401	Abx72401 Human NOV
542	12.6	42.0	31	8	ACC44511	Acc44511 HVV fragm	c 615	12.4	41.3	22	12	ADNG62254	Adng62254 Human NOV
543	12.6	42.0	32	2	AAV18399	Aav18399 Synthetic	c 616	12.4	41.3	23	2	AAAT01534	Aat01534 Human her
544	12.6	42.0	32	2	AAV59033	Aav59033 Human tra	c 617	12.4	41.3	23	3	AAAT03719	Aat03719 Human her
545	12.6	42.0	32	6	ABL91400	Abi91400 Chlamydia	c 618	12.4	41.3	23	3	AAA47528	Aaa47528 Primer fo
546	12.6	42.0	32	10	ADK71640	Adk71640 Drug-tole	c 619	12.4	41.3	23	12	ADHI0689	Adhi0689 Human CX3
547	12.6	42.0	33	2	AAQ69213	Aaq69213 Recombina	c 620	12.4	41.3	23	12	ADI44500	Adi44500 P. praten
548	12.6	42.0	33	2	AAQ59865	Aaq59865 Primer OT	c 621	12.4	41.3	24	2	AAV11542	Aav11542 Recombina
549	12.6	42.0	33	3	AAA49409	Aaa49409 Primer us	c 622	12.4	41.3	24	12	ADL70387	Adl70387 Target se
550	12.6	42.0	34	2	AAQ29333	Aaq29333 Retinoic	c 623	12.4	41.3	24	12	ADL011711	Adl011711 Single mu
551	12.6	42.0	35	1	AAV60581	Aav60581 Sequence	c 624	12.4	41.3	25	3	AAZ37265	Aaz37265 PCR prime
552	12.6	42.0	35	2	AAV08566	Aav08566 Human CSF	c 625	12.4	41.3	25	6	ABV82638	Abv82638 Human HTP
553	12.6	42.0	35	2	AAV66887	Aav66887 Human imm	c 626	12.4	41.3	25	6	ABV82650	Abv82650 Human HTP
554	12.6	42.0	35	4	AAAD10997	Aad10997 Forward p	c 627	12.4	41.3	25	6	ABV93389	Abv93389 Human POS
555	12.6	42.0	35	8	ABZ24417	Abz24417 Primer RP	c 628	12.4	41.3	25	6	ABV93388	Abv93388 Human POS
556	12.6	42.0	35	8	ABV76084	Abv76084 Primer RP	c 629	12.4	41.3	25	8	ADB03956	Adb03956 Human MDZ
557	12.6	42.0	35	10	ADD06167	Add06167 Rhabdovir	c 630	12.4	41.3	25	8	ADB03955	Adb03955 Human MDZ
558	12.6	42.0	36	6	AAAL49318	Aal49318 Rat Glut1	c 631	12.4	41.3	25	8	ADB03957	Adb03957 Human MDZ
559	12.6	42.0	37	3	AAA08890	Aaa08890 PCR prime	c 632	12.4	41.3	25	8	ADB03958	Adb03958 Human MDZ
560	12.6	42.0	37	6	ABK98987	Abk98987 Feline PC	c 633	12.4	41.3	25	9	ACI49090	Act49090 Human mlc
561	12.6	42.0	37	12	ADJ92414	Adj92414 Human Cys	c 634	12.4	41.3	25	9	ACK03973	Ack03973 Human mlc
562	12.6	42.0	37	12	ADJ92410	Adj92410 Human Cys	c 635	12.4	41.3	25	9	ACK03973	Ack03973 Human mlc
563	12.6	42.0	38	12	ADM36296	Adm36296 Modified	c 636	12.4	41.3	25	9	ACK24895	Ack24895 Human mic
564	12.6	42.0	40	2	AAT70799	Aat70799 Stenotic	c 637	12.4	41.3	25	9	ACI36583	Act36583 Human mic
565	12.6	42.0	40	2	AAT71195	Aat71195 HPV type	c 638	12.4	41.3	25	9	ACI06410	Act06410 Human mic
566	12.6	42.0	40	4	ACA91703	Act91703 Mouse fat	c 639	12.4	41.3	25	9	ACI58763	Act58763 Human mic
567	12.6	42.0	40	8	ACA61849	Act61849 Human C5a	c 640	12.4	41.3	25	9	ACI88219	Act88219 Human mic
568	12.6	42.0	40	10	ADI57945	Adi57945 Monoclonal	c 641	12.4	41.3	25	9	ACI13244	Act13244 Human mic
569	12.6	42.0	40	12	ADF90241	Adf90241 Human HMG	c 642	12.4	41.3	25	9	ACI64681	Act64681 Human mic
570	12.6	42.0	41	2	AAV26914	Aav26914 Human C5a	c 643	12.4	41.3	25	9	ACI99858	Act99858 Human mic
571	12.6	42.0	41	2	AAV50020	Aav50020 PCR prime	c 644	12.4	41.3	25	9	ACI07783	Act07783 Human mic
572	12.6	42.0	41	2	AAV18236	Aav18236 Primer #2	c 645	12.4	41.3	25	9	ACI99859	Act99859 Human mic
573	12.6	42.0	41	3	AAA88387	Aaa88387 Human C5a	c 646	12.4	41.3	25	9	ACI97509	Act97509 Human mic
574	12.6	42.0	41	4	AAV27382	Aav27382 Human C5a	c 647	12.4	41.3	25	9	ACK28622	Ack28622 Human mic
575	12.6	42.0	41	4	AAI65753	Aai65753 PCR prime	c 648	12.4	41.3	25	9	ACK27600	Ack27600 Human mic
576	12.6	42.0	41	12	ADI37091	Adi37091 Yeast cel	c 649	12.4	41.3	25	9	ACI11747	Act11747 Human mic
577	12.6	42.0	42	2	AAQ54958	Aaq54958 cyd-lacZ	c 650	12.4	41.3	25	9	ACI88218	Act88218 Human mic
578	12.6	42.0	45	8	ABT34125	Abt34125 Human pig	c 651	12.4	41.3	25	9	ACI46710	Act46710 Human mic
579	12.6	42.0	47	2	AZ010336	Aaz010336 Probe for	c 652	12.4	41.3	25	9	ACI46710	Act46710 Human mic
580	12.6	42.0	47	2	AZ010335	Aaz010335 Probe for	c 653	12.4	41.3	25	9	ACI00776	Act00776 Human mic
581	12.6	42.0	47	3	AAZ66851	Aaz66851 Human map	c 654	12.4	41.3	25	9	ACK11683	Ack11683 Human mic
582	12.6	42.0	47	10	ADF34426	Adf34426 Murine 5'	c 655	12.4	41.3	25	9	ACI86335	Act86335 Human mic
583	12.6	42.0	47	12	ADM90556	Adm90556 Mouse 5'	c 656	12.4	41.3	25	9	ACI80498	Act80498 Human mic
584	12.6	42.0	48	2	AAV15688	Aav15688 PCR prime	c 657	12.4	41.3	25	10	ADC61196	Adc61196 Full-leng
585	12.6	42.0	48	3	AAV58561	Aav58561 Human DNA	c 658	12.4	41.3	25	12	ADP15002	Adp15002 Renal cel
586	12.6	42.0	48	10	ADC02710	Adc02710 Ex vivo s	c 659	12.4	41.3	25	12	ADP15005	Adp15005 Renal cel
587	12.6	42.0	48	10	ADC02706	Adc02706 Ex vivo s	c 660	12.4	41.3	25	12	ADP15004	Adp15004 Renal cel
588	12.6	42.0	48	12	ADI58385	Adi58385 Human int	c 661	12.4	41.3	27	2	AAV74150	Aav74150 Mouse fit
589	12.6	42.0	48	12	ADI58381	Adi58381 Human int	c 662	12.4	41.3	27	2	AAV94070	Aav94070 Human IL-
590	12.6	42.0	49	10	ADFI6998	Adfi6998 Human alb	c 663	12.4	41.3	27	12	ADMA41126	Adm41126 GeneRacer
591	12.6	42.0	49	12	ADO38208	Ado38208 HIV envel	c 664	12.4	41.3	28	4	AAAD13133	Aaad13133 Human mem
592	12.6	42.0	49	12	ADO38097	Ado38097 HIV envel	c 665	12.4	41.3	28	4	AAQ83999	Aaq83999 pMON5853
593	12.6	42.0	50	2	AAV30010	Aav30010 Detector	c 666	12.4	41.3	29	3	AAA04598	Aaa04598 Polymorph
594	12.6	42.0	50	3	AAK99538	Aak99538 50-mer ol	c 667	12.4	41.3	29	6	ABV74250	Abv74250 Interleuk
595	12.6	42.0	50	4	AAAL33924	Aaal33924 Human SNP	c 668	12.4	41.3	29	6	ABV74062	Abv74062 Interleuk
596	12.6	42.0	50	6	ABZ03457	Abz03457 Human leu	c 669	12.4	41.3	29	10	ADC02673	Adc02673 Ex vivo s
597	12.6	42.0	50	6	ABZ08145	Abz08145 Human leu	c 670	12.4	41.3	29	10	ADC02107	Adc02107 Ex vivo s
598	12.4	41.3	17	6	ABV80641	Abv80641 Human HTP	c 671	12.4	41.3	29	10	ADC02374	Adc02374 Ex vivo s
599	12.4	41.3	17	6	ABV80645	Abv80645 Human HTP	c 672	12.4	41.3	29	10	ADI58348	Adi58348 Human int
600	12.4	41.3	17	6	ABV80804	Abv80804 Human mul	c 673	12.4	41.3	30	2	AAV21494	Aav21494 Plaemid p
601	12.4	41.3	17	8	ABT38793	Abt38793 Tumour su	c 674	12.4	41.3	30	4	AAH441958	Aah441958 Human WAV
602	12.4	41.3	17	10	ADE25272	Adc25272 Plant gro	c 675	12.4	41.3	30	4	AAH441958	Aah441958 Murine CA
603	12.4	41.3	19	10	ADF49915	Adf49915 Human BCL	c 676	12.4	41.3	30	10	ABZ23494	Abz23494 PCR prime
604	12.4	41.3	19	10	ADF49501	Adf49501 Human BCL	c 677	12.4	41.3	30	12	ADI37222	Adi37222 Mouse PN-
605	12.4	41.3	19	10	ABF77193	Abf77193 Mouse alp	c 678	12.4	41.3	30	12	ADP08793	Adp08793 PCR prime

C 679	12.4	41.3	30	12	ADP08806	Adp08806 PCR prime	752	12.2	40.7	19	10	ADG36508	ADG36508 HIV siNA
C 680	12.4	41.3	31	4	AA0303503	Aad03503 Dog p-gly	C 753	12.2	40.7	19	10	ADG35458	ADG35458 HIV siNA
C 681	12.4	41.3	31	10	ADL15940	Adel15940 Silkworm	754	12.2	40.7	20	3	AAA12081	AAA12081 Human ICA
C 682	12.4	41.3	32	6	ABL91396	Ab191396 Chlamydia	755	12.2	40.7	20	3	AAA61966	AAA61966 Human MEK
C 683	12.4	41.3	33	2	AAA19836	Aaa19836 Bacterioph	756	12.2	40.7	20	3	AAA61965	AAA61965 Human MEK
C 684	12.4	41.3	33	3	AAA29784	Aaa29784 Bacterioph	757	12.2	40.7	20	4	AAC67702	AAC67702 Oligonucle
C 685	12.4	41.3	33	3	AAA29784	Aaa29784 Bacterioph	C 758	12.2	40.7	20	6	AAD41824	Aad41824 Target su
C 686	12.4	41.3	33	5	AA021590	Aad21590 Bacterioph	C 759	12.2	40.7	20	6	AAD41824	Aad41824 Target su
C 687	12.4	41.3	33	8	ABZ70725	Abz70725 Human Bol	C 760	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 688	12.4	41.3	33	10	ACF57878	Acf57878 Human SCN	C 761	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 689	12.4	41.3	33	12	ADL72630	Adl72630 Foldback	C 762	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 690	12.4	41.3	35	3	AAA37474	Aaa37474 Arabidops	C 763	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 691	12.4	41.3	38	12	ADK67669	Adk67669 T7 promot	C 764	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 692	12.4	41.3	39	9	ADA15916	Ada15916 Primer fo	C 765	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 693	12.4	41.3	39	11	ABD18991	Abd18991 Human ade	C 766	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 694	12.4	41.3	41	6	ABA97154	Aba97154 Human pro	C 767	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 695	12.4	41.3	41	6	ABA97155	Aba97155 Human pro	C 768	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 696	12.4	41.3	41	6	ABA00595	Aba00595 LIM homol	C 769	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 697	12.4	41.3	41	6	ABA00596	Aba00596 LIM homol	C 770	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 698	12.4	41.3	41	6	ABZ49831	Abz49831 Human car	C 771	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 699	12.4	41.3	41	6	ABZ43647	Abz43647 Human car	C 772	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 700	12.4	41.3	41	6	ABL55242	Ab155242 Myelin P0	C 773	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 701	12.4	41.3	41	6	AA148376	Aa148376 Cytohesin	C 774	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 702	12.4	41.3	41	8	ABZ70727	Abz70727 Human Bol	C 775	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 703	12.4	41.3	41	12	ADL70390	Adl70390 Target se	C 776	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 704	12.4	41.3	42	2	AAV35222	Aav35222 E. coli G	C 777	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 705	12.4	41.3	42	2	AAV28133	Aav28133 GroEL apl	C 778	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 706	12.4	41.3	42	10	ADG44249	Adg44249 Anti-path	C 779	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 707	12.4	41.3	42	10	ADG44235	Adg44235 Anti-path	C 780	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 708	12.4	41.3	42	10	ADG44248	Adg44248 Anti-path	C 781	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 709	12.4	41.3	42	10	ADG44236	Adg44236 Anti-path	C 782	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 710	12.4	41.3	43	2	AAV19604	Aav19604 Human int	C 783	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 711	12.4	41.3	43	2	AAV19573	Aav19573 Human int	C 784	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 712	12.4	41.3	43	2	AAV15333	Aav15333 Interfero	C 785	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 713	12.4	41.3	43	2	AAV15367	Aav15367 Interfero	C 786	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 714	12.4	41.3	46	2	AAV06352	Aav06352 Phosphati	C 787	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 715	12.4	41.3	47	3	AAZ87009	Aaz87009 RBP-7 bia	C 788	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 716	12.4	41.3	47	3	AAZ66228	Aaz66228 Human map	C 789	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 717	12.4	41.3	47	3	AAZ67790	Aaz67790 Human map	C 790	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 718	12.4	41.3	47	4	AAH88369	Aah88369 CNS disor	C 791	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 719	12.4	41.3	47	4	AAI66149	Aai66149 Hepatitis	C 792	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 720	12.4	41.3	48	2	AAAT0495	Aat0495 Bacterioph	C 793	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 721	12.4	41.3	48	8	ACA09597	Aca09597 Necrosis	C 794	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 722	12.4	41.3	49	4	AAE81330	Aae81330 Human cac	C 795	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 723	12.4	41.3	50	4	AAE67710	Aae67710 HSI fragm	C 796	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 724	12.4	41.3	50	5	ABL00149	Ab100149 Human sil	C 797	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 725	12.4	41.3	50	6	ABQ95778	Abq95778 Tumour su	C 798	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 726	12.4	41.3	50	6	ABZ03330	Abz03330 Human leu	C 799	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 727	12.4	41.3	50	6	ABZ02112	Abz02112 Human leu	C 800	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 728	12.4	41.3	50	6	ABZ04715	Abz04715 Human leu	C 801	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 729	12.4	41.3	50	6	ABZ04942	Abz04942 Human leu	C 802	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 730	12.4	41.3	50	6	ABZ00546	Abz00546 Human leu	C 803	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 731	12.4	41.3	50	6	ABZ05064	Abz05064 Human leu	C 804	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 732	12.4	41.3	50	6	ABZ04065	Abz04065 Human leu	C 805	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 733	12.2	40.7	17	2	AAK63953	Aak63953 Fibrillar	C 806	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 734	12.2	40.7	17	2	AAK22660	Aak22660 Integrin	C 807	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 735	12.2	40.7	17	3	AAA36052	Aaa36052 Human gen	C 808	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 736	12.2	40.7	17	4	ABA80688	Ab80688 LDLR muta	C 809	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 737	12.2	40.7	17	4	ABA80689	Ab80689 LDLR muta	C 810	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 738	12.2	40.7	17	4	ABA80680	Ab80680 LDLR muta	C 811	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 739	12.2	40.7	17	4	ABA80681	Ab80681 LDLR muta	C 812	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 740	12.2	40.7	17	6	ABN00555	Abn00555 Human GDM	C 813	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 741	12.2	40.7	17	8	ACC65590	Acc65590 Murine ol	C 814	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 742	12.2	40.7	18	8	ACC67239	Acc67239 Murine ol	C 815	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 743	12.2	40.7	18	2	AAQ82204	Aaq82204 Chromosom	C 816	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 744	12.2	40.7	19	3	AAA83217	Aaa83217 cdk7 ribo	C 817	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 745	12.2	40.7	19	5	AAH58379	Aah58379 Cell-cycl	C 818	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 746	12.2	40.7	19	10	ADE27263	Ade27263 Stearoyl-	C 819	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 747	12.2	40.7	19	10	ADE27553	Ade27553 Stearoyl-	C 820	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 748	12.2	40.7	19	10	ADG36192	Adg36192 HIV siNA	C 821	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 749	12.2	40.7	19	10	ADG35454	Adg35454 HIV siNA	C 822	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 750	12.2	40.7	19	10	ADG36196	Adg36196 HIV siNA	C 823	12.2	40.7	20	6	AA141039	AA141039 3'UTR la
C 751	12.2	40.7	19	10	ADG35770	Adg35770 HIV siNA	C 824	12.2	40.7	20	6	AA141039	AA141039 3'UTR la

C 825	12.2	40.7	25	9	ACK14105	ACK14105 Human mic	898	12.2	40.7	31	8	ACD43689	ACD43689 Human gen
C 826	12.2	40.7	25	9	ACK51027	ACK51027 Human mic	899	12.2	40.7	32	2	AAT18046	AAT18046 Sense pri
C 827	12.2	40.7	25	9	ACK5065	ACK5065 Human mic	900	12.2	40.7	33	2	AAQ67095	AAQ67095 Human TNF
C 828	12.2	40.7	25	9	ACT196205	ACT196205 Human mic	901	12.2	40.7	33	2	AAQ67215	AAQ67215 Mutant TN
C 829	12.2	40.7	25	9	ACT180607	ACT180607 Human mic	902	12.2	40.7	33	2	AAQ7124	AAQ7124 Sense pri
C 830	12.2	40.7	25	9	ACT162221	ACT162221 Human mic	903	12.2	40.7	33	2	AAV13820	AAV13820 Primer fo
C 831	12.2	40.7	25	9	ACT192666	ACT192666 Human mic	904	12.2	40.7	33	2	AAQ03154	AAQ03154 PCR prime
C 832	12.2	40.7	25	9	ACT152734	ACT152734 Human mic	905	12.2	40.7	33	2	AAQ35617	AAQ35617 PCR prime
C 833	12.2	40.7	25	9	ACT165931	ACT165931 Human mic	906	12.2	40.7	33	2	AAQ59071	AAQ59071 MOP7 PCR
C 834	12.2	40.7	25	9	ACT104378	ACT104378 Human mic	907	12.2	40.7	33	2	AAI64380	AAI64380 PCR prime
C 835	12.2	40.7	25	9	ACT187713	ACT187713 Human mic	908	12.2	40.7	33	6	AAI51702	AAI51702 Kruppel-t
C 836	12.2	40.7	25	9	ACT178581	ACT178581 Human mic	909	12.2	40.7	33	6	ABN87529	ABN87529 Na/K aden
C 837	12.2	40.7	25	9	ACK06806	ACK06806 Human mic	910	12.2	40.7	33	9	ACFS7357	ACFS7357 Variable
C 838	12.2	40.7	25	9	ACT175396	ACT175396 Human mic	911	12.2	40.7	33	12	ADL00380	ADL00380 Antibacte
C 839	12.2	40.7	25	9	ACT175397	ACT175397 Human mic	912	12.2	40.7	34	2	AAZ34503	AAZ34503 Human LYS
C 840	12.2	40.7	25	9	ACT139293	ACT139293 Human mic	913	12.2	40.7	34	6	AAAL47815	AAAL47815 Mammalian
C 841	12.2	40.7	25	9	ACT112545	ACT112545 Human mic	914	12.2	40.7	35	2	AAV03359	AAV03359 Synthetic
C 842	12.2	40.7	25	9	ACT165537	ACT165537 Human mic	915	12.2	40.7	35	3	AAAG9507	AAAG9507 PRRSV att
C 843	12.2	40.7	25	9	ACK07270	ACK07270 Human mic	916	12.2	40.7	35	8	ACD40430	ACD40430 Human AIP
C 844	12.2	40.7	25	9	ACT141126	ACT141126 Human mic	917	12.2	40.7	35	10	ABZ23571	ABZ23571 PCR prime
C 845	12.2	40.7	25	9	ACK15818	ACK15818 Human mic	918	12.2	40.7	36	2	AAQ11735	AAQ11735 Sequence
C 846	12.2	40.7	25	9	ACT144058	ACT144058 Human mic	919	12.2	40.7	36	4	AAQ03317	AAQ03317 Human PAC
C 847	12.2	40.7	25	9	ACT148041	ACT148041 Human mic	920	12.2	40.7	36	10	ADRF69055	ADRF69055 Human bet
C 848	12.2	40.7	25	9	ACT148577	ACT148577 Human mic	921	12.2	40.7	37	2	AAQ28515	AAQ28515 Hypercalc
C 849	12.2	40.7	25	9	ACH54893	ACH54893 DNA target	922	12.2	40.7	38	12	ADP96589	ADP96589 PCR prime
C 850	12.2	40.7	25	12	ADM66525	ADM66525 Human coa	923	12.2	40.7	39	2	AAV13824	AAV13824 Primer fo
C 851	12.2	40.7	25	12	ADM66524	ADM66524 Human coa	924	12.2	40.7	39	2	AAV16046	AAV16046 PCR prime
C 852	12.2	40.7	25	12	ADP18080	ADP18080 Renal cel	925	12.2	40.7	39	2	AAV16042	AAV16042 PCR prime
C 853	12.2	40.7	25	12	ADP18079	ADP18079 Renal cel	926	12.2	40.7	39	2	AZ266899	AZ266899 Human chr
C 854	12.2	40.7	26	2	AAQ32845	AAQ32845 "Drop-in/	927	12.2	40.7	39	2	AAQ03158	AAQ03158 PCR prime
C 855	12.2	40.7	26	2	AAQ30090	AAQ30090 Sequence	928	12.2	40.7	39	2	AAZ435621	AAZ435621 PCR prime
C 856	12.2	40.7	26	2	AAQ74489	AAQ74489 Probe for	929	12.2	40.7	39	3	AAZ43301	AAZ43301 Murine ty
C 857	12.2	40.7	26	2	AAQ74564	AAQ74564 Probe for	930	12.2	40.7	39	3	AAZ43305	AAZ43305 Murine ty
C 858	12.2	40.7	26	2	AAQ74536	AAQ74536 Probe for	931	12.2	40.7	39	3	AAO5286	AAO5286 PCR prime
C 859	12.2	40.7	26	2	AAQ74550	AAQ74550 Probe for	932	12.2	40.7	39	3	AAO5290	AAO5290 PCR prime
C 860	12.2	40.7	26	2	AAQ86618	AAQ86618 Human imm	933	12.2	40.7	39	4	AAI64384	AAI64384 PCR prime
C 861	12.2	40.7	26	2	AAI15563	AAI15563 Human imm	934	12.2	40.7	40	2	AAAT70732	AAAT70732 Stenotic
C 862	12.2	40.7	26	2	AAAT40188	AAAT40188 HIV target	935	12.2	40.7	40	2	AAAT77030	AAAT77030 Hybrid DN
C 863	12.2	40.7	26	2	AAV55993	AAV55993 Human cel	936	12.2	40.7	40	10	ADD36559	ADD36559 Human pap
C 864	12.2	40.7	26	2	AAV66341	AAV66341 Human imm	937	12.2	40.7	40	12	ADD22177	ADD22177 HPV E6 ge
C 865	12.2	40.7	26	2	AAV23183	AAV23183 HIV regio	938	12.2	40.7	40	12	AD128597	AD128597 Horse int
C 866	12.2	40.7	26	10	AAQ62565	AAQ62565 Human imm	939	12.2	40.7	40	12	AD128558	AD128558 Human int
C 867	12.2	40.7	26	10	ADF43588	ADF43588 HIV detec	940	12.2	40.7	41	4	AAI68109	AAI68109 Human mit
C 868	12.2	40.7	26	10	ADF75976	ADF75976 Complement	941	12.2	40.7	41	6	ABZ48538	ABZ48538 Human oli
C 869	12.2	40.7	26	10	ADF75924	ADF75924 DNA hybr	942	12.2	40.7	41	6	ABZ45702	ABZ45702 Human ATP
C 870	12.2	40.7	26	10	ADF75990	ADF75990 RNA Hybri	943	12.2	40.7	41	6	ABZ48035	ABZ48035 Human ATP
C 871	12.2	40.7	26	10	ADF76004	ADF76004 Complement	944	12.2	40.7	41	6	ABZ44144	ABZ44144 Human NDU
C 872	12.2	40.7	26	10	ABV74096	ABV74096 HIV PCR p	945	12.2	40.7	41	6	ABZ50154	ABZ50154 Human NDU
C 873	12.2	40.7	26	12	ADO47270	ADO47270 LTR U5 se	946	12.2	40.7	41	9	ACC41985	ACC41985 Human HER
C 874	12.2	40.7	27	2	AAQ27975	AAQ27975 Primer E.	947	12.2	40.7	41	12	ADH06187	ADH06187 Gene poly
C 875	12.2	40.7	27	2	AAZ73866	AAZ73866 Mouse flt	948	12.2	40.7	41	12	ADH91974	ADH91974 1-beta-me
C 876	12.2	40.7	27	2	AAV13611	AAV13611 Hepatitis	949	12.2	40.7	46	2	AAQ80266	AAQ80266 NDF prime
C 877	12.2	40.7	27	6	ABZ63389	ABZ63389 Human Fv	950	12.2	40.7	46	2	AAZ27007	AAZ27007 Human chr
C 878	12.2	40.7	27	6	ABZ67771	ABZ67771 Antibody	951	12.2	40.7	47	2	AAAT02926	AAAT02926 Human glu
C 879	12.2	40.7	27	12	ADF91540	ADF91540 Human TNF	952	12.2	40.7	47	3	AAZ69545	AAZ69545 Human map
C 880	12.2	40.7	28	2	AAV17941	AAV17941 Simian er	953	12.2	40.7	47	3	AAZ69508	AAZ69508 Human map
C 881	12.2	40.7	28	3	AZ49126	AZ49126 PCR prime	954	12.2	40.7	47	3	AAZ67112	AAZ67112 Human map
C 882	12.2	40.7	28	10	ADG37163	ADG37163 RbA rela	955	12.2	40.7	47	3	AAZ65758	AAZ65758 Human map
C 883	12.2	40.7	29	2	AAQ94527	AAQ94527 Human/mur	956	12.2	40.7	47	3	AAAG62923	AAAG62923 PCR prime
C 884	12.2	40.7	29	2	AAQ94516	AAQ94516 Human/mur	957	12.2	40.7	48	2	AAAT29039	AAAT29039 Antisense
C 885	12.2	40.7	29	2	AAAT31756	AAAT31756 Probe for	958	12.2	40.7	48	6	ABA02540	ABA02540 Mouse bet
C 886	12.2	40.7	29	2	AAT38630	AAT38630 Chimaeric	959	12.2	40.7	49	2	AAQ69368	AAQ69368 Human pre
C 887	12.2	40.7	29	2	AAT38641	AAT38641 Chimaeric	960	12.2	40.7	49	2	AAT63830	AAT63830 Human pre
C 888	12.2	40.7	29	2	AAT42075	AAT42075 Human bet	961	12.2	40.7	49	2	AAI17118	AAI17118 Test sequ
C 889	12.2	40.7	30	3	AAAS3134	AAAS3134 Chimeric	962	12.2	40.7	49	4	AAAS09289	AAAS09289 U1A bindi
C 890	12.2	40.7	30	4	AAAF88177	AAAF88177 Murine CS	963	12.2	40.7	49	6	ABK82609	ABK82609 DNA bindi
C 891	12.2	40.7	30	8	ACC79717	ACC79717 TA p73 re	964	12.2	40.7	49	12	ADE80148	ADE80148 Duplex ol
C 892	12.2	40.7	30	12	ADO12252	ADO12252 Single mu	965	12.2	40.7	50	6	ABZ04867	ABZ04867 Human leu
C 893	12.2	40.7	30	12	ADO12298	ADO12298 Single mu	966	12.2	40.7	50	6	ABZ02936	ABZ02936 Human leu
C 894	12.2	40.7	30	12	ADO48556	ADO48556 Human neu	967	12	40.0	17	6	ABK19219	ABK19219 Human ERG
C 895	12.2	40.7	31	2	AAQ46948	AAQ46948 Chronic m	968	12	40.0	18	2	AAV30178	AAV30178 Protein k
C 896	12.2	40.7	31	2	AAV67716	AAV67716 Nucleotid	969	12	40.0	18	3	AAZ29136	AAZ29136 Primer L3
C 897	12.2	40.7	31	2	AAV67535	AAV67535 Nucleotid	970	12	40.0	20	2	AAT17556	AAT17556 Fibronect

c 971 12 40.0 20 2 AAT17566
 c 972 12 40.0 20 2 AAT17564
 c 973 12 40.0 20 2 AAX93651
 c 974 12 40.0 20 3 AAG63906
 c 975 12 40.0 20 4 AAD20444
 c 976 12 40.0 20 5 AAF69688
 c 977 12 40.0 20 5 ABA82295
 c 978 12 40.0 20 6 ABK23092
 c 979 12 40.0 20 6 ABI96132
 c 980 12 40.0 20 8 ACC45675
 c 981 12 40.0 20 10 ADB98373
 c 982 12 40.0 20 10 ABZ57978
 c 983 12 40.0 20 12 ADG98202
 c 984 12 40.0 20 12 ADI66976
 c 985 12 40.0 20 12 ADI66915
 c 986 12 40.0 20 12 ADK96478
 c 987 12 40.0 20 12 ADK96675
 c 988 12 40.0 21 2 AAV01121
 c 989 12 40.0 21 2 AAV67401
 c 990 12 40.0 21 3 AAA95916
 c 991 12 40.0 21 4 AAF96817
 c 992 12 40.0 21 4 AAH62122
 c 993 12 40.0 22 4 AAS23793
 c 994 12 40.0 22 6 ABZ30785
 c 995 12 40.0 22 10 ADF87878
 c 996 12 40.0 23 6 AAL46190
 c 997 12 40.0 23 9 ADA25523
 c 998 12 40.0 23 10 ADG29581
 c 999 12 40.0 24 2 AAV68426
 1000 12 40.0 24 2 AAX57133

ALIGNMENTS

RESULT 1
 ACF35783
 ID ACF35783 standard; DNA; 30 BP.
 XX
 AC ACF35783;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Internal control (IC)-specific probe ST2535Cy5F15.
 XX
 KW Nucleic acid purification; nucleic acid amplification; cancer;
 KW sickle cell anemia; blood screening; probe; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1 /tag= a
 FT /note= "Cys fluorophore attached to 5' terminus"
 FT modified_base 13..14 /tag= b
 FT /note= "HEX label incorporated between these nucleotides"
 FT
 PN WO2003057910-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 04-JAN-2003; 2003WO-EP000039.
 XX
 PR 08-JAN-2002; 2002US-0347327P.
 XX
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Pintel-Ober J, Wenzig P, Weindel K, Bartl K, Schoenbrunner R;
 PI Malhotra K, O'donnell P, Kyger E;
 XX WPI; 2003-587135/55.

XX Purification and amplification of target nucleic acid from biological
 PT sample used in diagnosis of cancer or in screening blood, involves
 PT binding target nucleic acid with unmodified silica surface, followed by
 PT amplification.
 XX
 PS Example 1; Page 23; 33pp; English.
 XX
 CC The invention relates to purification and amplification of target nucleic
 CC acid from biological sample. The method involves and binding target
 CC nucleic acid (TNA) in the sample with a material comprising an unmodified
 CC silica surface, separating the material from the sample and amplifying
 CC TNA in the presence of the material. The method is useful in diagnosis of
 CC certain diseases such as inherited diseases like sickle cell anemia and
 CC certain types of cancer or in screening blood for presence of target
 CC nucleic acid from virus. The method improves reaction efficiency and
 CC detection sensitivity of target nucleic acids. The present sequence
 CC represents an internal control (IC)-specific probe used in the method of
 CC the invention
 XX
 SQ Sequence 30 BP; 4 A; 10 C; 5 G; 11 T; 0 U; 0 Other;
 Query Match 100.0%; Score 30; DB 9; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
 Db 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
 RESULT 2
 AAD43286
 ID AAD43286 standard; DNA; 31 BP.
 XX
 AC AAD43286;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE ST2535 probe used to illustrate the methods of the invention.
 XX
 KW Amplification; target nucleic acid; probe; ss.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1 /tag= a
 FT /note= "Linked to Cy5 where Cy5 is Oligonucleotid-
 FT derivatisation with pentamethin-di-indocarbocyanin using
 FT alkylphosphatidyl-linker"
 FT stem_loop 2..12 /tag= b
 FT misc_binding 2..15 /tag= c
 FT /bound_moiety= "Nucleotides 12-9"
 FT misc_binding 9..12 /tag= d
 FT /bound_moiety= "Nucleotides 5-2"
 FT misc_feature 13..14 /tag= e
 FT /note= "Linked via HEXs where HEXs is Oligonucleotid-
 FT derivatisation with hexachloro-6-carboxy-fluorescein
 FT using 2-(Amino-cyclohexyl)propan-1,3-diol-linker"
 FT stem_loop 15..26 /tag= f
 FT misc_binding 15..17 /tag= g
 FT /bound_moiety= "Nucleotides 26-24"
 FT misc_binding 24..26 /tag= h
 FT /bound_moiety= "Nucleotides 17-15"
 FT modified_base 31

```

FT FT /*tag= i
FT FT /mod_base= OTHER
FT FT /note= "phosphorylated"
PN PN EPI236805-A1.
XX XX
PD PD 04-SEP-2002.
XX XX
XX XX 27-FEB-2002; 2002EP-00004483.
XX XX
XX XX 02-MAR-2001; 2001EP-00105172.
XX XX
XX XX (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX XX
XX XX Jaeger S;
XX XX
XX XX WPI; 2002-610695/66.
XX XX
XX XX Amplification of a target nucleic acid region using a specific control
XX XX sequence.
XX XX
XX XX Example 1; Fig 3; 28pp; English.
XX XX
XX XX The invention relates to a method for amplification of a target nucleic
XX XX acid region in a sample using a specific control sequence. The invention
XX XX is also directed to a method of determination of a target nucleic acid
XX XX using a special control nucleic acid. Nucleic acids of the invention are
XX XX used as a control in a reaction for amplifying target nucleic acids and
XX XX as a control in a hybridisation reaction for determination of target
XX XX nucleic acids. The present sequence is a probe used to illustrate the
XX XX methods of the invention. Note: This sequence is stated to be same as
XX XX that shown as SEQ ID NO:4 in sequence listing. However this sequence has
XX XX additional T at its 3' end
XX XX
XX XX Sequence 31 BP; 4 A; 10 C; 5 G; 12 T; 0 U; 0 Other;
XX XX
XX XX Query Match 100.0%; Score 30; DB 6; Length 31;
XX XX Best Local Similarity 100.0%; Pred. NO. 0.0017;
XX XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
Qy 1 TGGACTCAGTCCTGGTCATCTCACCTTCT 30
Db 1 TGGACTCAGTCCTGGTCATCTCACCTTCT 30
XX XX
RESULT 3
RAD43738
XX XX
XX XX AAD43738 standard; DNA; 31 BP.
XX XX
XX XX AAD43738;
XX XX
XX XX 14-NOV-2002 (first entry)
XX XX
XX XX ST535 probe to illustrate the method of the invention.
DE ST535 target nucleic acid; control nucleic acid; probe; ss.
XX XX
XX XX Amplification; target nucleic acid; control nucleic acid; probe; ss.
XX XX
XX XX Unidentified.
XX XX
XX XX Key Location/Qualifiers
XX XX misc_feature 1
XX XX /*tag= a
XX XX /note= "Linked to Cy5 where Cy5 is Oligonucleotid-
XX XX derivatisation with pentamethin-di-indocarbocyanin using
XX XX alkylphosphatidyl-linker"
XX XX 2..12
XX XX /*tag= b
XX XX 2..5
XX XX /*tag= c
XX XX /bound_moiety= "Nucleotides 12-9"
XX XX 9..12
XX XX /*tag= d
XX XX

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FT FT misc_feature /bound_moiety= "Nucleotides 5-2"
FT FT 13..14
FT FT /*tag= e
FT FT /note= "Linked via HEXs where HEXs is Oligonucleotid-
FT FT derivatisation with hexachloro-6-carboxy-fluorescein
FT FT using 2-(Amino-cyclohexyl)propan-1,3-diol-linker"
FT FT 15..26
FT FT /*tag= f
FT FT 15..17
FT FT /*tag= g
FT FT /bound_moiety= "Nucleotides 26-24"
FT FT 24..26
FT FT /*tag= h
FT FT /bound_moiety= "Nucleotides 17-15"
FT FT 31
FT FT /*tag= i
FT FT /mod_base= OTHER
FT FT /note= "Phosphorylated"
XX XX
XX XX EPI236804-A1.
XX XX
XX XX 04-SEP-2002.
XX XX
XX XX 02-MAR-2001; 2001EP-00105172.
XX XX
XX XX 02-MAR-2001; 2001EP-00105172.
XX XX (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX XX
XX XX Jaeger S;
XX XX
XX XX WPI; 2002-610694/66.
XX XX
XX XX Amplification of a target nucleic acid region using control sequences.
XX XX
XX XX Example 1; Fig 2; 29pp; English.
XX XX
XX XX The invention relates to a method for amplification of a target nucleic
XX XX acid region. The method is useful for amplification of a nucleic acid
XX XX molecule using control nucleic acid sequences. The control nucleic acid
XX XX sequences are at least in part parallel-complementary to the sequence of
XX XX the target nucleic acid. The present sequence is ST2535 probe used to the
XX XX method of the invention. Note: This sequence is stated to be same as that
XX XX shown as SEQ ID NO:4 in sequence listing. However this sequence has
XX XX additional T at its 3' end
XX XX
XX XX Sequence 31 BP; 4 A; 10 C; 5 G; 12 T; 0 U; 0 Other;
XX XX
XX XX Query Match 100.0%; Score 30; DB 6; Length 31;
XX XX Best Local Similarity 100.0%; Pred. NO. 0.0017;
XX XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
Qy 1 TGGACTCAGTCCTGGTCATCTCACCTTCT 30
Db 1 TGGACTCAGTCCTGGTCATCTCACCTTCT 30
XX XX
RESULT 4
AAH25420
XX XX ID AAH25420 standard; DNA; 31 BP.
XX XX
XX XX AAH25420;
XX XX
XX XX 22-AUG-2001 (first entry)
XX XX
XX XX Nucleotide sequence of a detection probe.
XX XX
XX XX Magnetic glass particle; nucleic acid purification; probe; ss.
XX XX
XX XX Synthetic.
XX XX
XX XX Key Location/Qualifiers
XX XX

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```
FT modified_base 1 /*tag= a
FT /*note= "derivatisation with a pentamethine-di-
FT indocarbocyanine via an alkylphosphatidyl linker"
FT misc_feature 14 /*tag= b
FT /*note= "2-(amino-cyclohexyl)-propane-1,3-diol-linker
FT derivatised with 6-carboxy-fluorescein"
FT modified_base 30 /*tag= c
FT /*note= "derivatised with a 3'-terminal phosphate group"
FT
FT PN WO200137291-A1.
FT XX
FT XX 25-MAY-2001.
FT XX
FT XX 17-NOV-2000; 2000WO-EP011459.
FT PR 17-NOV-1999; 99EP-00122853.
FT PR 12-MAY-2000; 2000EP-00110165.
FT XX
FT PA (HOFF ) ROCHE DIAGNOSTICS GMBH.
FT XX
FT PI Weindel K, Riedling M, Geiger A;
FT XX WPI; 2001-381247/40.
FT DR
FT XX Novel composition of magnetic glass particles for purification of DNA or
FT PT RNA in automated processes.
FT PS Example 7; Page 101; 105pp; English.
FT XX
FT CC The specification describes a composition of magnetic glass particles,
FT CC which contain at least one magnetic object with a mean diameter between 5
FT CC -500 nm. The composition is useful for the purification of nucleic acids.
FT CC The composition can be used to process large quantities of nucleic acid
FT CC samples, because it does not involve the particles being centrifuged or
FT CC the fluids being drawn through glass fiber filters. The present sequence
FT CC represents a probe which is used in the course of the invention
FT XX
FT SQ Sequence 31 BP; 4 A; 10 C; 5 G; 11 T; 0 U; 1 Other;
FT
FT Query Match 63.3%; Score 19; DB 4; Length 31;
FT Best Local Similarity 96.8%; Pred. No. 1.2e+02;
FT Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
FT
FT QY 1 TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
FT Db 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 31
FT
FT RESULT 5
FT AAT32453/c
FT ID AAT32453 standard; DNA; 33 BP.
FT XX
FT AC AAT32453;
FT XX
FT DT 17-JAN-1997 (first entry)
FT DE
FT DE Probe, SK535, for detection of internal quantification standard.
FT XX
FT XX Probe; internal quantification standard; amplification; detection; ss.
FT OS Synthetic.
FT XX
FT PN EP713921-A2.
FT XX
FT PD 29-MAY-1996.
FT XX
FT PF 15-NOV-1995; 95EP-00117981.
FT XX
FT PR 23-NOV-1994; 94US-00347657.
FT XX
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PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Picone TK;
XX
XX WPI; 1996-261341/27.
XX
XX Detecting a change in length of an oligonucleotide with a light-emitting
XX label - by measuring light emission in the presence of a DNA binding epd.
XX
XX Example 1; Page 11; 16pp; English.
XX
XX The present sequence is the oligonucleotide probe SK535, which is
XX hexachlorofluorescein labelled, and used for the detection of an internal
XX quantification standard (IQS). The amplification of the IQS is used to
XX prep. a standard curve, to which the amplification of an unknown sample,
XX which is detected using a fluorescein labelled probe, is compared
XX
XX SQ Sequence 33 BP; 12 A; 5 C; 11 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 63.3%; Score 19; DB 2; Length 33;
XX Best Local Similarity 96.8%; Pred. No. 1.2e+02;
XX Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX QY 1 TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
XX Db 31 TGGACTCAGTCCTTGGTCATCTCACCTTCT 1
XX
XX RESULT 6
XX ADK11540/c
XX ID ADK11540 standard; DNA; 48 BP.
XX
XX AC ADK11540;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE RNAi primer 553 for isolating Drosophila genes.
XX
XX KW ss; cytosstatic; cardiovascular; immunosuppressive; nephrotropic;
XX antirheumatic; antiarthritic; dermatological; antipsoriatic;
XX antiinflammatory; fungicide; gene therapy; Drosophila; diagnosis;
XX cardiovascular disorder; autoimmune disease; glomerulonephritis;
XX rheumatoid arthritis; dermatological disorder; psoriasis;
XX inflammatory disorder; malaria; emphysema; alopecia; primer.
XX
XX OS Drosophila melanogaster.
XX
XX PN WO20003040301-A2.
XX
XX PD 15-MAY-2003.
XX
XX PF 23-OCT-2002; 2002WO-GB004780.
XX
XX PR 05-NOV-2001; 2001GB-00026506.
XX PR 27-NOV-2001; 2001GB-00028384.
XX PR 11-FEB-2002; 2002GB-00003185.
XX
XX PA (CYCL-) CYCLACEL LTD.
XX
XX PI Deak P, Frenz L, Glover D, Midgley C;
XX
XX WPI; 2003-441540/41.
XX
XX New Drosophila polypeptides and polynucleotides, useful for diagnosing,
XX preventing and/or treating disorders, such as cancer, glomerulonephritis,
XX rheumatoid arthritis, psoriasis, malaria, emphysema and alopecia.
XX
XX PS Disclosure; Page 79; 265pp; English.
XX
XX The invention relates to novel Drosophila species DNA sequences and their
XX encoded proteins with their corresponding human homologues. The proteins
XX or their encoding polynucleotides are useful in a method of prevention,
XX treatment or diagnosis of a disease in an individual, and used to
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CC identify a substance capable of binding to the polypeptide or modulating
 CC the function of the polypeptide comprising incubating the polypeptide
 CC with a candidate substance and determining whether the substance binds to
 CC the polypeptide. The compositions are administered to an individual in
 CC need of such treatment. The method of diagnosis, in which the presence or
 CC absence of a polynucleotide is detected in a biological sample, comprises
 CC brining the biological sample containing the nucleic acid such as DNA or
 CC RNA into contact with a probe comprising a fragment of at least 15
 CC nucleotides of the polynucleotide, and detecting any duplex formed
 CC between the probe and nucleic acid in the sample. The method also
 CC comprises providing an antibody capable of binding to the polypeptide,
 CC incubating a biological sample with the antibody to allow the formation
 CC of an antibody-antigen complex, and determining whether antibody-antigen
 CC complex comprising the antibody is formed. The disease comprises a
 CC proliferative disease such as cancer. The antibody or identified
 CC substance is also useful in inhibiting the function of a polypeptide
 CC and/or regulating a cell division cycle function. The diseases also
 CC include cardiovascular disorders, autoimmune diseases such as
 CC glomerulonephritis and rheumatoid arthritis, and dermatological disorders
 CC such as psoriasis, inflammatory, fungal, and parasitic disorders such as
 CC malaria, emphysema and alopecia. The Drosophila sequences were isolated
 CC by a knockout mutation method using a P element and short interfering RNA
 CC (siRNA). Identification and isolation of the genes was done using RNAi
 CC primer targeted to the siRNA sequences. This sequence corresponds to
 CC primer used to amplify the Drosophila genes.

XX SQ Sequence 48 BP; 17 A; 11 C; 11 G; 9 T; 0 U; 0 Other;
 Query Match 58.7%; Score 17.6; DB 10; Length 48;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 4;

Qy 2 GGACTCAGTCCTTGGTCATCTCAC 25
 ||||| ||||| ||||| ||||| |||||
 Db 41 GGCCTTGGCTCTTGGTCATCTCCC 18

RESULT 7
 ADG78921/c
 ID ADG78921 standard; DNA; 38 BP.
 XX AC ADG78921;
 XX DT 11-MAR-2004 (first entry)
 XX DE Schizophrenia diagnosis method-related PCR-sequencing primer #8.
 XX KW schizophrenia; polymorphism detection; calcineurin; CN;
 XX KW CN-interacting molecule; PCR; primer; ss; sequencing.
 XX OS Unidentified.

XX PN W02003082210-A2.
 XX PD 09-OCT-2003.
 XX PF 26-MAR-2003; 2003WO-US009578.
 XX PR 26-MAR-2002; 2002US-0367944P.
 XX PR 07-MAR-2003; 2003US-0452813P.
 XX XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX PA (UVRV) UNIV ROCKEFELLER.

XX PI Gerber DJ, Karaviorgou M, Miyakawa T, Toneygawa S;
 XX WPI; 2003-803944/75.
 XX DR
 XX PT Diagnosing schizophrenia or susceptibility to schizophrenia comprises
 XX PT detecting a polymorphic variant of a polymorphism in a coding or non-
 XX PT coding portion of a gene encoding a calcineurin (CN) subunit or a CN
 XX PT interacting molecule.

PS Disclosure; Page 162; 177pp; English.
 XX CC The invention comprises a method of diagnosing schizophrenia or a
 CC susceptibility to schizophrenia. The method involves detecting a
 CC polymorphism in a gene encoding a calcineurin (CN) subunit or CN-
 CC interacting molecule. The method of the invention is useful for the
 CC diagnosis of schizophrenia or a susceptibility to schizophrenia. The
 CC present DNA sequence represents a PCR-sequencing primer that was used in
 CC the exemplification of the invention.

XX SQ Sequence 38 BP; 12 A; 13 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 56.0%; Score 16.8; DB 10; Length 38;
 Best Local Similarity 75.0%; Pred. No. 1.2e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGACTCAGTCCTTGGTCATCTCACCTTC 29
 ||||| ||||| ||||| ||||| |||||
 Db 31 GGACTCAGTATTGGTCATAGCTGTTTC 4

RESULT 8
 ACI99856
 ID ACI99856 standard; DNA; 25 BP.
 XX AC ACI99856;
 XX DT 14-OCT-2003 (first entry)
 XX DE Human microarray DNA oligonucleotide SEQ ID NO 99847.

XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 XX KW genetic variation; biallelic marker; polymorphism; human;
 XX KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.
 XX PD 05-JUN-2003.
 XX PF 15-MAR-2002; 2002US-00098263.
 XX PR 16-MAR-2001; 2001US-0276759P.
 XX PA (APFY-) APFYMATRIX INC.

XX PI Mittmann MP;
 XX WPI; 2003-567953/53.

XX PT New array of nucleic acid probes, useful for in situ hybridization, in
 XX PT Southern, Northern or dot-blot hybridization to identify or detect the
 XX PT sequence or specific mutations of any gene.

XX PS Claim 1; SEQ ID NO 99847; 9pp; English.

XX CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific

CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 3 A; 8 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 55.3%; Score 16.6; DB 9; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GACTCAGTCTTGCTGTCATCTCAC 25
|||||
DB 3 GACTCAGTCTTGCTGTCATCTC 25

RESULT 9
AAQ35233/c
ID AAQ35233 standard; DNA; 24 BP.

XX AAQ35233;
XX
XX
XX 25-MAR-2003 (revised)
DT 25-MAY-1993 (first entry)
XX
XX ANF detection primer 167-191.

XX Primer; atrial natriuretic factor; ANF; recombination; hormone; atrial;
KW cardiomyocytes; arterial pressure; cardiac output; vascular resistance;
KW intravascular volume; FOI; hypotension; familial orthostatic intolerance;
KW dizziness; mitral valve prolapse; clearance receptor; PCRFLP;
KW linkage relationship; ss.

XX Synthetic.

XX WO9300445-A1.

XX 07-JAN-1993.

XX 04-JUN-1992; 92WO-US004764.

XX 20-JUN-1991; 91US-00718006.

XX (UYVA-) UNIV VANDERBILT.

XX Phillips JA, Vnencak-Jones CL;

XX WPI; 1993-036390/04.

XX Detecting gene deletions e.g. growth hormone deficiency - comprises PCR
PT amplification of fusion fragment and enzyme digestion.

XX Disclosure; Page 30; 46pp; English.

XX The sequences given in AAQ35233-34 are primers which were used to amplify
CC the atrial natriuretic factor (ANF) gene and to detect possible
CC recombination events. ANF is a small peptide hormone synthesised by
CC atrial cardiomyocytes. Infusion of ANF in man causes decreased arterial
CC pressure due to decreased cardiac output and vascular resistance and
CC decreased intravascular volume. Individuals with familial orthostatic
CC intolerance (FOI) develop hypotension and dizziness on standing and may
CC have mitral valve prolapse. Individuals in certain FOI kindreds have
CC paradoxical increases in ANF levels on standing suggesting possible
CC abnormalities in ANF or its clearance receptors. An intragenic ANF PCRFLP
CC was identified to map ANF and its linkage relationship to FOI was
CC studied. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 24 BP; 8 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 54.7%; Score 16.4; DB 2; Length 24;

Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GTCCTTGGTCATCTCACC 26
|||||
DB 24 GTCCTTGGTCATCTCACC 7

RESULT 10
AAK55829/c

ID AAK55829 standard; DNA; 46 BP.

XX
AC AAK55829;

XX 09-JUL-1999 (first entry)

DE PCR mutagenesis primer #912 from WO9918240 Example 6.

XX Labelling; tag; molecular species; identification; property;
KW characteristic; hybridisation; amplification; PCR primer; ss.
XX Synthetic.

XX WO9918240-A2.

XX 15-APR-1999.

XX 05-OCT-1998; 98WO-US020874.

XX 06-OCT-1997; 97US-00944410.

XX (SUTRA-) STRATAGENE.

XX Sorge JA;

XX WPI; 1999-264040/22.

XX Uniquely tagged molecules identifiable by a unique property or
PT characteristic.

XX Example 6; Page 94; 138pp; English.

XX The present invention describes a composition comprising a mixture of
CC different species of molecules where each species is linked to a tag that
CC is unique to that species and that encodes at least two variable
CC positions on that species, where the tags can be identified without the
CC need for first isolating each of the tags prior to identification. Liquid
CC phase hybridisation system may be used for simultaneous identification of
CC a large subset of targets out of a very large collection of similar of
CC dissimilar molecular species. It may also be used to create tagged
CC molecules that identify any collection of molecular species, e.g.
CC peptides, antibodies, nucleic acids. Method bar codes collections or
CC probes or analytes for use in a liquid phase hybridisation method. Tagged
CC probes able to detect small changes or mutations in the target specimen.
CC Use of molecular tags overcomes difficulties of prior art methods, e.g.
CC the concentration of the probe would not be limited by the solid support,
CC both the target nucleic acids and the probes can diffuse toward each
CC other, and signal amplification through cycling reactions could occur.
CC Sequencing DNA with tags in combination with DNA amplification techniques
CC means that there is no need for traditional sequencing methods or
CC attaching to a solid phase, either the materials to be analysed or the
CC tags. The present sequence represents a PCR primer which is used in an
XX example from the present invention

SQ Sequence 46 BP; 11 A; 13 C; 12 G; 10 T; 0 U; 0 Other;

Query Match 54.7%; Score 16.4; DB 2; Length 46;

Best Local Similarity 76.9%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GACTCAGTCTTGCTGTCATCTCACCCTT 28

DB 41 GACTCAGACCTTGTGATCTGACCTT 16

RESULT 11
ACK23341
ID ACK23341 standard; DNA; 25 BP.
XX
AC ACK23341;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 123322.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
FN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
WPI; 2003-567953/53.
XX
New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
XX
Claim 1; SEQ ID NO 123322; 9pp; English.
XX
The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.
CC
Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying allelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html
XX
Sequence 25 BP; 5 A; 8 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 54.0%; Score 16.2; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7 CAGTCTTGTCATCTCACT 27
DB 5 CAGTCCGGTCACTCACTT 25

RESULT 12
ADD19586/c
ID ADD19586 standard; DNA; 39 BP.
XX
AC ADD19586;
XX
DT 15-JAN-2004 (first entry)
XX
DE Oreochromis niloticus SNP OLA primer SEQ ID NO:221.
XX
KW single nucleotide polymorphism; SNP; fish; Salmo salar;
KW Oreochromis niloticus; Atlantic halibut; microsatellite; cod;
KW polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
XX detection; primer; ss.
OS Synthetic.
OS Oreochromis niloticus.
XX
FN WO2003060160-A2.
XX
PD 24-JUL-2003.
XX
PF 17-JAN-2003; 2003WO-IB000112.
XX
PR 18-JAN-2002; 2002US-0349950P.
PR 16-AUG-2002; 2002US-0404200P.
XX
PA (GENO-) GENOMAR ASA.
XX
PI Lie O, Slettan A, Hoyum M, Lingaas F;
XX
WPI; 2003-627388/59.
XX
Novel isolated nucleic acid molecule comprising single nucleotide polymorphism associated with fish, useful for forming PCR primers which are used for detecting single nucleotide polymorphisms in fish nucleic acids.
XX
Claim 6; SEQ ID NO 221; 233pp; English.
XX
The present invention describes an isolated nucleic acid (I) comprising a single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs; (ii) a nucleic acid having nucleotide sequence that hybridises to (i), or its complement under highly stringent hybridisation conditions. Also described: (1) an isolated oligonucleotide (II) comprising at least 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O. niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod polymorphic sites and seabass polymorphic sites, or their complement; (2) a primer pair (III) suitable for use in PCR, comprising two (II) capable of amplifying a nucleotide sequence chosen from S. salar SNPs and O. niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod polymorphic sites and seabass polymorphic sites; and determining (M1) the origin of fish sample comprising providing a parent genotype database comprising a collection of candidate parent genotypes, where each of the candidate parent genotype represents a distinct origin, and comparing a sample genotype to the parent genotype database, where a match between the sample genotype and one of the candidate parent genotype identifies the origin of the sample. (M1) is useful for determining the origin of a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus, rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for detecting nucleic acid molecule comprising SNP in a sample, which involves contacting the sample containing nucleic acids with one or more (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus SNPs, and identifying nucleic acid that hybridises to (II). (II) is useful for detecting nucleic acid molecule comprising a polymorphic sequence in a sample, comprising contacting the sample containing nucleic acids with one or more (II) which is derived from O. niloticus microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic sites or seabass polymorphic sites, and identifying a nucleic acid that hybridises to (II). (III) is useful for detecting nucleic acid molecule comprising a microsatellite sequence in sample. The present sequence is used in the exemplification of the present invention.


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XX 09-JAN-2003 (first entry)
XX Human leukocyte gene expression profiling probe SEQ ID NO 405.
XX
XX T7: leukocyte; gene expression profiling; allograft rejection;
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.
XX Homo sapiens.
XX WO2000257414-A2.
XX
XX 25-JUL-2002.
XX
XX 22-OCT-2001; 2001WO-US047856.
XX
XX 20-OCT-2000; 2000US-0241994P.
XX
XX 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
XX Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quattermous T, Johnson F;
XX
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 1; Page 338; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
XX Sequence 50 BP; 8 A; 14 C; 10 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 52.0%; Score 15.6; DB 6; Length 50;
XX Best Local Similarity 70.0%; Pred. No. 4.2e+03;
XX Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX QY 1 TGGACTCAGCTCTTGGTCATCTCACCTTCT 30
XX ||||| ||||| ||||| ||||| |||||
XX Db 13 TGCACCCAGTTCCTCTTATCTCAACTTAT 42
XX
XX RESULT 16
XX ABZ04927
XX ID ABZ04927 standard; DNA; 50 BP.
XX
XX AC ABZ04927;
XX
XX DT 09-JAN-2003 (first entry)
XX
XX DE Human leukocyte gene expression profiling probe SEQ ID NO 4918.
XX
XX T7: leukocyte; gene expression profiling; allograft rejection;
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.
XX
XX Homo sapiens.
XX WO2000257414-A2.
XX
XX 25-JUL-2002.
XX
XX 22-OCT-2001; 2001WO-US047856.
XX
XX 20-OCT-2000; 2000US-0241994P.
XX
XX 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
XX Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quattermous T, Johnson F;
XX
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 1; Page 338; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
XX Sequence 50 BP; 8 A; 14 C; 10 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 52.0%; Score 15.6; DB 6; Length 50;
XX Best Local Similarity 70.0%; Pred. No. 4.2e+03;
XX Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX QY 1 TGGACTCAGCTCTTGGTCATCTCACCTTCT 30
XX ||||| ||||| ||||| ||||| |||||
XX Db 13 TGCACCCAGTTCCTCTTATCTCAACTTAT 42
XX
XX RESULT 17
XX ADP12630
XX ID ADP12630 standard; DNA; 50 BP.
XX
XX AC ADP12630;
XX
XX DT 12-AUG-2004 (first entry)
XX
XX DE 50-mer oligonucleotide array probe #13.
XX
XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; probe; ss.
XX
XX Homo sapiens.
XX WO2004042346-A2.
XX
XX 21-MAY-2004.
XX
XX 24-APR-2003; 2003WO-US012946.
XX
XX 24-APR-2002; 2002US-00131831.
XX
XX 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

```


PT of a particular phenotype or disorder (e.g. diabetes) associated with a
particular genotype.

PS Claim 1; Page 121; 145pp; English.

XX The invention relates to the identification of nucleic acid molecules
CC (AA129513-AA131314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing

XX Sequence 31 BP; 7 A; 8 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 51.3%; Score 15.4; DB 4; Length 31;

Best Local Similarity 76.0%; Pred. No. 4.7e+03;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCCTTGGTCATCTCAC 25

Db 31 TGGACTAAGCCTTGGCCATGCC 7

RESULT 20

AAD29041/c

ID AAD29041 standard; DNA; 22 BP.

XX AAD29041;

DT 07-MAY-2002 (first entry)

XX Human G-protein coupled-receptor 7 gene expressing reverse PCR primer #1.

XX G-protein coupled-receptor; GPCR; therapy; diabetes; obesity; anorexia;
KW cancer; neurodegenerative disorders; Alzheimer's; Parkinson's; dementia;
KW haematopoietic disorder; immune disorder; cardiac disorder; haemostatic;
KW Crohn's disease; angina pectoris; schizophrenia; Huntington's disease;
KW Gilles de la Tourette's syndrome; hypotension; hypertension; neuroleptic;
KW human immuno deficiency virus; HIV; neuroprotective; immunomodulatory;
KW asthma; immunogen; vaccine; nontropic; anorectic; anabolic; cytostatic;
KW depression; ulcer; cardiant; hypotensive; hypertensive; osteoporosis;
KW anticonvulsant; antiinflammatory; gastrointestinal; PCR primer; ss.

XX Homo sapiens.

XX WO200208289-A2.

XX 31-JAN-2002.

XX 26-JUL-2001; 2001WO-US023576.

XX 26-JUL-2000; 2000US-0221336P.

PR 05-OCT-2000; 2000US-0238333P.

PR 10-JAN-2001; 2001US-0260675P.

PR 22-FEB-2001; 2001US-0271025P.

PR 23-MAR-2001; 2001US-0278164P.

PR 02-APR-2001; 2001US-0280876P.

XX (CURA-) CURAGEN CORP.

XX Padigar M, Mezes P, Mishra V, Burgess C, Casman S, Smithson G;
XX WPI; 2002-148464/19.

XX New G-protein coupled-receptor polypeptides and nucleic acids encoding
XX them are useful in therapeutics e.g. cancer.

XX Example 1; Page 149; 160pp; English.

XX The present invention relates to an isolated G-protein coupled-receptor

CC

CC (GPCRX) polypeptide and its nucleic acid. GPCR is useful in treating or
CC preventing a GPCR-associated disorder and the predisposition to a
CC disease associated with altered expression levels of this polypeptide.
CC GPCR is useful for treating or preventing disorders such as; diabetes,
CC obesity, anorexia, cancer, neurodegenerative disorders, Alzheimer's,
CC Parkinson's, haematopoietic disorders, immune disorders, asthma, cardiac
CC disorders, Crohn's disease, angina pectoris, ulcer, schizophrenia,
CC depression, dementia, Huntington's disease, Gilles de la Tourette's
CC syndrome, human immuno deficiency virus (HIV), hypotension, hypertension
CC and osteoporosis. GPCR can be used as an immunogen to produce antibodies
CC specific for the invention, as vaccines and in screening for potential
CC agonistic and antagonistic compounds. The present sequence is human GPCR
CC gene expressing PCR primer

XX Sequence 22 BP; 11 A; 0 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 6; Length 22;

Best Local Similarity 85.0%; Pred. No. 5.4e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TCCTTGGTCATCTCACCTTC 29

Db 21 TCCTTTCATCTCTCCTTC 2

RESULT 21

AAD29038/c

ID AAD29038 standard; DNA; 22 BP.

XX AAD29038;

DT 07-MAY-2002 (first entry)

XX Human G-protein coupled-receptor 6a gene expressing reverse PCR primer.

XX G-protein coupled-receptor; GPCR; therapy; diabetes; obesity; anorexia;
KW cancer; neurodegenerative disorders; Alzheimer's; Parkinson's; dementia;
KW haematopoietic disorder; immune disorder; cardiac disorder; haemostatic;
KW Crohn's disease; angina pectoris; schizophrenia; Huntington's disease;
KW Gilles de la Tourette's syndrome; hypotension; hypertension; neuroleptic;
KW human immuno deficiency virus; HIV; neuroprotective; immunomodulatory;
KW asthma; immunogen; vaccine; nontropic; anorectic; anabolic; cytostatic;
KW depression; ulcer; cardiant; hypotensive; hypertensive; osteoporosis;
KW anticonvulsant; antiinflammatory; gastrointestinal; PCR primer; ss.

XX Homo sapiens.

XX WO200208289-A2.

XX 31-JAN-2002.

XX 26-JUL-2001; 2001WO-US023576.

XX 26-JUL-2000; 2000US-0221336P.

PR 05-OCT-2000; 2000US-0238333P.

PR 10-JAN-2001; 2001US-0260675P.

PR 22-FEB-2001; 2001US-0271025P.

PR 23-MAR-2001; 2001US-0278164P.

PR 02-APR-2001; 2001US-0280876P.

XX (CURA-) CURAGEN CORP.

XX Padigar M, Mezes P, Mishra V, Burgess C, Casman S, Smithson G;
XX WPI; 2002-148464/19.

XX New G-protein coupled-receptor polypeptides and nucleic acids encoding
XX them are useful in therapeutics e.g. cancer.

XX Example 1; Page 146; 168pp; English.

XX The present invention relates to an isolated G-protein coupled-receptor

CC (GPCRX) polypeptide and its nucleic acid. GPCR is useful in treating or

CC preventing a GPCR-associated disorder and the predisposition to a
 CC disease associated with altered expression levels of this polypeptide.
 CC GPCR is useful for treating or preventing disorders such as; diabetes,
 CC obesity, anorexia, cancer, neurodegenerative disorders, Alzheimer's,
 CC Parkinson's, haematopoietic disorders, immune disorders, asthma, cardiac
 CC disorders, Crohn's disease, angina pectoris, ulcer, schizophrenia,
 CC depression, dementia, Huntington's disease, Gilles de la Tourette's
 CC syndrome, human immuno deficiency virus (HIV), hypotension, hypertension
 CC and osteoporosis. GPCR can be used as an immunogen to produce antibodies
 CC specific for the invention, as vaccines and in screening for potential
 CC agonistic and antagonistic compounds. The present sequence is human GPCR
 CC gene expressing PCR primer
 XX

SQ Sequence 22 BP; 11 A; 0 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 6; Length 22;
 Best Local Similarity 85.0%; Pred. No. 5.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 TCCTTGTCATCTCACCTTC 29
 ||||| ||||| |||||
 Db 21 TCCTTCTCATCTCTCCTTC 2

RESULT 22

ABN89142/c
 ID ABN89142 standard; DNA; 22 BP.

AC ABN89142;

XX 28-AUG-2002 (first entry)

DE Human GPCR2 reverse PCR primer SEQ ID NO:82.

XX Human; GPCR; GPCR; G protein-coupled receptor; antiatherosclerotic;
 KW anorectic; antibacterial; fungicide; protozoacide; virucide; analgesic;
 KW cytotatic; immunomodulator; metabolic; antiasthmatic; antiparkinsonian;
 KW hypertensive; hypotensive; osteopathic; antiinflammatory; anti-HIV;
 KW antiinfertility; neuroprotective; antidiabetic; cardiatic; antiulcer;
 KW antiallergic; nootropic; tranquilizer; neuroleptic; antidepressant;
 KW antimanic; anticonvulsant; haemostatic; immunosuppressive; hepatotropic;
 KW cerebroprotective; dermatological; antiaddictive; gynaecological; cancer;
 KW nephrotropic; gene therapy; vaccine; developmental disease; diabetes;
 KW cardiomyopathy; atherosclerosis; neurodegenerative disorder;
 KW autoimmune disorder; infectious disease; PCR primer; ss.

OS Homo sapiens.

OS Synthetic.

XX WO200226985-A2.

PN 04-APR-2002.

PD 28-SEP-2001; 2001WO-US030552.

XX 28-SEP-2000; 2000US-0236284P.

PR 28-SEP-2000; 2000US-0236286P.

PR 03-OCT-2000; 2000US-0237581P.

PR 06-OCT-2000; 2000US-0238735P.

PR 16-OCT-2000; 2000US-0240736P.

PR 05-JAN-2001; 2001US-0260019P.

PR 08-JAN-2001; 2001US-0260338P.

PR 17-JAN-2001; 2001US-0262156P.

PR 18-JAN-2001; 2001US-0262498P.

PR 19-JAN-2001; 2001US-0263133P.

PR 24-JAN-2001; 2001US-0263691P.

PR 02-FEB-2001; 2001US-0266109P.

PR 26-FEB-2001; 2001US-0271634P.

PR 27-SEP-2001; 2001US-00965422.

XX (CURA-) CURAGEN CORP.

PA Spytek KA, Casman S, Padigar M, Dickson K, Vernet C;

XX 04-APR-2002.

PI Spaderna SK, Shenoy S, Gerlach V, Ellerman K, Edinger S;
 PI MacDougall JR, Smithson G, Li L, Malyankar UM, Taylor S, Gunther E;
 PI Tchernev VT;
 XX
 XX WPI; 2002-499868/53.
 XX Novel G-protein coupled-receptor polypeptides and nucleic acids for
 PT diagnosing, treating cardiomyopathy, atherosclerosis, cancer,
 PT neurodegenerative, autoimmune disorders, infectious diseases and
 PT diabetes.

PS Example 1; Page 158; 213pp; English.

XX ABN89112 to ABN89130 encoding the human G protein-coupled receptor
 CC (GPCR) proteins given in ABN81440 to ABN81458. GPCR proteins can have
 CC antiatherosclerotic, anorectic, antibacterial, fungicide, protozoacide,
 CC virucide, analgesic, cytotatic, immunomodulator, metabolic, hypotensive,
 CC antiasthmatic, antiparkinsonian, hypertensive, osteopathic, anti-HIV,
 CC antiinflammatory, antiinfertility, neuroprotective, antidiabetic, antiallergic,
 CC cardiatic, antiulcer, tranquilizer, neuroleptic, hepatotropic,
 CC immunosuppressive, antimanic, anticonvulsant, haemostatic, antiaddictive,
 CC nephrotropic and gynaecological activities, and can be used in vaccines
 CC and gene therapy. GPCR proteins and polynucleotides can be used for
 CC treating or preventing a GPCR-associated disorder such as
 CC cardiomyopathy, atherosclerosis, a disorder related to cell signal
 CC processing and metabolic pathway modulation, in a human. GPCR proteins
 CC and polynucleotides can also be used in the manufacture of a medicament
 CC for preventing or treating disorders or syndromes including developmental
 CC diseases, cardiomyopathy, atherosclerosis, cancer, neurodegenerative
 CC disorders, autoimmune disorders, infectious diseases and diabetes.
 CC ABN89131 to ABN89187 represent PCR primers and probes used in the
 CC exemplification of the present invention
 XX

SQ Sequence 22 BP; 11 A; 0 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 6; Length 22;
 Best Local Similarity 85.0%; Pred. No. 5.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 TCCTTGTCATCTCACCTTC 29
 ||||| ||||| |||||
 Db 21 TCCTTCTCATCTCTCCTTC 2

RESULT 23

ABN89136/c

ID ABN89136 standard; DNA; 22 BP.

XX AC ABN89136;

XX 28-AUG-2002 (first entry)

DE Human GPCR2 reverse PCR primer SEQ ID NO:76.

XX Human; GPCR; GPCR; G protein-coupled receptor; antiatherosclerotic;
 KW anorectic; antibacterial; fungicide; protozoacide; virucide; analgesic;
 KW cytotatic; immunomodulator; metabolic; antiasthmatic; antiparkinsonian;
 KW hypertensive; hypotensive; osteopathic; antiinflammatory; anti-HIV;
 KW antiinfertility; neuroprotective; antidiabetic; cardiatic; antiulcer;
 KW antiallergic; nootropic; tranquilizer; neuroleptic; antidepressant;
 KW antimanic; anticonvulsant; haemostatic; immunosuppressive; hepatotropic;
 KW cerebroprotective; dermatological; antiaddictive; gynaecological; cancer;
 KW nephrotropic; gene therapy; vaccine; developmental disease; diabetes;
 KW cardiomyopathy; atherosclerosis; neurodegenerative disorder;
 KW autoimmune disorder; infectious disease; PCR primer; ss.

OS Homo sapiens.

OS Synthetic.

XX WO200226985-A2.

PN 04-APR-2002.


```

XX PF 28-SEP-2001; 2001WO-US030552.
XX PR 28-SEP-2000; 2000US-0236284P.
XX PR 28-SEP-2000; 2000US-0236286P.
XX PR 03-OCT-2000; 2000US-0237581P.
XX PR 06-OCT-2000; 2000US-0238735P.
XX PR 16-OCT-2000; 2000US-0240736P.
XX PR 05-JAN-2001; 2001US-0260019P.
XX PR 08-JAN-2001; 2001US-0260338P.
XX PR 17-JAN-2001; 2001US-0262156P.
XX PR 18-JAN-2001; 2001US-0262498P.
XX PR 19-JAN-2001; 2001US-0263133P.
XX PR 24-JAN-2001; 2001US-0263691P.
XX PR 02-FEB-2001; 2001US-0266109P.
XX PR 26-FEB-2001; 2001US-0271634P.
XX PR 27-SEP-2001; 2001US-00965422.
XX PA (CURA-) CURAGEN CORP.
XX OS Spytek KA, Casman S, Padigar M, Dickson K, Vernet C;
XX PI Spaderna SK, Shenoy S, Gerlach V, Ellerman K, Edinger S;
XX PI McDougall JR, Smithson G, Li L, Malyankar UM, Taylor S, Gunther E;
XX PI Tchernev VT;
XX PD WPI; 2002-499868/53.
XX DR Novel G-protein coupled-receptor polypeptides and nucleic acids for
XX PT diagnosing, treating cardiomyopathy, atherosclerosis, cancer,
XX PT neurodegenerative, autoimmune disorders, infectious diseases and
XX PT diabetes.
XX PS Example 1; Page 158; 213pp; English.
XX CC ABN89112 to ABN89130 encoding the human G protein-coupled receptor
XX CC (GPCRX) proteins given in ABN81440 to ABN81458. GPCRX proteins can have
XX CC antiatherosclerotic, anorectic, antibacterial, fungicide, protozoacide,
XX CC virucide, analgesic, cytostatic, immunomodulator, metabolic, hypotensive,
XX CC antiasthmatic, antiparkinsonian, hypertensive, osteopathic, anti-HIV,
XX CC antiinflammatory, antifertility, neuroprotective, antiangiinal,
XX CC cardiant, antiulcer, antiallergic, nootropic, tranquiliser, neuroleptic,
XX CC antidepressant, antimanic, anticonvulsant, haemostatic, hepatotropic,
XX CC immunosuppressive, cerebroprotective, dermatological, antiaddictive,
XX CC nephrotropic and gynaecological activities, and can be used in vaccines
XX CC and gene therapy. GPCRX proteins and polynucleotides can be used for
XX CC treating or preventing a GPCRX-associated disorder such as
XX CC cardiomyopathy, atherosclerosis, a disorder related to cell signal
XX CC processing and metabolic pathway modulation, in a human. GPCRX proteins
XX CC and polynucleotides can also be used in the manufacture of a medicament
XX CC for preventing or treating disorders or syndromes including developmental
XX CC diseases, cardiomyopathy, atherosclerosis, cancer, neurodegenerative
XX CC disorders, autoimmune disorders, infectious diseases and diabetes.
XX CC ABN89111 to ABN89187 represent PCR primers and probes used in the
XX CC exemplification of the present invention
XX SQ Sequence 22 BP; 11 A; 0 C; 10 G; 1 T; 0 U; 0 Other;
      Query Match          50.7%; Score 15.2; DB 6; Length 22;
      Best Local Similarity 85.0%; Pred. No. 5.4e+03;
      Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 10 TCCTTGGTCATCTCACCTTC 29
Db 21 TCCTTTCATCTCTCTTC 2
RESULT 24
ABT05749/c
ID ABT05749 standard; DNA; 22 BP.
XX AC ABT05749;
XX XX
XX DT 16-OCT-2002 (first entry)

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XX DE GPCR related reverse PCR primer SEQ ID No 202.
XX KW Antidiabetic; cytostatic; anorectic; nootropic; neuroprotective; GPCRX;
XX KW antiparkinsonian; cardiant; antiarteriosclerotic; immunosuppressive;
XX KW hypotensive; haemostatic; antifertility; antiasthmatic; antiinflammatory;
XX KW anti-HIV; G-protein coupled receptor X; cardiomyopathy; atherosclerosis;
XX KW diabetes; metabolic disorder; diabetes; obesity; infectious disease;
XX KW Parkinson's disorder; immune disorder; Alzheimer's disease; dyslipidaemia;
XX KW anorexia; neurodegenerative disorder; haematopoietic disorder; obesity;
XX KW metabolic syndrome X; wasting disorder; cancer; hypertension; neoplasm;
XX KW congenital heart defect; aortic stenosis; subaortic stenosis; lymphoma;
XX KW transplacental; adrenoleukodystrophy; congenital adrenal hyperplasia;
XX KW prostate cancer; adenocarcinoma; uterus cancer; fertility; haemophilia;
XX KW hypercoagulation; idiopathic thrombocytopenic purpura; immunodeficiency;
XX KW graft versus host disease; AIDS; bronchial asthma; Crohn's disease;
XX KW multiple sclerosis; chromosomal mapping; tissue typing; forensic biology;
XX KW gene therapy; transgenic animal; PCR; primer; ss.
XX OS Unidentified.
XX XX WO200246229-A2.
XX PN 13-JUN-2002.
XX PD 05-DEC-2001; 2001WO-US046530.
XX PF 05-DEC-2000; 2000US-0251459P.
XX PR 29-DEC-2000; 2000US-0259007P.
XX PR 04-DEC-2001; 2001US-00005041.
XX PA (CURA-) CURAGEN CORP.
XX PI Casman SJ, Padigar M, Burgess CE, Shimkets RA, Spytek KA;
XX PI Gilbert JA, Mayotte JE, Baumgartner JC, Mishra V, Vernet CM;
XX PI Dickinson KS, Ballinger RA, Wolenc AR;
XX DR WPI; 2002-537559/57.
XX PT Novel isolated G-protein coupled receptor polypeptide, designated NOVX,
XX PT useful for treating or preventing in human receptor-associated disorders
XX PT e.g. cardiomyopathy, atherosclerosis or diabetes.
XX PS Example 2; Page 247; 264pp; English.
XX CC The invention relates to a novel isolated G-protein coupled receptor X
XX CC (GPCRX) polypeptide. The isolated protein, its encoding polynucleotide
XX CC and the antibody of the isolated protein is useful for treating or
XX CC preventing a GPCRX-associated disorder in a subject, preferably human,
XX CC where the disorder is cardiomyopathy, atherosclerosis or diabetes. The
XX CC isolated protein, its encoding polynucleotide and the antibody of the
XX CC isolated protein is useful for treating or preventing metabolic
XX CC disorders, diabetes, obesity, infectious disease, anorexia,
XX CC neurodegenerative disorder, Alzheimer's disease, Parkinson's disorder,
XX CC immune disorders, haematopoietic disorders, and various dyslipidaemias,
XX CC metabolic disturbances associated with obesity, the metabolic syndrome X,
XX CC wasting disorders associated with chronic diseases, and cancer. The
XX CC disorders also include cardiomyopathy, atherosclerosis, hypertension,
XX CC congenital heart defects, aortic stenosis, subaortic stenosis,
XX CC transplacental, adrenoleukodystrophy, congenital adrenal hyperplasia,
XX CC prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer,
XX CC fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic
XX CC purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial
XX CC asthma, Crohn's disease, and multiple sclerosis. The isolated protein,
XX CC its encoding polynucleotide and the antibody of the isolated protein is
XX CC useful in screening assays, detection assays (e.g., chromosomal mapping,
XX CC tissue typing, forensic biology). The isolated polynucleotide is useful
XX CC in gene therapy, to express the isolated protein, to detect GPCRX mRNA or
XX CC a genetic lesion in a GPCRX gene, and to modulate GPCRX activity. The
XX CC cell of the invention is useful for producing non-human transgenic
XX CC animals. This polynucleotide sequence represents a reverse PCR primer of
XX CC a GPCRX protein of the invention

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SQ Sequence 22 BP; 11 A; 0 C; 10 G; 1 T; 0 U; 0 Other;
Query Match 50.7%; Score 15.2; DB 6; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 10 TCCTTGGTCATCTCACCTTC 29
DB 21 TCCTTTCATCTCTCCTTC 2

RESULT 25
AAV27123/c
ID AAV27123 standard; DNA; 24 BP.
XX
AC AAV27123;
XX
DT 28-SEP-1998 (first entry)
XX
DE Synthetic human prollyl-4-hydroxylase PCR primer.
XX
KW collagen III; yeast expression vector; production; prollyl-4-hydroxylase;
KW PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9818918-A1.
XX
PD 07-MAY-1998.
XX
PF 29-OCT-1997; 97WO-AU000721.
XX
PR 29-OCT-1996; 96AU-00003310.
PR 19-DEC-1996; 96AU-00004306.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Vaughan PR, Galanis M, Ramshaw JAM, Werkmeister JA;
XX WPI; 1998-272214/24.
XX
PT Stable expression of hydroxylated triple helical proteins - using yeast
PT transformed with nucleotide sequences encoding prollyl 4-hydroxylase
PT subunits and products such as collagen polypeptides.
XX
PS Example 1; Page 11; 45pp; English.
XX
CC The sequence is that of a PCR primer which was used in the construction
CC of a yeast vector for the co-ordinated co-expression of the alpha and
CC beta subunits of Prollyl-4-hydroxylase
XX
SQ Sequence 24 BP; 9 A; 4 C; 10 G; 1 T; 0 U; 0 Other;
Query Match 50.7%; Score 15.2; DB 2; Length 24;
Best Local Similarity 85.0%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 10 TCCTTGGTCATCTCACCTTC 29
DB 20 TCCTTGGTCACCTCCCTTC 1

RESULT 26
AAL56525/c
ID AAL56525 standard; DNA; 33 BP.
XX
AC AAL56525;
XX
DT 04-DEC-2003 (first entry)
XX
DE PCR primer 1b related to human clathrin light chain polypeptide 9-02.
XX

KW Human clathrin light chain polypeptide-9.02; cancer; HIV infection; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN CN1381482-A.
XX
PD 27-NOV-2002.
XX
PF 18-APR-2001; 2001CN-00112630.
XX
PR 18-APR-2001; 2001CN-00112630.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2003-258235/26.
XX
PT Polypeptide-clathrin light chain -9.02 and polynucleotide for coding it.
PS Disclosure; Page 31; Opp; Chinese.
XX
CC This invention relates to a clathrin light chain polypeptide-9.02 and the
CC nucleotide sequence encoding the polypeptide of the invention. The
CC polypeptide may be used to treat diseases such as cancer and HIV
CC infection. The present sequence is that of PCR primer 1b related to the
CC human clathrin light chain polypeptide-9.02 of the invention and used in
CC example 5 of the specification. Note: This sequence, assigned Seq ID 5 in
CC the sequence listing differs from Seq ID 5 in example 5 of the
CC specification. The alternative sequence is given in AAL56517
XX
SQ Sequence 33 BP; 12 A; 10 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 50.7%; Score 15.2; DB 10; Length 33;
Best Local Similarity 71.4%; Pred. No. 5.8e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3 GACTCAGTCCTTGGTCATCTCACCTTCT 30
DB 32 GAGTCAGTCCTTGGTCATCTCACCTTCT 5

RESULT 27
AAZ32382/c
ID AAZ32382 standard; DNA; 37 BP.
XX
AC AAZ32382;
XX
DT 26-JAN-2000 (first entry)
XX
DE Receptor construct IR-Delta-685 sense PCR primer.
XX
KW Receptor construct; soluble insulin receptor; IgG; immunoglobulin G;
KW fusion protein; insulin binding protein; growth factor; PCR primer;
KW insulin specific tyrosine kinase; screening; mimetic; ss.
XX
OS Synthetic.
XX
PN EP957164-A1.
XX
PD 17-NOV-1999.
XX
PF 15-MAY-1998; 98EP-00201633.
XX
PR 15-MAY-1998; 98EP-00201633.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Kristensen C;
XX
DR WPI; 1999-621951/54.
XX

PT Polypeptides used for the screening of ligands capable of binding to an
 XX insulin specific tyrosine kinase.
 PS Example 1; Page 7; 17pp; English.
 XX The present invention describes a polypeptide (I), with a molecular
 CC weight of 40-100KD, which is capable of binding to insulin. Also
 CC described are: (1) a fusion polypeptide comprising (I) and another
 CC polypeptide capable of facilitating expression, purification and/or
 CC crystallisation of the polypeptide; (2) a process of producing a
 CC polypeptide, where a cell containing a recombinant expression vector
 CC comprising a DNA fragment encoding (I), is cultured to promote the
 CC expression of (I), (I) being recovered from the culture; and (3) an
 CC insulin mimetic which has insulin activity when bound to an insulin
 CC receptor in vivo, and which is capable of binding to (I). (I) is used for
 CC the screening of ligands binding to the polypeptide, and for screening
 CC for insulin mimetics. The insulin mimetics isolated may be oral insulin
 CC mimetics which can be formulated into tablets or other oral medicaments.
 CC The polypeptide due to its size, may be co-crystallised with insulin
 CC making it possible to obtain knowledge of the structure- activity
 CC relationship. The present sequence represents a PCR primer used in the
 CC construction of receptor constructs, which are expressed as soluble
 CC insulin receptor (IR) immunoglobulin G (IgG) fusion proteins, in the
 CC exemplification of the present invention
 XX
 SQ Sequence 37 BP; 12 A; 11 C; 8 G; 6 T; 0 U; 0 Other;
 Query Match 50.7%; Score 15.2; DB 2; Length 37;
 Best Local Similarity 71.4%; Pred. No. 6e+03;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 3 GACTCAGCTCTGGTCATCTACCTTCT 30
 DB 29 GAGTCTGCTTTGGACAGCTAGCCTTGT 2
 RESULT 28
 AAT91980
 ID AAT91980 standard; DNA; 39 BP.
 XX
 AC AAT91980;
 XX
 DT 13-FEB-1998 (first entry)
 DE Primer 8 for rat thrombomodulin DNA amplification.
 KW rat; thrombomodulin; thrombin; activation; protein C;
 KW recombinant production; PCR primer; amplify; ss.
 XX
 OS Synthetic.
 XX JP09268200-A.
 XX 14-OCT-1997.
 XX
 PF 01-APR-1996; 96JP-00078494.
 XX
 PR 01-APR-1996; 96JP-00078494.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 DR WPI; 1997-554712/51.
 XX
 PT Recombinant production of rat thrombomodulin - which promotes thrombin
 PT activation of protein C.
 XX
 PS Example 3; Page 22; 28pp; Japanese.
 XX
 CC This PCR primer was used to amplify DNA encoding rat thrombomodulin (TM).
 CC TM upon binding thrombin, promotes thrombin activation of protein C. Host
 CC cells transformed with the DNA can be used for the large scale
 CC recombinant production of the peptide, or rat thrombomodulin
 XX

SQ Sequence 39 BP; 11 A; 12 C; 7 G; 9 T; 0 U; 0 Other;
 Query Match 50.7%; Score 15.2; DB 2; Length 39;
 Best Local Similarity 85.0%; Pred. No. 6e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7 CAGTCCTTGGTCATCTACCC 26
 DB 14 CAGTCCTTGGTCATCTGACC 33
 RESULT 29
 ADQ94820
 ID ADQ94820 standard; DNA; 50 BP.
 XX
 AC ADQ94820;
 XX
 DT 23-SEP-2004 (first entry)
 DE Generic binding agent associated primer seqid 13.
 DE binding agent; beta barrel conformation; replicable vector;
 KW binding agent library; machine-accessible medium; immunoassay; PCR;
 KW primer; ss.
 XX
 OS Synthetic.
 XX
 PN US2004126769-A1.
 XX
 PD 01-JUL-2004.
 XX
 PF 30-DEC-2002; 2002US-00335181.
 XX
 PR 30-DEC-2002; 2002US-00335181.
 XX
 PA (QUIR/) QUIRK S.
 XX
 PI Quirk S;
 XX
 DR WPI; 2004-591378/57.
 XX
 PT New isolated binding agents, useful for binding, detecting or identifying
 PT a target molecule (e.g. antigen or antigenic epitope), or for detecting
 PT or isolating a target in a sample suspected of containing the target.
 XX
 PS Example 1; SEQ ID NO 13; 60pp; English.
 XX
 CC The invention describes an isolated binding agent comprising a
 CC polypeptide: having an amino acid sequence selected from 2 sequences of
 CC 134 amino acids (SEQ ID NO: 2 and 4) given in the specification; or
 CC having a beta barrel conformation, where the polypeptide comprises a
 CC sequence of 134 amino acids (SEQ ID NO: 37) given in the specification.
 CC Also described are: an isolated nucleic acid encoding SEQ ID NO: 2 or 4,
 CC or comprising SEQ ID NO: 25, 26, 27, 28 or 29 (sequences not defined in
 CC the specification); an expression vector comprising a promoter and a
 CC nucleic acid encoding a polypeptide comprising SEQ ID NO: 2, 4 or 37; a
 CC library of binding agents where each binding agent in the library
 CC comprises a polypeptide comprising SEQ ID NO: 2 or 37; making a library
 CC of binding agent nucleic acids; making a library of replicable vectors
 CC that encode binding agent polypeptides; making a library of binding agent
 CC polypeptides; a computer implemented method of making a library of
 CC binding agents; a system for generating peptide sequences; and a machine-
 CC accessible medium. The specifically claimed binding agent comprises a
 CC sequence selected from 2 fully defined sequences of 134 amino acids (SEQ
 CC ID NO: 2 and 4) given in the specification. The binding agents can be
 CC used to bind, detect or identify a target molecule, such as an antigen or
 CC antigenic epitope, to detect or isolate a target in a sample suspected of
 CC containing the target, in immunoassays where antibodies are commonly
 CC employed. This sequence represents a primer used in the creation of
 CC generic binding agent DNA ADQ94810.
 XX
 SQ Sequence 50 BP; 9 A; 13 C; 11 G; 17 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 12; Length 50;
Best Local Similarity 71.4%; Pred. No. 6.3e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTGGTTCATCTCACCCTTCT 30
| | | | | | | | | | | | | | | | | | | |
Db 6 GACTCTGTTAAAGGTCGTTTCCACCATCT 33

RESULT 30
ACK06327
ID ACK06327 standard; DNA; 25 BP.
XX
AC ACK06327;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 106308.
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 106308; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 3 A; 8 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 50.0%; Score 15; DB 9; Length 25;
Best Local Similarity 78.3%; Pred. No. 6.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTCTGTCATCTC 23
| | | | | | | | | | | | | | | | | | | |
Db 3 TGGACCCTCTACTTGGTCTTCTC 25

RESULT 31
ACK06326
ID ACK06326 standard; DNA; 25 BP.
XX
AC ACK06326;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 106307.
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 106307; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 2 A; 8 C; 4 G; 11 T; 0 U; 0 Other;

QY 1 TGGACTCAGTCTTGGTCATCTC 23
Db 3 TGGACCCCTCTTCTGGTCTCTC 25

RESULT 32
ACI99857
ID ACI99857 standard; DNA; 25 BP.
XX AC ACI99857;
XX 14-OCT-2003 (first entry)
XX Human microarray DNA oligonucleotide SEQ ID NO 99848.
DE EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX Homo sapiens.
OS US2003104410-A1.
PN 05-JUN-2003.
PD 15-MAR-2002; 2002US-00098263.
XX 16-MAR-2001; 2001US-0276759P.
PR (APFY-) APFYMATRIX INC.
XX Mittmann MP;
PI WPI; 2003-567953/53.
DR New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX Claim 1; SEQ ID NO 99848; 9pp; English.

CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX Sequence 25 BP; 4 A; 8 C; 6 G; 7 T; 0 U; 0 Other;
SQ Query Match 50.0%; Score 15; DB 9; Length 25;
Best Local Similarity 78.3%; Pred. No. 6.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTGGTCATCTC 25
|||||

Db 3 GACTCAGTCCTAGGTCGTCTCTC 25

RESULT 33
ADM35884
ID ADM35884 standard; DNA; 42 BP.
XX AC ADM35884;
XX 03-JUN-2004 (first entry)
XX Human RANTES/ER retention signal PCR primer, SEQ ID NO:28.
DE Human; RANTES; chemokine; chemokine receptor 5; CCR5;
XX expression inhibition; intracellular immunisation; animal model;
KW HIV-1 resistant phenotype; HIV-1 infection;
KW chemokine receptor-related disease; anti-HIV; gene therapy;
KW endoplasmic reticulum retention signal; PCR; primer; ss.
XX Homo sapiens.
OS Synthetic.
OS WO2004013330-A1.
PN 12-FEB-2004.
PD 10-JUL-2003; 2003WO-ES000350.
XX 26-JUL-2002; 2002ES-00001776.
PR (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX (GENE-) GENETRIX SL.
XX Gonzalez De La Pena MA, Serrano Gomez F, Abad Minguez JL;
PI Bernard Miana A, Llorente Gomez MDLM, Martinez Alonso C;
PI Garmendia Mendizabal C;
XX WPI; 2004-157133/15.

PT New genetic construct that inhibits expression of the CCR5 receptor,
PT useful for preparing vectors for gene therapy of human immune deficiency
PT virus infection and a murine model of immunization.
XX Example 15; SEQ ID NO 28; 92pp; Spanish.

CC The invention relates to a genetic construct that, when expressed
CC intracellularly, specifically inhibits expression of the human chemokine
CC receptor CCR5. The genetic construct may encode a ribozyme directed
CC against the CCR5 mRNA (ADM35860), or a multicatalytic ribozyme containing
CC several consecutive functional units from one or more ribozymes
CC (ADM35869). In addition to a ribozyme, the construct may also encode the
CC chemokine RANTES which is modified to contain an endoplasmic reticulum
CC retention signal (ADM35872) and which is preferably mutated to inactivate
CC its signalling properties. Alternatively, the genetic construct of the
CC invention may encode an N-terminal part of CCR5 (including 2-6
CC transmembrane domains) with an endoplasmic reticulum retention signal and
CC in which the region corresponding to the extracellular part is replaced
CC with a domain which binds the N-terminal region of CCR5 (such as RANTES),
CC and the construct may additionally encode an anti-CCR5 ribozyme in the
CC 3'UTR. The invention also relates to a eukaryotic expression vector or a
CC retroviral vector containing a genetic construct of the invention; a
CC eukaryotic cell transformed with the vector; and an animal model of
CC intracellular immunisation against HIV-1 developed from NOD/Scid mice
CC using the vectors. The genetic constructs of the invention inhibit
CC surface expression of CCR5, thereby mimicking the phenotype of HIV-1
CC resistance in individuals where CCR5 is inactivated by mutation. The
CC constructs are used to prepare expression or retroviral vectors for the
CC establishment of a murine model of intracellular immunisation against HIV
CC to test the effectiveness of the genetic constructs in restricting
CC infection with macrophage-tropic strains of HIV-1. The vectors may also
CC be used in gene therapy of humans who are seropositive for HIV-1,
CC particularly in the early stages of infection, or who have a disease that
CC involves chemokine receptors closely related, structurally and


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XX Human; calmodulin 9.02; phosphatidylinositol signal pathway dysfunction;  
KW PCR; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX CN1333273-A.  
XX  
XX 30-JAN-2002.  
XX  
XX 07-JUL-2000; 2000CN-00117090.  
XX  
XX 07-JUL-2000; 2000CN-00117090.  
PR (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.  
XX  
XX Mao Y, Xie Y;  
XX WPI; 2002-305590/35.  
XX  
XX Novel polypeptide human calmodulin 9.02 and polynucleotide for encoding  
PT said polypeptide.  
XX  
XX Example 2; Page 18 (Disclosure); 33pp; Chinese.  
XX  
XX The invention relates to human calmodulin 9.02 (AB883796), the  
CC polynucleotide (ABN85528) encoding said polypeptide and the method for  
CC producing this polypeptide by recombinant DNA technology. The invention  
CC also discloses the method for curing several diseases, such as  
CC phosphatidylinositol signal pathway dysfunction related diseases by the  
CC polypeptide. The invention also discloses an antagonist for resisting the  
CC polypeptide and its therapeutic action and the application of  
CC polynucleotide coding this novel human calmodulin 9.02. The present  
CC sequence is that of a human calmodulin 9.02 PCR primer, useful in  
CC examples of the invention  
XX  
SQ Sequence 24 BP; 0 A; 10 C; 3 G; 11 T; 0 U; 0 Other;  
Query Match 49.3%; Score 14.8; DB 6; Length 24;  
Best Local Similarity 88.9%; Pred. No. 8.3e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 12 CTTGGTCATCTCACCTTC 29  
Db 1 CTTGGTCATCTCACCTTC 18  
RESULT 37  
ADN97703  
ID ADN97703 standard; DNA; 30 BP.  
XX  
XX ADN97703;  
XX  
XX 15-JUL-2004 (first entry)  
DT Primer KP43.  
DE  
XX  
XX antibacterial; immunosuppressive; antirheumatic; antiarthritic;  
KW antihelminthic; insecticide; biosynthesis; macrolide; antibiotic;  
KW spiramycin; veterinary medicine; immunosuppressant; transplant rejection;  
KW rheumatoid arthritis; autoimmune disease; insecticide; antihelminthic;  
KW avermectin; primer; ss.  
XX  
XX Streptomyces ambofaciens.  
OS  
XX WO2004033689-A2.  
PN  
XX 22-APR-2004.  
XX  
XX 08-OCT-2003; 2003WO-FR002962.  
PF  
XX 08-OCT-2003; 2002FR-00012489.  
XX  
PR 27-FEB-2003; 2003FR-00002439.  
PR
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PR 07-AUG-2003; 2003US-0493490P.  
XX (AVET ) AVENTIS PHARMA SA.  
PA (CNRS.) CNRS.  
XX  
XX Blondelet-Rouault M, Dominguez H, Darbon-Rongere E, Gerbaud C;  
PI Gondran A, Karray F, Lacroix P, Oestreicher-Mermet- Bouvier N;  
PI Pernodet J, Tuphile K;  
XX WPI; 2004-330455/30.  
XX  
XX New polynucleotides encoding proteins involved in spiramycin  
PT biosynthesis, useful for improving synthesis of macrolide antibiotics or  
PT for generating new hybrid macrolides.  
XX  
XX Example 28; SEQ ID NO 154; 480pp; French.  
XX  
XX The invention relates to polynucleotides that encode polypeptides  
CC involved in biosynthesis of the macrolide antibiotic spiramycin (A), or  
CC equivalents within the degeneracy of the genetic code. The  
CC polynucleotides and polypeptides are used: (a) to improve production  
CC (optionally also purity) of macrolides (M), especially spiramycins; and  
CC (b) to produce hybrid antibiotics. The macrolides are useful in human and  
CC veterinary medicine as antibiotics, but some are also immunosuppressants  
CC (e.g. FK506) useful for treating transplant rejection, rheumatoid  
CC arthritis and other autoimmune diseases; or insecticides and  
CC anthelmintics (e.g. avermectin). This sequence corresponds to a PCR  
CC primer to amplify the spiramycin biosynthetic genes from Streptomyces  
CC ambofaciens.  
XX  
SQ Sequence 30 BP; 5 A; 9 C; 6 G; 10 T; 0 U; 0 Other;  
Query Match 49.3%; Score 14.8; DB 12; Length 30;  
Best Local Similarity 88.9%; Pred. No. 8.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 11 CTTGGTCATCTCACCTT 28  
Db 13 CTTGGTCATCTCGCCTT 30  
RESULT 38  
AAX55831/c  
ID AAX55831 standard; DNA; 46 BP.  
XX  
XX AAX55831;  
XX  
XX 09-JUL-1999 (first entry)  
DT  
XX  
XX PCR mutagenesis primer #914 from WO9918240 Example 6.  
DE  
XX  
XX Labelling; tag; molecular species; identification; property;  
KW characteristic; hybridisation; amplification; PCR primer; ss.  
XX  
XX Synthetic.  
OS  
XX WO9918240-A2.  
PN  
XX 15-APR-1999.  
PD  
XX 05-OCT-1998; 98WO-US020874.  
PF  
XX 06-OCT-1997; 97US-00944410.  
PR  
XX (STRA-) STRATAGENE.  
PA  
XX Sorge JA;  
PI  
XX WPI; 1999-264040/22.  
DR  
XX Uniquely tagged molecules identifiable by a unique property or  
PT characteristic.  
XX
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PS Example 6; Page 94; 138pp; English.
XX
CC The present invention describes a composition comprising a mixture of
CC different species of molecules where each species is linked to a tag that
CC is unique to that species and that encodes at least two variable
CC positions on that species, where the tags can be identified without the
CC need for first isolating each of the tags prior to identification. Liquid
CC phase hybridisation system may be used for simultaneous identification of
CC a large subset of targets out of a very large collection of similar of
CC dissimilar molecular species. It may also be used to create tagged
CC molecules that identify any collection of molecular species, e.g.
CC peptides, antibodies, nucleic acids. Method bar codes collections or
CC probes or analytes for use in a liquid phase hybridisation method. Tagged
CC probes able to detect small changes or mutations in the target specimen.
CC Use of molecular tags overcomes difficulties of prior art methods, e.g.
CC the concentration of the probe would not be limited by the solid support,
CC both the target nucleic acids and the probes can diffuse toward each
CC other, and signal amplification through cycling reactions could occur.
CC Sequencing DNA with tags in combination with DNA amplification techniques
CC means that there is no need for traditional sequencing methods or
CC attaching to a solid phase, either the materials to be analysed or the
CC tags. The present sequence represents a PCR primer which is used in an
CC example from the present invention
XX
SQ Sequence 46 BP; 10 A; 13 C; 13 G; 10 T; 0 U; 0 Other;
Query Match 49.3%; Score 14.8; DB 2; Length 46;
Best Local Similarity 73.1%; Pred. No. 9.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGGTCATCTCACCTT 28
DB 41 GACTCAGACCTTGTGCGAGCTGACGTT 16

RESULT 39
AA55830/c
ID AAX55830 standard; DNA; 46 BP.
AC AAX55830;
XX
XX 09-JUL-1999 (first entry)
DE PCR mutagenesis primer #913 from WO9918240 Example 6.
KW Labelling; tag; molecular species; identification; property;
KW characteristic; hybridisation; amplification; PCR primer; ss.
XX Synthetic.
OS
XX WO9918240-A2.
PN
XX 15-APR-1999.
PD
XX 05-OCT-1998; 98WO-US020874.
PF
XX 06-OCT-1997; 97US-00944410.
PR (STRA-) STRATAGENE.
XX Sorge JA;
PI
XX WPI; 1999-264040/22.
DR
XX Uniquely tagged molecules identifiable by a unique property or
XX characteristic.
PS Example 6; Page 94; 138pp; English.
XX
CC The present invention describes a composition comprising a mixture of
CC different species of molecules where each species is linked to a tag that
CC is unique to that species and that encodes at least two variable
CC positions on that species, where the tags can be identified without the
CC need for first isolating each of the tags prior to identification. Liquid
CC phase hybridisation system may be used for simultaneous identification of
CC a large subset of targets out of a very large collection of similar of
CC dissimilar molecular species. It may also be used to create tagged
CC molecules that identify any collection of molecular species, e.g.
CC peptides, antibodies, nucleic acids. Method bar codes collections or
CC probes or analytes for use in a liquid phase hybridisation method. Tagged
CC probes able to detect small changes or mutations in the target specimen.
CC Use of molecular tags overcomes difficulties of prior art methods, e.g.
CC the concentration of the probe would not be limited by the solid support,
CC both the target nucleic acids and the probes can diffuse toward each
CC other, and signal amplification through cycling reactions could occur.
CC Sequencing DNA with tags in combination with DNA amplification techniques
CC means that there is no need for traditional sequencing methods or
CC attaching to a solid phase, either the materials to be analysed or the
CC tags. The present sequence represents a PCR primer which is used in an
CC example from the present invention
XX
SQ Sequence 46 BP; 10 A; 13 C; 13 G; 10 T; 0 U; 0 Other;
Query Match 49.3%; Score 14.8; DB 2; Length 46;
Best Local Similarity 73.1%; Pred. No. 9.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGGTCATCTCACCTT 28
DB 41 GACTCAGACCTTGTGCGAGCTGACGTT 16

RESULT 40
AA55832/c
ID AAX55832 standard; DNA; 46 BP.
XX
AC AAX55832;
XX
XX 09-JUL-1999 (first entry)
DE PCR mutagenesis primer #915 from WO9918240 Example 6.
KW Labelling; tag; molecular species; identification; property;
KW characteristic; hybridisation; amplification; PCR primer; ss.
XX Synthetic.
OS
XX WO9918240-A2.
PN
XX 15-APR-1999.
PD
XX 05-OCT-1998; 98WO-US020874.
PF
XX 06-OCT-1997; 97US-00944410.
PR (STRA-) STRATAGENE.
XX Sorge JA;
PI
XX WPI; 1999-264040/22.
DR
XX Uniquely tagged molecules identifiable by a unique property or
XX characteristic.
PS Example 6; Page 94; 138pp; English.
XX
CC The present invention describes a composition comprising a mixture of
CC different species of molecules where each species is linked to a tag that
CC is unique to that species and that encodes at least two variable
CC positions on that species, where the tags can be identified without the
CC need for first isolating each of the tags prior to identification. Liquid
CC phase hybridisation system may be used for simultaneous identification of
CC a large subset of targets out of a very large collection of similar of
CC dissimilar molecular species. It may also be used to create tagged
CC molecules that identify any collection of molecular species, e.g.
CC peptides, antibodies, nucleic acids. Method bar codes collections or

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CC probes or analytes for use in a liquid phase hybridisation method. Tagged
CC probes able to detect small changes or mutations in the target specimen.
CC Use of molecular tags overcomes difficulties of prior art methods, e.g.
CC the concentration of the probe would not be limited by the solid support,
CC both the target nucleic acids and the probes can diffuse toward each
CC other, and signal amplification through cycling reactions could occur.
CC Sequencing DNA with tags in combination with DNA amplification techniques
CC means that there is no need for traditional sequencing methods or
CC attaching to a solid phase, either the materials to be analysed or the
CC tags. The present sequence represents a PCR primer which is used in an
CC example from the present invention
XX
SQ Sequence 46 BP; 10 A; 13 C; 12 G; 11 T; 0 U; 0 Other;

Query Match 49.3%; Score 14.8; DB 2; Length 46;
Best Local Similarity 73.1%; Pred. No. 9.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 GACTCAGTCCTTGGTCATCTCACCTT 28
Db 41 GACTCAGACCTTGTGCGAACTGACGTT 16

Search completed: November 23, 2004, 17:28:24
Job time : 190.011 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	19	63.3	33	1	US-08-299-682-13
C 2	19	63.3	33	1	US-08-347-657-1
C 3	16.4	54.7	46	4	US-08-944-410-52
C 4	15.2	50.7	24	4	US-09-297-269-7
C 5	15.2	50.7	47	4	US-09-671-317-930
C 6	14.8	49.3	46	4	US-08-944-410-53
C 7	14.8	49.3	46	4	US-08-944-410-54
C 8	14.8	49.3	46	4	US-08-944-410-55
C 9	14.8	49.3	47	4	US-09-422-978-1893
C 10	14.6	48.7	36	4	US-09-916-510A-20
C 11	14.6	48.7	42	4	US-09-139-28
C 12	14.6	48.7	49	3	US-09-710-200-40
C 13	14.6	48.7	49	4	US-09-975-408-40
C 14	14.4	48.0	27	1	US-08-758-306-368
C 15	14.4	48.0	34	4	US-09-029-941-6
C 16	14.2	47.3	24	4	US-09-297-269-6
C 17	14.2	47.3	34	2	US-09-132-619-18
C 18	14.2	47.3	39	3	US-09-079-984A-13
C 19	14.2	47.3	39	4	US-09-390-729-13
C 20	14.2	47.3	45	1	US-08-221-816B-18
C 21	14.2	47.3	45	4	US-10-112-547-18
C 22	14.2	47.3	45	4	US-10-112-241-18
C 23	14.2	47.3	45	4	US-09-639-667-1
C 24	14.2	47.3	45	4	US-10-104-611-18
C 25	14.2	47.3	45	4	US-10-109-368-18
C 26	14.2	47.3	47	3	US-09-338-907-269
C 27	14.2	47.3	47	3	US-09-218-207-269
C 28	14.2	47.3	20	4	US-08-591-432-18
C 29	14.2	47.3	20	4	US-08-591-432-19
C 30	14	46.7	28	2	US-08-859-998-670
C 31	14	46.7	28	3	US-09-225-928-670
C 32	14	46.7	28	4	US-09-225-201B-670
C 33	14	46.7	40	5	PCT-US94-08052-9
C 34	14	46.7	44	2	US-08-401-068-9
C 35	14	46.7	44	2	US-08-846-338-9
C 36	14	46.7	47	4	US-09-422-978-2989
C 37	13.8	46.0	28	3	US-09-006-636-6
C 38	13.8	46.0	28	3	US-09-006-632-6
C 39	13.8	46.0	28	3	US-09-325-274-6
C 40	13.8	46.0	36	3	US-09-416-756A-14
C 41	13.8	46.0	36	3	US-09-686-172-2
C 42	13.8	46.0	36	4	US-09-955-726A-19
C 43	13.8	46.0	36	4	US-09-680-310-16
C 44	13.6	45.3	22	4	US-09-559-306-4
C 45	13.6	45.3	29	1	US-08-538-875-3
C 46	13.6	45.3	30	3	US-08-297-395-43
C 47	13.6	45.3	31	3	US-08-679-645-437
C 48	13.4	44.7	28	3	US-08-348-548-90
C 49	13.4	44.7	28	5	PCT-US95-15716-90
C 50	13.4	44.7	32	3	US-09-026-033-8
C 51	13.4	44.7	37	4	US-09-434-837-3
C 52	13.4	44.7	42	1	US-08-381-572-3
C 53	13.4	44.7	42	1	US-08-592-820-3
C 54	13.4	44.7	42	4	US-08-944-410-80
C 55	13.4	44.7	45	4	US-09-546-934-32
C 56	13.4	44.7	47	4	US-09-422-978-1446
C 57	13.2	44.0	22	4	US-09-791-105B-11
C 58	13.2	44.0	29	2	US-08-494-151-3
C 59	13.2	44.0	30	2	US-08-305-764C-52
C 60	13.2	44.0	30	2	US-08-892-403A-14
C 61	13.2	44.0	30	4	US-09-291-894-14
C 62	13.2	44.0	34	4	US-09-086-118-19
C 63	13.2	44.0	36	3	US-08-961-083-291
C 64	13.2	44.0	36	4	US-09-536-784-291
C 65	13.2	44.0	46	4	US-08-944-410-49
C 66	13.2	44.0	46	4	US-08-944-410-50
C 67	13.2	44.0	46	4	US-08-944-410-51
C 68	13.2	44.0	46	4	US-08-944-410-56
C 69	13.2	44.0	46	4	US-08-944-410-57
C 70	13.2	44.0	47	4	US-09-671-317-802
C 71	13.2	44.0	47	4	US-09-671-317-945
C 72	13.2	44.0	47	4	US-09-422-978-1615
C 73	13.2	44.0	47	4	US-09-422-978-2521
C 74	13	43.3	20	4	US-09-027-444-4
C 75	13	43.3	20	5	PCT-US94-07091-8
C 76	13	43.3	22	2	US-09-205-144-2
C 77	13	43.3	27	3	US-08-979-917A-17
C 78	13	43.3	30	4	US-09-269-262B-12
C 79	13	43.3	30	4	US-09-380-287A-37
C 80	13	43.3	32	3	US-08-816-977-45
C 81	13	43.3	32	4	US-09-334-477-45
C 82	13	43.3	34	1	US-07-971-819A-26
C 83	13	43.3	34	1	US-08-475-231-26
C 84	13	43.3	35	3	US-08-814-412-25
C 85	13	43.3	35	5	PCT-US94-14106-27
C 86	13	43.3	36	1	US-08-411-389-16
C 87	13	43.3	39	3	US-07-987-264-33
C 88	13	43.3	41	1	US-08-356-405-12
C 89	13	43.3	47	4	US-09-422-978-2988
C 90	13	43.3	48	1	US-08-317-102-1
C 91	13	43.3	48	1	US-08-317-102-2
C 92	13	43.3	48	1	US-08-411-796-165
C 93	13	43.3	48	1	US-08-411-796-169
C 94	13	43.3	48	3	US-08-471-039-165
C 95	13	43.3	48	3	US-08-471-039-169
C 96	13	43.3	48	3	US-08-706-945D-70
C 97	13	43.3	48	4	US-08-559-390-165
C 98	13	43.3	48	4	US-08-559-390-169
C 99	13	43.3	48	5	PCT-US93-11198-165
C 100	13	43.3	48	5	PCT-US93-11198-169

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Sequence 3, Appli
Sequence 43, Appl
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Sequence 27, Appl
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Sequence 12, Appl
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Sequence 2, Appli
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Sequence 169, App
Sequence 169, App
Sequence 70, Appl
Sequence 165, App
Sequence 169, App
Sequence 169, App
Sequence 169, App

c 101	13	43.3	50	1	US-08-171-389-393	Sequence 393, App	174	12.6	42.0	26	4	US-08-749-955-19	Sequence 19, Appl
c 102	13	43.3	50	1	US-08-123-936-393	Sequence 393, App	c 175	12.6	42.0	26	4	US-08-749-955-20	Sequence 20, Appl
c 103	13	43.3	50	2	US-08-475-228A-393	Sequence 393, App	176	12.6	42.0	29	4	US-09-915-815-18	Sequence 18, Appl
c 104	13	43.3	50	3	US-08-482-080A-393	Sequence 393, App	177	12.6	42.0	32	4	US-09-194-300A-7	Sequence 7, Appl
c 105	13	43.3	50	3	US-09-354-947-393	Sequence 393, App	178	12.6	42.0	33	4	US-09-207-388-84	Sequence 84, Appl
c 106	13	43.3	50	4	US-09-554-929-70	Sequence 70, Appl	179	12.6	42.0	37	3	US-09-161-241-70	Sequence 70, Appl
c 107	13	43.3	50	4	US-09-554-929-71	Sequence 71, Appl	c 180	12.6	42.0	41	1	US-08-464-531-63	Sequence 63, Appl
c 108	13	43.3	50	4	US-09-554-929-123	Sequence 123, App	c 181	12.6	42.0	41	2	US-08-461-598-63	Sequence 63, Appl
c 109	13	43.3	50	5	PCT-US93-12388-393	Sequence 393, App	c 182	12.6	42.0	41	3	US-08-323-137-63	Sequence 63, Appl
c 110	12.8	42.7	18	4	US-09-422-978-6022	Sequence 6022, App	c 183	12.6	42.0	41	3	US-08-936-632B-19	Sequence 19, Appl
c 111	12.8	42.7	20	3	US-09-124-238A-15	Sequence 15, Appl	c 184	12.6	42.0	41	3	US-08-582-333A-71	Sequence 71, Appl
c 112	12.8	42.7	20	4	US-09-721-975-15	Sequence 15, Appl	c 185	12.6	42.0	42	1	US-08-367-122-50	Sequence 50, Appl
c 113	12.8	42.7	20	4	US-09-986-621-15	Sequence 15, Appl	c 186	12.6	42.0	42	1	US-09-338-907-132	Sequence 192, App
c 114	12.8	42.7	21	3	US-09-124-238A-24	Sequence 24, Appl	c 187	12.6	42.0	47	3	US-09-338-907-193	Sequence 193, App
c 115	12.8	42.7	21	4	US-09-721-975-24	Sequence 24, Appl	c 188	12.6	42.0	47	3	US-09-218-207-132	Sequence 192, App
c 116	12.8	42.7	21	4	US-09-986-621-24	Sequence 24, Appl	c 189	12.6	42.0	47	3	US-09-218-207-193	Sequence 193, App
c 117	12.8	42.7	21	4	US-09-422-978-10245	Sequence 10245, A	c 190	12.6	42.0	47	4	US-09-641-638-803	Sequence 803, App
c 118	12.8	42.7	24	3	US-09-124-238A-27	Sequence 27, Appl	c 191	12.6	42.0	47	4	US-09-641-638-981	Sequence 981, App
c 119	12.8	42.7	24	4	US-09-721-975-27	Sequence 27, Appl	c 192	12.6	42.0	47	4	US-09-422-978-1198	Sequence 1198, App
c 120	12.8	42.7	24	4	US-09-986-621-27	Sequence 27, Appl	c 193	12.6	42.0	47	4	US-09-422-978-1547	Sequence 1547, App
c 121	12.8	42.7	24	4	US-09-986-621-27	Sequence 27, Appl	c 194	12.6	42.0	47	4	US-09-422-978-2807	Sequence 2807, App
c 122	12.8	42.7	27	1	US-08-758-308-1038	Sequence 1038, App	c 195	12.6	42.0	47	4	US-09-422-978-3752	Sequence 3752, App
c 123	12.8	42.7	34	3	US-08-584-048-371	Sequence 371, App	c 196	12.6	42.0	47	4	US-10-170-097-803	Sequence 803, App
c 124	12.8	42.7	38	4	US-09-517-740-1	Sequence 54, Appl	c 197	12.6	42.0	47	4	US-10-170-097-981	Sequence 981, App
c 125	12.8	42.7	40	3	US-09-626-923-3	Sequence 3, Appl	c 198	12.6	42.0	48	1	US-08-411-796-166	Sequence 166, App
c 126	12.8	42.7	40	3	US-09-484-850-3	Sequence 3, Appl	c 199	12.6	42.0	48	1	US-08-411-796-170	Sequence 170, App
c 127	12.8	42.7	40	3	US-09-408-392-3	Sequence 3, Appl	c 200	12.6	42.0	48	1	US-08-471-039-166	Sequence 166, App
c 128	12.8	42.7	40	4	US-09-626-930-3	Sequence 3, Appl	c 201	12.6	42.0	48	3	US-08-471-039-170	Sequence 170, App
c 129	12.8	42.7	40	4	US-09-626-930-3	Sequence 3, Appl	c 202	12.6	42.0	48	3	US-08-864-473-72	Sequence 72, Appl
c 130	12.8	42.7	40	4	US-09-626-930-3	Sequence 3, Appl	c 203	12.6	42.0	48	3	US-09-440-523-72	Sequence 72, Appl
c 131	12.8	42.7	40	4	US-09-626-930-3	Sequence 3, Appl	c 204	12.6	42.0	48	4	US-08-559-390-166	Sequence 166, App
c 132	12.8	42.7	40	4	US-09-626-930-3	Sequence 3, Appl	c 205	12.6	42.0	48	4	US-08-559-390-170	Sequence 170, App
c 133	12.8	42.7	43	3	US-09-668-195-5	Sequence 5, Appl	c 206	12.6	42.0	48	4	US-09-18-156-72	Sequence 72, Appl
c 134	12.8	42.7	47	4	US-09-671-317-734	Sequence 734, App	c 207	12.6	42.0	48	5	PCT-US93-11198-166	Sequence 166, App
c 135	12.8	42.7	47	4	US-09-422-978-1322	Sequence 1322, App	c 208	12.6	42.0	48	5	PCT-US93-11198-170	Sequence 170, App
c 136	12.6	42.0	20	1	US-08-635-309-31	Sequence 31, Appl	c 209	12.6	42.0	50	2	US-08-933-749-7	Sequence 7, Appl
c 137	12.6	42.0	20	3	US-09-345-882-96	Sequence 96, Appl	c 210	12.6	42.0	50	3	US-09-235-583-7	Sequence 7, Appl
c 138	12.6	42.0	20	4	US-08-469-260A-711	Sequence 711, App	c 211	12.6	42.0	50	3	US-09-599-164-7	Sequence 7, Appl
c 139	12.6	42.0	20	4	US-08-488-446-711	Sequence 711, App	c 212	12.4	41.3	20	4	US-09-198-452A-4748	Sequence 4748, App
c 140	12.6	42.0	20	4	US-08-467-344A-711	Sequence 711, App	c 213	12.4	41.3	20	4	US-09-081-385-123	Sequence 123, App
c 141	12.6	42.0	20	4	US-08-424-550B-711	Sequence 711, App	c 214	12.4	41.3	21	4	US-09-657-472-454	Sequence 454, App
c 142	12.6	42.0	23	1	US-08-412-614-57	Sequence 57, Appl	c 215	12.4	41.3	21	4	US-09-657-472-970	Sequence 970, App
c 143	12.6	42.0	23	1	US-08-412-614-58	Sequence 58, Appl	c 216	12.4	41.3	25	4	US-09-687-637B-4	Sequence 4, Appl
c 144	12.6	42.0	23	1	US-08-412-614-59	Sequence 59, Appl	c 217	12.4	41.3	26	1	US-07-971-819A-27	Sequence 27, Appl
c 145	12.6	42.0	23	1	US-08-412-614-60	Sequence 60, Appl	c 218	12.4	41.3	26	1	US-08-475-231-27	Sequence 27, Appl
c 146	12.6	42.0	23	2	US-08-635-761-57	Sequence 57, Appl	c 219	12.4	41.3	27	1	US-08-758-306-370	Sequence 370, App
c 147	12.6	42.0	23	2	US-08-635-761-58	Sequence 58, Appl	c 220	12.4	41.3	27	3	US-08-584-040-6900	Sequence 6900, App
c 148	12.6	42.0	23	2	US-08-635-761-59	Sequence 59, Appl	c 221	12.4	41.3	27	3	US-09-044-718-30	Sequence 30, Appl
c 149	12.6	42.0	23	2	US-08-635-761-60	Sequence 60, Appl	c 222	12.4	41.3	27	3	US-09-044-718-31	Sequence 31, Appl
c 150	12.6	42.0	23	3	US-09-312-520-57	Sequence 57, Appl	c 223	12.4	41.3	27	4	US-10-062-848-30	Sequence 30, Appl
c 151	12.6	42.0	23	3	US-09-312-520-58	Sequence 58, Appl	c 224	12.4	41.3	27	4	US-10-062-848-31	Sequence 31, Appl
c 152	12.6	42.0	23	3	US-09-312-520-59	Sequence 59, Appl	c 225	12.4	41.3	29	1	US-08-081-539-8	Sequence 8, Appl
c 153	12.6	42.0	23	3	US-09-312-520-60	Sequence 60, Appl	c 226	12.4	41.3	29	1	US-08-466-647-8	Sequence 8, Appl
c 154	12.6	42.0	23	4	US-09-863-086-57	Sequence 57, Appl	c 227	12.4	41.3	29	1	US-08-411-795B-133	Sequence 133, App
c 155	12.6	42.0	23	4	US-09-863-086-58	Sequence 58, Appl	c 228	12.4	41.3	29	1	US-08-411-795B-400	Sequence 400, App
c 156	12.6	42.0	23	4	US-09-863-086-59	Sequence 59, Appl	c 229	12.4	41.3	29	1	US-08-411-796-133	Sequence 133, App
c 157	12.6	42.0	23	4	US-09-863-086-60	Sequence 60, Appl	c 230	12.4	41.3	29	1	US-08-469-319A-133	Sequence 133, App
c 158	12.6	42.0	25	4	US-09-866-108A-3476	Sequence 3476, App	c 231	12.4	41.3	29	1	US-08-469-319A-400	Sequence 400, App
c 159	12.6	42.0	25	4	US-09-866-108A-3477	Sequence 3477, App	c 232	12.4	41.3	29	3	US-08-471-039-133	Sequence 133, App
c 160	12.6	42.0	25	4	US-09-866-108A-3478	Sequence 3478, App	c 233	12.4	41.3	29	4	US-08-764-114-133	Sequence 133, App
c 161	12.6	42.0	25	4	US-09-866-108A-3479	Sequence 3479, App	c 234	12.4	41.3	29	4	US-08-764-114-400	Sequence 400, App
c 162	12.6	42.0	25	4	US-09-866-108A-3480	Sequence 3480, App	c 235	12.4	41.3	29	4	US-08-469-419-133	Sequence 133, App
c 163	12.6	42.0	25	4	US-09-866-108A-3481	Sequence 3481, App	c 236	12.4	41.3	29	4	US-08-469-419-400	Sequence 400, App
c 164	12.6	42.0	25	4	US-09-866-108A-3482	Sequence 3482, App	c 237	12.4	41.3	29	4	US-08-559-390-133	Sequence 133, App
c 165	12.6	42.0	25	4	US-09-866-108A-14154	Sequence 14154, A	c 238	12.4	41.3	29	4	US-09-304-232-798	Sequence 798, App
c 166	12.6	42.0	25	4	US-09-866-108A-14155	Sequence 14155, A	c 239	12.4	41.3	29	5	PCT-US93-11198-133	Sequence 133, App
c 167	12.6	42.0	25	4	US-09-866-108A-14156	Sequence 14156, A	c 240	12.4	41.3	31	4	US-09-672-725C-21	Sequence 21, Appl
c 168	12.6	42.0	25	4	US-09-866-108A-14157	Sequence 14157, A	c 241	12.4	41.3	33	4	US-09-894-799-16	Sequence 16, Appl
c 169	12.6	42.0	25	4	US-09-866-108A-14158	Sequence 14158, A	c 242	12.4	41.3	46	4	US-08-832-571-11	Sequence 11, Appl
c 170	12.6	42.0	25	4	US-09-866-108A-14159	Sequence 14159, A	c 243	12.4	41.3	47	3	US-09-345-882-45	Sequence 46, Appl
c 171	12.6	42.0	25	4	US-09-866-108A-14160	Sequence 14160, A	c 244	12.4	41.3	47	4	US-09-422-978-1776	Sequence 1776, App
c 172	12.6	42.0	26	4	US-08-749-955-17	Sequence 17, Appl	c 245	12.4	41.3	47	4	US-09-422-978-1988	Sequence 1988, App
c 173	12.6	42.0	26	4	US-08-749-955-18	Sequence 18, Appl	c 246	12.4	41.3	48	1	US-08-160-670A-46	Sequence 46, Appl

247	12.2	40.7	17	1	US-08-390-850-585	Sequence 585, App	320	12.2	40.7	39	4	US-09-390-729-7	Sequence 7, Appli
248	12.2	40.7	17	1	US-08-435-634-585	Sequence 585, App	321	12.2	40.7	46	3	US-09-262-773-182	Sequence 182, App
c 249	12.2	40.7	17	1	US-09-866-108A-547	Sequence 547, App	c 322	12.2	40.7	47	1	US-08-119-773-10	Sequence 10, Appl
c 250	12.2	40.7	17	4	US-09-404-912-109	Sequence 109, App	c 323	12.2	40.7	47	4	US-09-422-978-105	Sequence 105, App
251	12.2	40.7	18	2	US-08-117-952-204	Sequence 204, App	324	12.2	40.7	47	4	US-09-422-978-1042	Sequence 1042, Ap
252	12.2	40.7	19	4	US-09-696-731-803	Sequence 803, App	325	12.2	40.7	47	4	US-09-422-978-1459	Sequence 1459, Ap
253	12.2	40.7	20	3	US-08-359-757-17	Sequence 17, Appl	326	12.2	40.7	48	1	US-08-168-317-12	Sequence 12, Appl
254	12.2	40.7	20	3	US-09-359-757-18	Sequence 18, Appl	c 327	12.2	40.7	48	1	US-08-391-000-13	Sequence 13, Appl
255	12.2	40.7	20	3	US-09-428-584-22	Sequence 22, Appl	c 328	12.2	40.7	48	2	US-08-741-931-13	Sequence 13, Appl
c 256	12.2	40.7	20	3	US-08-622-543-3	Sequence 3, Appli	329	12.2	40.7	48	2	US-08-460-510-12	Sequence 12, Appl
c 257	12.2	40.7	20	4	US-09-929-486-3	Sequence 3, Appli	330	12.2	40.7	48	3	US-08-460-490-12	Sequence 12, Appl
c 258	12.2	40.7	20	4	US-10-259-903-3	Sequence 3, Appli	331	12.2	40.7	48	3	US-09-035-665-8	Sequence 8, Appli
259	12.2	40.7	20	4	US-10-259-903-4	Sequence 4, Appli	332	12.2	40.7	48	3	US-09-035-665-9	Sequence 9, Appli
c 260	12.2	40.7	20	6	5219727-55	Patent No. 5219727	333	12.2	40.7	48	5	PCT-US92-00730-12	Sequence 12, Appl
c 261	12.2	40.7	21	1	US-07-906-930E-22	Sequence 22, Appl	c 334	12.2	40.7	48	5	PCT-US92-10430-7	Sequence 7, Appli
c 262	12.2	40.7	21	1	US-07-906-930E-27	Sequence 27, Appl	335	12.2	40.7	49	1	US-08-171-389-118	Sequence 118, App
c 263	12.2	40.7	21	3	US-08-338-579A-80	Sequence 80, Appl	336	12.2	40.7	49	1	US-08-123-936-118	Sequence 118, App
c 264	12.2	40.7	21	3	US-09-301-978C-7	Sequence 7, Appli	337	12.2	40.7	49	2	US-08-475-228A-118	Sequence 118, App
c 265	12.2	40.7	21	5	PCT-US94-09851-80	Sequence 80, Appl	338	12.2	40.7	49	3	US-08-482-080A-118	Sequence 118, App
c 266	12.2	40.7	23	3	US-08-905-223-32	Sequence 32, Appl	339	12.2	40.7	49	3	US-09-354-947-118	Sequence 118, App
c 267	12.2	40.7	23	3	US-09-247-155-32	Sequence 32, Appl	340	12.2	40.7	49	5	PCT-US93-12388-118	Sequence 118, App
c 268	12.2	40.7	23	4	US-09-599-360B-18	Sequence 18, Appl	c 341	12	40.0	18	2	US-08-970-269A-8	Sequence 8, Appli
c 269	12.2	40.7	23	4	US-09-663-600A-32	Sequence 32, Appl	c 342	12	40.0	18	3	US-09-407-562-8	Sequence 8, Appli
c 270	12.2	40.7	23	4	US-09-621-976-18	Sequence 18, Appl	c 343	12	40.0	18	3	US-09-080-525-17	Sequence 17, Appl
c 271	12.2	40.7	23	4	US-08-513-999C-18	Sequence 18, Appl	c 344	12	40.0	18	4	US-09-695-782-17	Sequence 17, Appl
c 272	12.2	40.7	25	4	US-09-866-108A-3483	Sequence 3483, Ap	c 345	12	40.0	20	3	US-08-804-180C-12	Sequence 12, Appl
c 273	12.2	40.7	25	4	US-09-866-108A-3484	Sequence 3484, Ap	346	12	40.0	20	4	US-09-198-452A-2977	Sequence 2977, Ap
c 274	12.2	40.7	26	1	US-08-033-072-1	Sequence 1, Appli	c 347	12	40.0	20	4	US-09-544-398B-320	Sequence 320, App
c 275	12.2	40.7	26	1	US-08-479-852-4	Sequence 4, Appli	348	12	40.0	22	4	US-09-792-024-474	Sequence 474, App
c 276	12.2	40.7	26	1	US-08-479-852-56	Sequence 56, Appl	c 349	12	40.0	24	3	US-08-896-449A-10	Sequence 10, Appl
c 277	12.2	40.7	26	1	US-08-479-852-70	Sequence 70, Appl	c 350	12	40.0	24	3	US-09-132-652-10	Sequence 10, Appl
c 278	12.2	40.7	26	1	US-08-479-852-84	Sequence 84, Appl	351	12	40.0	24	4	US-09-177-650-81	Sequence 81, Appl
c 279	12.2	40.7	26	2	US-08-462-646-4	Sequence 4, Appli	c 352	12	40.0	24	4	US-09-886-900A-10	Sequence 10, Appl
c 280	12.2	40.7	26	2	US-08-462-646-56	Sequence 56, Appl	c 353	12	40.0	24	4	US-09-662-478C-10	Sequence 10, Appl
c 281	12.2	40.7	26	2	US-08-462-646-70	Sequence 70, Appl	c 354	12	40.0	24	4	US-09-551-161-3	Sequence 3, Appli
c 282	12.2	40.7	26	2	US-08-462-646-84	Sequence 84, Appl	c 355	12	40.0	25	2	US-08-632-787-35	Sequence 35, Appl
c 283	12.2	40.7	26	2	US-07-695-201B-12	Sequence 12, Appl	356	12	40.0	25	3	US-09-097-199-35	Sequence 35, Appl
c 284	12.2	40.7	26	3	US-08-470-532-12	Sequence 12, Appl	c 357	12	40.0	27	3	US-08-985-162-872	Sequence 872, App
c 285	12.2	40.7	26	3	US-09-013-406-4	Sequence 4, Appli	c 358	12	40.0	27	3	US-08-985-162-901	Sequence 901, App
c 286	12.2	40.7	26	3	US-09-013-406-56	Sequence 56, Appl	c 359	12	40.0	27	3	US-09-105-839D-17	Sequence 17, Appl
c 287	12.2	40.7	26	3	US-09-013-406-70	Sequence 70, Appl	c 360	12	40.0	27	3	US-08-584-040-4727	Sequence 4727, Ap
c 288	12.2	40.7	26	3	US-09-013-406-84	Sequence 84, Appl	c 361	12	40.0	27	4	US-09-344-040C-17	Sequence 17, Appl
c 289	12.2	40.7	26	4	US-09-168-947-10	Sequence 10, Appl	c 362	12	40.0	27	4	US-09-401-063-872	Sequence 872, App
c 290	12.2	40.7	26	4	US-08-968-208-12	Sequence 12, Appl	c 363	12	40.0	27	4	US-09-401-063-901	Sequence 901, App
c 291	12.2	40.7	26	4	US-09-766-095-4	Sequence 4, Appli	c 364	12	40.0	28	1	US-08-833-039A-17	Sequence 17, Appl
c 292	12.2	40.7	26	4	US-09-766-095-56	Sequence 56, Appl	365	12	40.0	28	1	US-08-485-107-6	Sequence 6, Appli
c 293	12.2	40.7	26	4	US-09-766-095-70	Sequence 70, Appl	366	12	40.0	28	2	US-08-472-719-5	Sequence 6, Appli
c 294	12.2	40.7	26	4	US-08-766-095-84	Sequence 84, Appl	c 367	12	40.0	28	4	US-09-304-232-551	Sequence 551, App
c 295	12.2	40.7	27	3	US-08-584-040-6616	Sequence 6616, Ap	368	12	40.0	30	3	US-08-876-078-9	Sequence 9, Appli
c 296	12.2	40.7	28	3	US-09-327-681-1	Sequence 1, Appli	369	12	40.0	30	3	US-08-831-823-9	Sequence 9, Appli
c 297	12.2	40.7	28	4	US-09-091-134-7	Sequence 7, Appli	370	12	40.0	33	1	US-08-752-238-10	Sequence 10, Appl
c 298	12.2	40.7	29	1	US-08-345-505A-7	Sequence 7, Appli	c 371	12	40.0	33	3	US-09-085-603B-10	Sequence 10, Appl
c 299	12.2	40.7	29	3	US-08-913-778-2	Sequence 2, Appli	c 372	12	40.0	34	4	US-09-551-161-5	Sequence 5, Appli
c 300	12.2	40.7	29	3	US-08-646-265A-67	Sequence 67, Appl	373	12	40.0	37	3	US-09-363-939A-213	Sequence 213, App
c 301	12.2	40.7	29	3	US-08-646-265A-83	Sequence 83, Appl	374	12	40.0	37	4	US-09-791-301-213	Sequence 213, App
c 302	12.2	40.7	30	3	US-09-178-869A-11	Sequence 11, Appl	c 375	12	40.0	39	3	US-09-052-995-4	Sequence 4, Appli
c 303	12.2	40.7	30	4	US-09-761-413-11	Sequence 11, Appl	c 376	12	40.0	39	4	US-09-535-008-25	Sequence 25, Appl
c 304	12.2	40.7	31	1	US-07-940-652-15	Sequence 15, Appl	c 377	12	40.0	39	4	US-09-220-557-16	Sequence 16, Appl
c 305	12.2	40.7	31	1	US-08-255-553-15	Sequence 15, Appl	c 378	12	40.0	40	2	US-09-262-773-91	Sequence 91, Appl
c 306	12.2	40.7	33	1	US-08-538-875-8	Sequence 8, Appli	c 379	12	40.0	40	3	US-08-343-443B-60	Sequence 60, Appl
c 307	12.2	40.7	33	1	US-08-600-783-6	Sequence 6, Appli	380	12	40.0	42	4	US-09-359-304B-23	Sequence 23, Appl
c 308	12.2	40.7	33	3	US-09-079-984A-3	Sequence 3, Appli	c 381	12	40.0	42	6	5231166-15	Patent No. 5231166
c 309	12.2	40.7	33	4	US-09-390-729-3	Sequence 3, Appli	c 382	12	40.0	44	2	US-08-441-887A-20	Sequence 20, Appl
c 310	12.2	40.7	34	4	US-08-845-381E-20	Sequence 20, Appl	c 383	12	40.0	44	3	US-08-544-381B-117	Sequence 117, App
c 311	12.2	40.7	34	6	5182196-15	Patent No. 5182196	384	12	40.0	45	3	US-09-312-285-6	Sequence 6, Appli
c 312	12.2	40.7	36	3	US-09-446-504-81	Sequence 81, Appl	385	12	40.0	45	3	US-09-312-286-6	Sequence 6, Appli
c 313	12.2	40.7	36	3	US-09-712-266-81	Sequence 81, Appl	386	12	40.0	45	3	US-09-312-038-6	Sequence 6, Appli
c 314	12.2	40.7	39	2	US-08-857-946-42	Sequence 42, Appl	387	12	40.0	45	3	US-09-554-511-13	Sequence 13, Appl
c 315	12.2	40.7	39	2	US-08-857-946-46	Sequence 46, Appl	388	12	40.0	45	4	US-09-728-764-6	Sequence 6, Appli
c 316	12.2	40.7	39	3	US-08-970-740-42	Sequence 42, Appl	389	12	40.0	45	4	US-09-312-304B-4	Sequence 4, Appli
c 317	12.2	40.7	39	3	US-08-970-740-46	Sequence 46, Appl	390	12	40.0	45	4	US-09-728-792-6	Sequence 6, Appli
c 318	12.2	40.7	39	3	US-09-262-773-74	Sequence 74, Appl	391	12	40.0	45	4	US-09-850-964-6	Sequence 6, Appli
c 319	12.2	40.7	39	3	US-09-079-984A-7	Sequence 7, Appli	392	12	40.0	45	4	US-09-532-806-7	Sequence 7, Appli

C 393	12	40.0	47	1	US-08-171-389-15	Sequence 15, Appl	466	11.8	39.3	33	4	US-09-758-282B-45	Sequence 45, Appl
C 394	12	40.0	47	1	US-08-123-936-15	Sequence 15, Appl	467	11.8	39.3	33	4	US-09-577-304A-45	Sequence 45, Appl
C 395	12	40.0	47	1	US-08-475-228A-15	Sequence 15, Appl	468	11.8	39.3	34	2	US-08-577-492-15	Sequence 15, Appl
C 396	12	40.0	47	3	US-08-482-080A-15	Sequence 15, Appl	469	11.8	39.3	34	3	US-09-073-630-15	Sequence 15, Appl
C 397	12	40.0	47	3	US-08-961-083-391	Sequence 391, Appl	c 470	11.8	39.3	35	3	US-08-903-632-12	Sequence 12, Appl
C 398	12	40.0	47	3	US-09-354-947-15	Sequence 15, Appl	c 471	11.8	39.3	36	2	US-08-418-085-31	Sequence 31, Appl
C 399	12	40.0	47	4	US-09-641-638-775	Sequence 775, Appl	472	11.8	39.3	36	3	US-09-099-011A-31	Sequence 31, Appl
C 400	12	40.0	47	4	US-09-422-978-575	Sequence 575, Appl	473	11.8	39.3	36	4	US-09-098-877B-31	Sequence 31, Appl
C 401	12	40.0	47	4	US-09-422-978-1243	Sequence 1243, Ap	c 474	11.8	39.3	38	4	US-09-474-432B-1264	Sequence 1264, Ap
C 402	12	40.0	47	4	US-09-422-978-2137	Sequence 2137, Ap	c 475	11.8	39.3	38	4	US-09-476-387-1263	Sequence 1263, Ap
C 403	12	40.0	47	4	US-09-422-978-2424	Sequence 2424, Ap	476	11.8	39.3	39	2	US-08-857-946-52	Sequence 52, Appl
C 404	12	40.0	47	4	US-09-536-784-391	Sequence 391, Appl	477	11.8	39.3	39	3	US-08-970-740-52	Sequence 52, Appl
C 405	12	40.0	47	4	US-10-170-097-775	Sequence 775, Appl	478	11.8	39.3	39	4	US-09-517-871-16	Sequence 16, Appl
C 406	12	40.0	47	5	PCT-US93-12388-15	Sequence 15, Appl	479	11.8	39.3	39	4	US-09-517-439-16	Sequence 16, Appl
C 407	12	40.0	49	3	US-08-535-057A-8	Sequence 8, Appli	480	11.8	39.3	40	1	US-08-171-389-166	Sequence 166, Appl
C 408	12	40.0	49	4	US-09-503-252-8	Sequence 8, Appli	481	11.8	39.3	40	1	US-08-123-936-166	Sequence 166, Appl
C 409	12	40.0	50	4	US-09-443-199C-986	Sequence 986, Appl	482	11.8	39.3	40	1	US-08-436-463-12	Sequence 12, Appl
C 410	12	40.0	50	4	US-09-844-525A-63	Sequence 988, Appl	483	11.8	39.3	40	2	US-08-475-228A-166	Sequence 166, Appl
C 411	11.8	39.3	17	2	US-08-389-423-33	Sequence 33, Appl	484	11.8	39.3	40	3	US-08-482-080A-166	Sequence 166, Appl
C 412	11.8	39.3	17	4	US-09-189-028-33	Sequence 33, Appl	485	11.8	39.3	40	3	US-09-354-947-166	Sequence 166, Appl
C 413	11.8	39.3	18	3	US-09-448-176-8	Sequence 8, Appli	486	11.8	39.3	40	5	PCT-US93-12388-166	Sequence 166, Appl
C 414	11.8	39.3	19	4	US-09-647-504-6	Sequence 6, Appli	487	11.8	39.3	42	3	US-08-454-098-17	Sequence 17, Appli
C 415	11.8	39.3	20	1	US-08-441-430-67	Sequence 67, Appl	488	11.8	39.3	43	4	US-09-647-390-6	Sequence 6, Appli
C 416	11.8	39.3	20	4	US-09-844-525A-63	Sequence 63, Appl	c 489	11.8	39.3	45	4	US-09-517-871-15	Sequence 15, Appl
C 417	11.8	39.3	21	4	US-09-657-472-480	Sequence 480, Appl	c 490	11.8	39.3	45	4	US-09-517-439-15	Sequence 15, Appl
C 418	11.8	39.3	21	4	US-09-696-791-4479	Sequence 4479, Ap	c 491	11.8	39.3	47	4	US-09-422-978-1087	Sequence 1087, Ap
C 419	11.8	39.3	22	4	US-09-755-665-113	Sequence 113, Appl	492	11.8	39.3	47	4	US-09-422-978-1204	Sequence 1204, Ap
C 420	11.8	39.3	22	4	US-09-755-665-114	Sequence 114, Appl	493	11.8	39.3	47	4	US-09-422-978-3052	Sequence 3052, Ap
C 421	11.8	39.3	23	3	US-08-781-891-13	Sequence 13, Appl	c 494	11.8	39.3	47	4	US-09-422-978-3864	Sequence 3864, Ap
C 422	11.8	39.3	23	4	US-09-707-388-58	Sequence 58, Appl	495	11.8	39.3	47	4	US-09-422-978-3901	Sequence 3901, Ap
C 423	11.8	39.3	23	4	US-09-618-166-13	Sequence 13, Appl	c 496	11.8	39.3	50	1	US-07-994-469A-27	Sequence 27, Appl
C 424	11.8	39.3	24	4	US-09-904-389-6	Sequence 6, Appli	c 497	11.6	38.7	18	1	US-08-390-850-1131	Sequence 1131, Ap
C 425	11.8	39.3	25	3	US-08-776-971-91	Sequence 91, Appl	498	11.6	38.7	18	1	US-08-435-634-1131	Sequence 1131, Ap
C 426	11.8	39.3	25	4	US-09-866-108A-4970	Sequence 4970, Ap	c 499	11.6	38.7	20	3	US-09-358-683-11	Sequence 11, Appl
C 427	11.8	39.3	25	4	US-09-866-108A-4971	Sequence 4971, Ap	c 500	11.6	38.7	20	4	US-09-487-792-42	Sequence 42, Appl
C 428	11.8	39.3	25	4	US-09-866-108A-4972	Sequence 4972, Ap	c 501	11.6	38.7	20	4	US-09-791-211-78	Sequence 78, Appl
C 429	11.8	39.3	25	4	US-09-576-290-91	Sequence 91, Appl	c 502	11.6	38.7	20	4	US-09-908-594-42	Sequence 42, Appl
C 430	11.8	39.3	26	3	US-08-859-998-778	Sequence 778, Appl	c 503	11.6	38.7	20	4	US-09-422-978-10056	Sequence 10056, A
C 431	11.8	39.3	26	3	US-09-225-928-778	Sequence 778, Appl	c 504	11.6	38.7	20	4	US-09-614-614-34	Sequence 34, Appl
C 432	11.8	39.3	26	4	US-09-225-201B-778	Sequence 778, Appl	c 505	11.6	38.7	20	4	US-09-198-452A-6076	Sequence 6076, Ap
C 433	11.8	39.3	26	4	US-09-665-615B-89	Sequence 89, Appl	c 506	11.6	38.7	20	4	US-09-356-806-11	Sequence 11, Appl
C 434	11.8	39.3	27	1	US-08-222-284A-3	Sequence 3, Appli	c 507	11.6	38.7	21	3	US-08-803-085-13	Sequence 13, Appl
C 435	11.8	39.3	27	1	US-08-640-517A-85	Sequence 85, Appl	c 508	11.6	38.7	21	3	US-09-231-227-6	Sequence 6, Appli
C 436	11.8	39.3	27	3	US-08-985-162-1111	Sequence 1111, Ap	509	11.6	38.7	21	3	US-08-943-731-541	Sequence 541, App
C 437	11.8	39.3	27	3	US-08-985-162-1396	Sequence 1396, Ap	c 510	11.6	38.7	21	4	US-09-768-585-6	Sequence 6, Appli
C 438	11.8	39.3	27	3	US-08-584-040-222	Sequence 222, Appl	511	11.6	38.7	21	4	US-09-814-351-32	Sequence 32, Appl
C 439	11.8	39.3	27	3	US-08-584-040-435	Sequence 435, Appl	512	11.6	38.7	21	4	US-09-657-472-1582	Sequence 1582, Ap
C 440	11.8	39.3	27	3	US-08-584-040-4637	Sequence 4637, Ap	513	11.6	38.7	22	4	US-09-680-420A-8	Sequence 8, Appli
C 441	11.8	39.3	27	3	US-08-584-040-6284	Sequence 6284, Ap	c 514	11.6	38.7	23	4	US-09-207-388-101	Sequence 101, App
C 442	11.8	39.3	27	3	US-08-584-040-6301	Sequence 6301, Ap	c 515	11.6	38.7	24	4	US-10-006-611-10	Sequence 10, Appl
C 443	11.8	39.3	27	3	US-08-679-645-908	Sequence 908, Appl	c 516	11.6	38.7	25	4	US-09-538-709-323	Sequence 323, Appl
C 444	11.8	39.3	27	4	US-09-401-063-1111	Sequence 1111, Ap	c 517	11.6	38.7	25	4	US-09-866-108A-3475	Sequence 3475, Ap
C 445	11.8	39.3	27	4	US-09-401-063-1396	Sequence 1396, Ap	518	11.6	38.7	25	4	US-09-866-108A-14153	Sequence 14153, A
C 446	11.8	39.3	28	3	US-09-162-021B-17	Sequence 17, Appl	519	11.6	38.7	26	3	US-09-245-041-74	Sequence 74, Appl
C 447	11.8	39.3	28	4	US-09-687-477-22	Sequence 22, Appl	520	11.6	38.7	26	4	US-09-060-482-6	Sequence 6, Appli
C 448	11.8	39.3	28	4	US-09-687-476-22	Sequence 22, Appl	521	11.6	38.7	26	4	US-09-358-055B-75	Sequence 75, Appl
C 449	11.8	39.3	28	4	US-09-687-373-22	Sequence 22, Appl	522	11.6	38.7	26	4	US-09-238-238-74	Sequence 74, Appl
C 450	11.8	39.3	28	4	US-09-975-553-22	Sequence 22, Appl	523	11.6	38.7	27	1	US-08-478-039-50	Sequence 50, Appl
C 451	11.8	39.3	28	4	US-10-270-795-22	Sequence 22, Appl	c 524	11.6	38.7	27	1	US-08-476-349A-50	Sequence 50, Appl
C 452	11.8	39.3	28	4	US-10-270-876-22	Sequence 22, Appl	c 525	11.6	38.7	27	3	US-08-523-894-43	Sequence 43, Appl
C 453	11.8	39.3	28	4	US-10-268-051-12	Sequence 12, Appl	c 526	11.6	38.7	27	3	US-08-341-560B-15	Sequence 15, Appl
C 454	11.8	39.3	29	1	US-07-977-284A-225	Sequence 225, Appl	527	11.6	38.7	27	3	PCT-US93-03895-15	Sequence 15, Appl
C 455	11.8	39.3	29	2	US-08-256-426B-225	Sequence 225, Appl	528	11.6	38.7	29	2	US-08-761-277A-77	Sequence 77, Appl
C 456	11.8	39.3	30	1	US-09-636-771-9	Sequence 9, Appli	c 529	11.6	38.7	29	2	US-09-304-232-214	Sequence 214, App
C 457	11.8	39.3	30	2	US-08-535-243-9	Sequence 9, Appli	c 530	11.6	38.7	29	4	US-09-304-232-726	Sequence 726, App
C 458	11.8	39.3	30	2	US-08-859-998-341	Sequence 341, Appl	c 531	11.6	38.7	29	4	US-09-304-232-726	Sequence 726, App
C 459	11.8	39.3	30	3	US-09-225-928-341	Sequence 341, Appl	532	11.6	38.7	29	4	US-09-304-232-809	Sequence 809, App
C 460	11.8	39.3	30	4	US-09-486-241-32	Sequence 32, Appl	c 533	11.6	38.7	30	2	US-08-373-190-59	Sequence 59, Appl
C 461	11.8	39.3	30	4	US-09-225-201B-341	Sequence 341, Appl	534	11.6	38.7	30	2	US-08-438-190A-59	Sequence 59, Appl
C 462	11.8	39.3	30	4	US-09-270-957-48	Sequence 48, Appl	535	11.6	38.7	30	2	US-09-100-388-16	Sequence 16, Appl
C 463	11.8	38.3	30	6	5466586-1	Patent No. 5466586	c 536	11.6	38.7	30	3	US-08-803-085-14	Sequence 14, Appl
C 464	11.8	39.3	32	2	US-08-912-129A-88	Sequence 88, Appl	c 537	11.6	38.7	30	3	US-09-287-145A-59	Sequence 59, Appl
C 465	11.8	39.3	33	2	US-08-731-272A-23	Sequence 23, Appl	c 538	11.6	38.7	30	3	US-09-556-111-59	Sequence 59, Appl

539	11.6	38.7	31	4	US-08-887-497A-63	Sequence 63, Appl	c 612	11.6	38.7	50	4	US-08-880-865-9	Sequence 9, Appl
540	11.6	38.7	31	4	US-08-887-497A-65	Sequence 65, Appl	613	11.4	38.0	17	3	US-08-584-040-5983	Sequence 5983, Ap
541	11.6	38.7	32	3	US-09-232-477A-4	Sequence 4, Appl	614	11.4	38.0	17	4	US-09-371-772B-2820	Sequence 2820, Ap
542	11.6	38.7	32	4	US-09-784-982-A	Sequence 4, Appl	c 615	11.4	38.0	17	4	US-09-371-772B-6276	Sequence 6276, Ap
543	11.6	38.7	32	4	US-09-581-070-6	Sequence 6, Appl	c 616	11.4	38.0	17	4	US-09-371-772B-6277	Sequence 6277, Ap
544	11.6	38.7	32	4	US-09-818-739-3	Sequence 3, Appl	c 617	11.4	38.0	19	1	US-07-377-284A-21	Sequence 21, Appl
545	11.6	38.7	33	2	US-08-636-602A-8	Sequence 8, Appl	c 618	11.4	38.0	19	2	US-08-256-426B-21	Sequence 21, Appl
546	11.6	38.7	33	3	US-09-265-314-8	Sequence 8, Appl	c 619	11.4	38.0	19	3	US-08-851-843A-90	Sequence 90, Appl
547	11.6	38.7	33	4	US-08-755-592A-10	Sequence 10, Appl	620	11.4	38.0	19	3	US-08-974-549A-382	Sequence 382, App
548	11.6	38.7	33	4	US-10-006-611-4	Sequence 4, Appl	621	11.4	38.0	19	3	US-08-854-050-90	Sequence 90, Appl
549	11.6	38.7	34	1	US-08-411-796-448	Sequence 448, App	622	11.4	38.0	19	3	US-09-430-323-90	Sequence 90, Appl
550	11.6	38.7	34	2	US-08-596-387B-41	Sequence 41, Appl	623	11.4	38.0	19	4	US-08-312-951-149	Sequence 149, App
551	11.6	38.7	34	3	US-08-471-039-448	Sequence 448, App	624	11.4	38.0	19	4	US-09-422-978-5040	Sequence 5040, Ap
552	11.6	38.7	34	3	US-08-960-190A-3	Sequence 3, Appl	625	11.4	38.0	19	4	US-09-402-181B-382	Sequence 382, App
553	11.6	38.7	34	3	US-09-067-615-41	Sequence 41, Appl	626	11.4	38.0	19	4	US-09-721-456-382	Sequence 382, App
554	11.6	38.7	34	4	US-08-559-390-448	Sequence 448, App	627	11.4	38.0	19	4	US-09-696-791-2023	Sequence 2023, Ap
555	11.6	38.7	34	5	PCT-US93-11198-448	Sequence 448, App	628	11.4	38.0	20	2	US-08-117-952-253	Sequence 253, App
556	11.6	38.7	34	5	PCT-US95-09816A-41	Sequence 41, Appl	629	11.4	38.0	20	4	US-09-446-754-14	Sequence 14, Appl
557	11.6	38.7	35	1	US-07-985-110-10	Sequence 10, Appl	630	11.4	38.0	20	4	US-09-446-754-15	Sequence 15, Appl
558	11.6	38.7	35	1	US-08-099-053-10	Sequence 10, Appl	631	11.4	38.0	20	4	US-09-733-294A-55	Sequence 55, Appl
559	11.6	38.7	35	1	US-08-135-511-9	Sequence 9, Appl	632	11.4	38.0	20	6	5487993-6	Patent No. 5487993
560	11.6	38.7	35	1	US-08-452-829-10	Sequence 10, Appl	633	11.4	38.0	21	2	US-09-211-930-9	Sequence 9, Appl
561	11.6	38.7	35	1	US-08-187-453-9	Sequence 9, Appl	634	11.4	38.0	21	3	US-09-340-993-9	Sequence 9, Appl
562	11.6	38.7	35	1	US-08-613-743-2	Sequence 2, Appl	635	11.4	38.0	21	3	US-09-254-023B-38	Sequence 38, Appl
563	11.6	38.7	35	4	US-10-153-064-126	Sequence 126, App	636	11.4	38.0	21	3	US-09-468-442-9	Sequence 9, Appl
564	11.6	38.7	36	3	US-10-153-064-128	Sequence 128, App	637	11.4	38.0	22	4	US-09-086-663A-34	Sequence 34, Appl
565	11.6	38.7	36	3	US-08-692-922-7	Sequence 7, Appl	c 638	11.4	38.0	22	5	PCT-US92-00283-35	Sequence 35, Appl
566	11.6	38.7	36	3	US-08-688-908-1	Sequence 1, Appl	639	11.4	38.0	23	3	US-09-087-232A-7	Sequence 7, Appl

685	11.4	38.0	33	2	US-08-646-367-19	Sequence 19, Appl	758	11.4	38.0	47	1	US-08-411-796-53	Sequence 53, Appl
686	11.4	38.0	33	2	US-08-690-184-7	Sequence 7, Appl	c 759	11.4	38.0	47	1	US-08-123-936-237	Sequence 237, App
c 687	11.4	38.0	33	3	US-09-028-649A-2	Sequence 2, Appl	c 760	11.4	38.0	47	2	US-08-475-228A-237	Sequence 237, App
688	11.4	38.0	33	3	US-08-523-373-12	Sequence 12, Appl	c 761	11.4	38.0	47	3	US-08-482-080A-237	Sequence 237, App
c 689	11.4	38.0	33	3	US-08-946-458-11	Sequence 11, Appl	c 762	11.4	38.0	47	3	US-08-471-039-53	Sequence 53, Appl
c 690	11.4	38.0	33	3	US-08-379-802-10	Sequence 10, Appl	c 763	11.4	38.0	47	3	US-09-354-947-237	Sequence 237, App
c 691	11.4	38.0	33	3	US-09-028-587-2	Sequence 2, Appl	c 764	11.4	38.0	47	4	US-08-559-390-53	Sequence 53, Appl
c 692	11.4	38.0	33	3	US-09-048-129-10	Sequence 10, Appl	c 765	11.4	38.0	47	4	US-09-671-317-551	Sequence 551, App
c 693	11.4	38.0	33	3	US-08-511-759B-8	Sequence 8, Appl	c 766	11.4	38.0	47	4	US-09-671-317-840	Sequence 840, App
c 694	11.4	38.0	33	3	US-09-028-652-2	Sequence 2, Appl	c 767	11.4	38.0	47	4	US-09-671-317-862	Sequence 862, App
c 695	11.4	38.0	33	3	US-08-487-107-2	Sequence 2, Appl	c 768	11.4	38.0	47	4	US-09-422-978-721	Sequence 721, App
c 696	11.4	38.0	33	3	US-09-048-079-10	Sequence 10, Appl	c 769	11.4	38.0	47	4	US-09-422-978-938	Sequence 938, App
c 697	11.4	38.0	33	3	US-09-291-823-7	Sequence 7, Appl	c 770	11.4	38.0	47	4	US-09-422-978-1106	Sequence 1106, Ap
c 698	11.4	38.0	33	3	US-09-592-197-8	Sequence 8, Appl	c 771	11.4	38.0	47	4	US-09-422-978-1646	Sequence 1646, Ap
c 699	11.4	38.0	33	3	US-08-892-704-8	Sequence 8, Appl	c 772	11.4	38.0	47	4	US-09-422-978-2772	Sequence 2772, Ap
c 700	11.4	38.0	34	2	US-08-793-410-19	Sequence 19, Appl	c 773	11.4	38.0	47	4	US-09-422-978-3131	Sequence 3131, Ap
701	11.4	38.0	35	4	US-09-915-060A-13	Sequence 13, Appl	c 774	11.4	38.0	47	5	PCT-US93-1198-53	Sequence 53, Appl
702	11.4	38.0	37	1	US-08-383-743A-21	Sequence 21, Appl	c 775	11.4	38.0	47	5	PCT-US93-11638-11	Sequence 11, Appl
703	11.4	38.0	37	3	US-08-808-881-21	Sequence 21, Appl	c 776	11.4	38.0	47	5	PCT-US93-12388-237	Sequence 237, App
704	11.4	38.0	37	3	US-09-017-631-21	Sequence 21, Appl	c 777	11.4	38.0	47	5	US-08-411-796-167	Sequence 167, App
705	11.4	38.0	37	3	US-09-455-960-22	Sequence 22, Appl	c 778	11.4	38.0	48	1	US-08-411-796-168	Sequence 168, App
706	11.4	38.0	37	4	US-09-520-118-21	Sequence 21, Appl	c 779	11.4	38.0	48	1	US-08-518-878B-6	Sequence 6, Appl
707	11.4	38.0	37	4	US-10-051-325-22	Sequence 22, Appl	c 780	11.4	38.0	48	1	US-08-518-878B-39	Sequence 39, Appl
708	11.4	38.0	37	5	PCT-US93-07116-21	Sequence 21, Appl	c 781	11.4	38.0	48	1	US-08-294-522B-6	Sequence 6, Appl
c 709	11.4	38.0	38	3	US-08-851-843A-108	Sequence 108, App	c 782	11.4	38.0	48	1	US-08-294-522B-39	Sequence 39, Appl
c 710	11.4	38.0	38	3	US-08-974-549A-595	Sequence 595, App	c 783	11.4	38.0	48	2	US-08-807-861A-6	Sequence 6, Appl
c 711	11.4	38.0	38	3	US-08-854-050-108	Sequence 108, App	c 784	11.4	38.0	48	2	US-08-807-861A-39	Sequence 39, Appl
c 712	11.4	38.0	38	3	US-09-430-323-108	Sequence 108, App	c 785	11.4	38.0	48	2	US-08-470-868A-6	Sequence 6, Appl
c 713	11.4	38.0	38	4	US-09-402-181B-595	Sequence 595, App	c 786	11.4	38.0	48	2	US-08-470-868A-39	Sequence 39, Appl
c 714	11.4	38.0	38	4	US-09-721-456-595	Sequence 595, App	c 787	11.4	38.0	48	2	US-08-470-868A-39	Sequence 39, Appl
c 715	11.4	38.0	40	3	US-09-277-016-11	Sequence 11, Appl	c 788	11.4	38.0	48	2	US-08-676-279-9	Sequence 9, Appl
c 716	11.4	38.0	40	4	US-10-153-064-108	Sequence 108, App	c 789	11.4	38.0	48	3	US-08-471-039-167	Sequence 167, App
c 717	11.4	38.0	41	1	US-07-931-473B-104	Sequence 104, App	c 790	11.4	38.0	48	3	US-08-471-039-168	Sequence 168, App
c 718	11.4	38.0	41	1	US-07-931-473B-156	Sequence 156, App	c 791	11.4	38.0	48	3	US-09-210-681-39	Sequence 39, Appl
719	11.4	38.0	41	1	US-07-931-473B-158	Sequence 158, App	c 792	11.4	38.0	48	3	US-08-946-719A-6	Sequence 6, Appl
720	11.4	38.0	41	1	US-07-714-131C-104	Sequence 104, App	c 793	11.4	38.0	48	3	US-08-946-719A-39	Sequence 39, Appl
721	11.4	38.0	41	1	US-07-714-131C-156	Sequence 156, App	c 794	11.4	38.0	48	4	US-08-559-390-167	Sequence 167, App
722	11.4	38.0	41	1	US-07-714-131C-158	Sequence 158, App	c 795	11.4	38.0	48	4	US-08-559-390-168	Sequence 168, App
723	11.4	38.0	41	1	US-08-412-110-104	Sequence 104, App	c 796	11.4	38.0	48	4	US-09-547-983-6	Sequence 6, Appl
724	11.4	38.0	41	1	US-08-412-110-156	Sequence 156, App	c 797	11.4	38.0	48	4	US-09-547-983-39	Sequence 39, Appl
725	11.4	38.0	41	1	US-08-412-110-158	Sequence 158, App	c 798	11.4	38.0	48	4	PCT-US93-11198-167	Sequence 167, App
726	11.4	38.0	41	1	US-08-409-442A-104	Sequence 104, App	c 799	11.4	38.0	48	5	PCT-US93-11198-168	Sequence 168, App
727	11.4	38.0	41	1	US-08-409-442A-156	Sequence 156, App	c 800	11.4	38.0	49	2	US-08-955-138-74	Sequence 74, Appl
728	11.4	38.0	41	1	US-08-409-442A-158	Sequence 158, App	c 801	11.4	38.0	49	2	PCT-US94-08052-8	Sequence 8, Appl
729	11.4	38.0	41	2	US-08-469-609A-104	Sequence 104, App	c 802	11.4	38.0	50	1	US-08-171-389-360	Sequence 360, App
730	11.4	38.0	41	2	US-08-469-609A-156	Sequence 156, App	c 803	11.4	38.0	50	1	US-08-171-389-582	Sequence 582, App
731	11.4	38.0	41	2	US-08-469-609A-158	Sequence 158, App	c 804	11.4	38.0	50	1	US-08-207-901-63	Sequence 63, Appl
732	11.4	38.0	41	3	US-09-143-190-104	Sequence 104, App	c 805	11.4	38.0	50	1	US-08-123-936-360	Sequence 360, App
733	11.4	38.0	41	3	US-09-143-190-156	Sequence 156, App	c 806	11.4	38.0	50	1	US-08-123-936-582	Sequence 582, App
734	11.4	38.0	41	3	US-09-143-190-158	Sequence 158, App	c 807	11.4	38.0	50	2	US-08-475-228A-360	Sequence 360, App
735	11.4	38.0	41	3	US-09-502-344-104	Sequence 104, App	c 808	11.4	38.0	50	2	US-08-475-228A-582	Sequence 582, App
736	11.4	38.0	41	3	US-09-502-344-156	Sequence 156, App	c 809	11.4	38.0	50	2	US-08-482-080A-360	Sequence 360, App
737	11.4	38.0	41	3	US-09-502-344-158	Sequence 158, App	c 810	11.4	38.0	50	3	US-08-482-080A-582	Sequence 582, App
c 738	11.4	38.0	41	3	US-09-564-805-102	Sequence 102, App	c 811	11.4	38.0	50	3	US-09-043-233-7	Sequence 7, Appl
c 739	11.4	38.0	42	1	US-08-233-009-53	Sequence 53, Appl	c 812	11.4	38.0	50	3	US-09-354-947-360	Sequence 360, App
c 740	11.4	38.0	42	1	US-08-233-009-54	Sequence 54, Appl	c 813	11.4	38.0	50	3	US-09-354-947-582	Sequence 582, App
c 741	11.4	38.0	42	3	US-08-864-357F-13	Sequence 13, Appl	c 814	11.4	38.0	50	4	PCT-US93-12388-360	Sequence 360, App
c 742	11.4	38.0	42	3	US-09-475-947A-324	Sequence 324, App	c 815	11.4	38.0	50	5	PCT-US93-12388-582	Sequence 582, App
c 743	11.4	38.0	42	4	US-09-475-947A-325	Sequence 325, App	c 816	11.4	38.0	50	5	US-08-390-850-584	Sequence 584, App
c 744	11.4	38.0	43	2	US-08-686-599A-14	Sequence 14, Appl	c 817	11.4	38.0	50	5	US-08-435-634-584	Sequence 584, App
c 745	11.4	38.0	43	3	US-09-061-702-13	Sequence 13, Appl	c 818	11.2	37.3	17	1	US-08-584-040-5991	Sequence 5991, Ap
c 746	11.4	38.0	43	3	US-09-748-451-13	Sequence 13, Appl	c 819	11.2	37.3	17	3	US-08-584-040-6042	Sequence 6042, Ap
c 747	11.4	38.0	43	3	US-09-312-285-7	Sequence 7, Appl	c 820	11.2	37.3	17	3	US-08-584-040-7634	Sequence 7634, Ap
c 748	11.4	38.0	43	3	US-09-312-266-7	Sequence 7, Appl	c 821	11.2	37.3	17	3	US-09-371-772B-2879	Sequence 2879, Ap
c 749	11.4	38.0	43	3	US-08-987-943-7	Sequence 7, Appl	c 822	11.2	37.3	17	4	US-09-371-772B-3426	Sequence 3426, Ap
c 750	11.4	38.0	43	3	US-08-312-038-7	Sequence 7, Appl	c 823	11.2	37.3	17	4	US-09-371-772B-3426	Sequence 3426, Ap
c 751	11.4	38.0	43	4	US-09-728-764-7	Sequence 7, Appl	c 824	11.2	37.3	17	4	US-09-866-108A-548	Sequence 548, App
c 752	11.4	38.0	43	4	US-09-728-764-7	Sequence 7, Appl	c 825	11.2	37.3	17	4	US-09-866-108A-548	Sequence 548, App
c 753	11.4	38.0	43	4	US-08-312-004B-5	Sequence 5, Appl	c 826	11.2	37.3	17	4	US-09-866-108A-548	Sequence 548, App
c 754	11.4	38.0	43	4	US-09-728-792-7	Sequence 7, Appl	c 827	11.2	37.3	17	4	US-09-866-108A-548	Sequence 548, App
c 755	11.4	38.0	43	4	US-09-850-964-7	Sequence 7, Appl	c 828	11.2	37.3	17	4	US-09-866-108A-548	Sequence 548, App
c 756	11.4	38.0	43	4	US-09-532-806-8	Sequence 8, Appl	c 829	11.2	37.3	17	4	US-09-866-108A-548	Sequence 548, App
c 757	11.4	38.0	43	4	US-08-381-691-12	Sequence 12, Appl	c 830	11.2	37.3	17	4	US-09-866-108A-548	Sequence 548, App
			46	2	US-08-171-389-237	Sequence 237, App							

831	11.2	37.3	17	4	US-09-866-108A-9263	Sequence 9263, Ap	904	11.2	37.3	28	2	US-08-859-998-1212	Sequence 1212, Ap
c 832	11.2	37.3	18	3	US-09-630-706-91	Sequence 91, Appl	c 905	11.2	37.3	28	3	US-08-648-263-15	Sequence 15, Appl
833	11.2	37.3	18	4	US-09-422-978-4787	Sequence 4787, Ap	906	11.2	37.3	28	3	US-09-397-238A-14	Sequence 14, Appl
834	11.2	37.3	18	4	US-09-422-978-9660	Sequence 9660, Ap	907	11.2	37.3	28	3	US-09-225-928-1212	Sequence 1212, Ap
c 835	11.2	37.3	19	3	US-08-072-064-11	Sequence 11, Appl	c 908	11.2	37.3	28	3	US-09-468-265-9	Sequence 9, Appl
836	11.2	37.3	19	4	US-09-060-295-54	Sequence 54, Appl	909	11.2	37.3	28	4	US-09-225-201B-1212	Sequence 1212, Ap
837	11.2	37.3	19	4	US-09-402-923A-54	Sequence 54, Appl	910	11.2	37.3	29	1	US-07-931-473B-125	Sequence 125, App
c 838	11.2	37.3	20	1	US-08-193-779-13	Sequence 13, Appl	911	11.2	37.3	29	1	US-07-714-131C-125	Sequence 125, App
c 839	11.2	37.3	20	3	US-08-578-615A-115	Sequence 115, Appl	912	11.2	37.3	29	1	US-08-409-442A-125	Sequence 125, App
840	11.2	37.3	20	3	US-09-359-757-19	Sequence 19, Appl	913	11.2	37.3	29	1	US-08-412-110-125	Sequence 125, App
841	11.2	37.3	20	3	US-09-428-584-21	Sequence 21, Appl	914	11.2	37.3	29	2	US-08-469-609A-125	Sequence 125, App
842	11.2	37.3	20	4	US-09-780-175-23	Sequence 23, Appl	c 915	11.2	37.3	29	2	US-08-787-902A-5	Sequence 5, Appl
843	11.2	37.3	20	4	US-09-676-610B-49	Sequence 49, Appl	916	11.2	37.3	29	3	US-09-143-130-125	Sequence 125, App
844	11.2	37.3	20	4	US-09-422-978-11629	Sequence 11629, A	917	11.2	37.3	29	3	US-09-302-344-125	Sequence 125, App
845	11.2	37.3	20	4	US-09-198-452A-5613	Sequence 5613, Ap	918	11.2	37.3	29	4	US-09-304-232-214	Sequence 214, App
846	11.2	37.3	20	4	US-09-495-714C-95	Sequence 95, Appl	c 919	11.2	37.3	29	4	US-10-119-466-2	Sequence 2, Appl
c 847	11.2	37.3	20	4	US-10-215-448-25	Sequence 25, Appl	c 920	11.2	37.3	30	1	US-07-955-718-38	Sequence 38, Appl
c 848	11.2	37.3	20	5	PCT-US94-07770-115	Sequence 115, Appl	c 921	11.2	37.3	30	2	US-08-629-001A-30	Sequence 30, Appl
849	11.2	37.3	21	2	US-08-798-738-9	Sequence 9, Appl	c 922	11.2	37.3	30	3	US-08-297-395-31	Sequence 31, Appl
c 850	11.2	37.3	21	2	US-08-738-922-6	Sequence 6, Appl	923	11.2	37.3	30	3	US-08-627-907A-8	Sequence 8, Appl
c 851	11.2	37.3	21	4	US-08-951-034B-4	Sequence 4, Appl	c 924	11.2	37.3	30	3	US-09-178-869-12	Sequence 12, Appl
c 852	11.2	37.3	23	1	US-08-211-202-81	Sequence 81, Appl	925	11.2	37.3	30	3	US-08-642-274D-109	Sequence 109, App
853	11.2	37.3	23	1	US-08-308-949A-11	Sequence 11, Appl	c 926	11.2	37.3	30	4	US-09-761-413-12	Sequence 12, Appl
c 854	11.2	37.3	23	1	US-08-307-619-52	Sequence 52, Appl	c 927	11.2	37.3	30	5	PCT-US91-05742-38	Sequence 38, Appl
c 855	11.2	37.3	23	1	US-08-299-187-3	Sequence 3, Appl	c 928	11.2	37.3	30	6	5217891-16	Patent No. 5217891
c 856	11.2	37.3	23	1	US-08-685-764-26	Sequence 26, Appl	c 929	11.2	37.3	31	3	US-08-951-923-45	Sequence 45, Appl
c 857	11.2	37.3	23	2	US-08-350-260A-98	Sequence 98, Appl	c 930	11.2	37.3	31	3	US-08-679-645-455	Sequence 455, App
c 858	11.2	37.3	23	2	US-08-350-260A-571	Sequence 571, Appl	c 931	11.2	37.3	32	1	US-08-021-623C-15	Sequence 15, Appl
c 859	11.2	37.3	23	3	US-09-050-783-52	Sequence 52, Appl	c 932	11.2	37.3	32	2	US-08-859-998-386	Sequence 386, App
c 860	11.2	37.3	23	4	US-09-104-337A-98	Sequence 98, Appl	c 933	11.2	37.3	32	3	US-08-535-057A-10	Sequence 10, Appl
c 861	11.2	37.3	23	4	US-09-104-337A-571	Sequence 571, Appl	c 934	11.2	37.3	32	3	US-09-225-928-386	Sequence 386, App
c 862	11.2	37.3	23	4	US-10-067-443-53	Sequence 53, Appl	c 935	11.2	37.3	32	4	US-09-225-201B-386	Sequence 386, App
c 863	11.2	37.3	23	4	US-10-067-443-65	Sequence 65, Appl	c 936	11.2	37.3	32	4	US-09-503-252-10	Sequence 10, Appl
c 864	11.2	37.3	23	4	US-10-153-064-53	Sequence 53, Appl	c 937	11.2	37.3	33	4	US-09-948-495A-9	Sequence 9, Appl
c 865	11.2	37.3	23	4	PCT-US95-11114-3	Sequence 65, Appl	938	11.2	37.3	34	1	US-07-796-106-8	Sequence 8, Appl
c 866	11.2	37.3	23	5	PCT-US95-11114-3	Sequence 3, Appl	c 939	11.2	37.3	35	2	US-08-850-049-27	Sequence 27, Appl
c 867	11.2	37.3	24	2	US-08-318-157B-50	Sequence 50, Appl	c 940	11.2	37.3	35	2	US-08-050-478-27	Sequence 27, Appl
c 868	11.2	37.3	24	2	US-08-687-080-129	Sequence 129, Appl	c 941	11.2	37.3	35	3	US-09-414-117-27	Sequence 27, Appl
c 869	11.2	37.3	24	3	US-08-646-861-34	Sequence 34, Appl	c 942	11.2	37.3	35	4	US-08-613-743-3	Sequence 3, Appl
c 870	11.2	37.3	24	4	US-09-253-794-50	Sequence 50, Appl	c 943	11.2	37.3	35	4	US-09-678-437-27	Sequence 27, Appl
c 871	11.2	37.3	25	1	US-08-394-210-3	Sequence 3, Appl	c 944	11.2	37.3	35	4	US-09-964-895-8	Sequence 8, Appl
872	11.2	37.3	25	1	US-08-394-210-16	Sequence 16, Appl	c 945	11.2	37.3	35	4	US-09-943-722-27	Sequence 27, Appl
c 873	11.2	37.3	25	2	US-08-273-402B-4	Sequence 4, Appl	946	11.2	37.3	36	2	US-08-717-123-9	Sequence 9, Appl
c 874	11.2	37.3	25	4	US-09-866-108A-3485	Sequence 3485, Ap	947	11.2	37.3	36	4	US-09-375-257-9	Sequence 9, Appl
875	11.2	37.3	25	4	US-09-866-108A-14151	Sequence 14151, A	c 948	11.2	37.3	37	1	US-08-399-696-61	Sequence 61, Appl
876	11.2	37.3	25	4	US-09-866-108A-14151	Sequence 14152, A	c 949	11.2	37.3	37	3	US-08-961-083-284	Sequence 284, App
877	11.2	37.3	25	4	US-09-866-108A-14162	Sequence 14162, A	950	11.2	37.3	37	3	US-08-536-784-284	Sequence 284, App
878	11.2	37.3	25	4	US-09-866-108A-14163	Sequence 14163, A	c 951	11.2	37.3	38	1	US-08-328-314-11	Sequence 11, Appl
879	11.2	37.3	25	4	US-09-142-108C-38	Sequence 38, Appl	c 952	11.2	37.3	38	1	US-08-731-045-11	Sequence 11, Appl
880	11.2	37.3	26	1	US-08-062-022-5	Sequence 5, Appl	c 953	11.2	37.3	38	3	US-08-535-057A-9	Sequence 9, Appl
881	11.2	37.3	26	1	US-08-495-743-5	Sequence 5, Appl	c 954	11.2	37.3	38	3	US-09-262-773-126	Sequence 126, App
882	11.2	37.3	26	1	US-08-495-739-5	Sequence 5, Appl	c 955	11.2	37.3	38	4	US-09-503-252-9	Sequence 9, Appl
883	11.2	37.3	26	1	US-08-495-741-5	Sequence 5, Appl	956	11.2	37.3	39	1	US-07-759-568-5	Sequence 5, Appl
884	11.2	37.3	26	1	US-08-257-073-123	Sequence 123, Appl	957	11.2	37.3	39	3	US-08-961-083-275	Sequence 275, App
c 885	11.2	37.3	26	3	US-08-062-023-5	Sequence 5, Appl	958	11.2	37.3	39	4	US-08-536-784-275	Sequence 275, App
c 886	11.2	37.3	26	4	US-07-953-726A-38	Sequence 38, Appl	959	11.2	37.3	40	4	US-09-313-221A-78	Sequence 78, Appl
c 887	11.2	37.3	26	4	US-08-062-021A-11	Sequence 11, Appl	960	11.2	37.3	41	1	US-07-931-473B-157	Sequence 157, App
c 888	11.2	37.3	27	1	US-08-758-306-456	Sequence 456, Appl	961	11.2	37.3	41	1	US-07-714-131C-157	Sequence 157, App
c 889	11.2	37.3	27	3	US-08-985-162-858	Sequence 858, App	c 962	11.2	37.3	41	1	US-08-211-202-91	Sequence 91, Appl
c 890	11.2	37.3	27	3	US-08-985-162-959	Sequence 959, App	963	11.2	37.3	41	1	US-08-412-110-157	Sequence 157, App
c 891	11.2	37.3	27	3	US-08-985-162-976	Sequence 976, App	964	11.2	37.3	41	1	US-08-409-442A-157	Sequence 157, App
c 892	11.2	37.3	27	3	US-08-584-040-695	Sequence 695, App	965	11.2	37.3	41	1	US-08-409-442A-361	Sequence 361, App
c 893	11.2	37.3	27	3	US-08-584-040-773	Sequence 773, App	c 966	11.2	37.3	41	1	US-08-307-619-60	Sequence 60, Appl
c 894	11.2	37.3	27	3	US-08-584-040-7710	Sequence 7710, Ap	967	11.2	37.3	41	2	US-08-469-609A-157	Sequence 157, App
c 895	11.2	37.3	27	3	US-08-584-040-4748	Sequence 4748, Ap	968	11.2	37.3	41	2	US-08-469-609A-361	Sequence 361, App
c 896	11.2	37.3	27	3	US-08-584-040-4948	Sequence 4948, Ap	c 969	11.2	37.3	41	2	US-08-350-260A-106	Sequence 106, App
c 897	11.2	37.3	27	3	US-08-584-040-5266	Sequence 5266, Ap	c 970	11.2	37.3	41	2	US-08-350-260A-207	Sequence 207, App
c 898	11.2	37.3	27	3	US-08-584-040-6910	Sequence 6910, Ap	971	11.2	37.3	41	2	US-08-576-626A-24	Sequence 24, Appl
c 899	11.2	37.3	27	4	US-09-401-063-858	Sequence 858, App	972	11.2	37.3	41	3	US-09-143-190-361	Sequence 157, App
c 900	11.2	37.3	27	4	US-09-401-063-959	Sequence 959, App	973	11.2	37.3	41	3	US-09-143-190-361	Sequence 361, App
c 901	11.2	37.3	27	4	US-09-401-063-976	Sequence 976, App	c 974	11.2	37.3	41	3	US-09-050-783-60	Sequence 60, Appl
902	11.2	37.3	28	2	US-08-948-569A-14	Sequence 14, Appl	975	11.2	37.3	41	3	US-09-502-344-157	Sequence 157, App
903	11.2	37.3	28	2	US-09-188-469-14	Sequence 14, Appl	976	11.2	37.3	41	3	US-09-502-344-361	Sequence 361, App

c 977 11.2 37.3 41 4 US-09-104-337A-106
c 978 11.2 37.3 41 4 US-09-104-337A-207
c 979 11.2 37.3 41 4 US-09-060-299-313
c 980 11.2 37.3 41 4 US-09-402-923A-313
c 981 11.2 37.3 42 3 US-09-136-421-2
c 982 11.2 37.3 42 4 US-09-276-533A-9
c 983 11.2 37.3 42 4 US-10-158-735-9
c 984 11.2 37.3 43 3 US-08-732-708C-18
c 985 11.2 37.3 44 2 US-08-350-260A-584
c 986 11.2 37.3 44 4 US-09-104-337A-584
c 987 11.2 37.3 45 2 US-08-749-852-13
c 988 11.2 37.3 46 1 US-08-119-773-14
c 989 11.2 37.3 46 1 US-08-427-640-25
c 990 11.2 37.3 46 3 US-09-173-043-14
c 991 11.2 37.3 46 3 US-09-209-525-22
c 992 11.2 37.3 47 4 US-09-641-638-1267
c 993 11.2 37.3 47 4 US-09-422-978-25
c 994 11.2 37.3 47 4 US-09-422-978-1398
c 995 11.2 37.3 47 4 US-09-422-978-2599
c 996 11.2 37.3 47 4 US-09-422-978-2606
c 997 11.2 37.3 47 4 US-09-422-978-2828
c 998 11.2 37.3 47 4 US-09-422-978-2931
c 999 11.2 37.3 47 4 US-10-170-097-1267
1000 11.2 37.3 48 4 US-09-538-709-121

ALIGNMENTS

RESULT 1
US-08-299-682-13/c
; Sequence 13, Application US/08299682
; Patent No. 5431063
; GENERAL INFORMATION:
; APPLICANT: Fisher, Mary Ellen
; APPLICANT: Watson, Robert Malcolm
; TITLE OF INVENTION: Methods for In-Solution Quenching of
; TITLE OF INVENTION: Fluorescently Labeled Oligonucleotide Probes
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/08/299,682
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION/DOCKET NUMBER: 35,321
REFERENCE/DOCKET INFORMATION: 9002
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-299-682-13
Query Match 63.3%; Score 19; DB 1; Length 33;
Best Local Similarity 96.8%; Pred. No. 20;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Query 1 TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
Db 31 TGGACTCAGTCCTCTGGTCATCTCACCTTCT 31

RESULT 3
US-08-944-410-52/c
; Sequence 52, Application US/08944410
; Patent No. 6607878
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121-0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial

Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
Db 31 TGGACTCAGTCCTCTGGTCATCTCACCTTCT 1

RESULT 2
US-08-347-657-1/c
; Sequence 1, Application US/08347657
; Patent No. 5571673
; GENERAL INFORMATION:
; APPLICANT: Picone, Teresa
; TITLE OF INVENTION: Methods for In-Solution Quenching of
; TITLE OF INVENTION: Fluorescently Labeled Oligonucleotide Probes
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/08/347,657
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION/DOCKET NUMBER: 35,321
REFERENCE/DOCKET INFORMATION: 9037
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-347-657-1
Query Match 63.3%; Score 19; DB 1; Length 33;
Best Local Similarity 96.8%; Pred. No. 20;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Query 1 TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
Db 31 TGGACTCAGTCCTCTGGTCATCTCACCTTCT 31

RESULT 3
US-08-944-410-52/c
; Sequence 52, Application US/08944410
; Patent No. 6607878
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121-0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial

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; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-52

Query Match          54.7%; Score 16.4; DB 4; Length 46;
Best Local Similarity 76.9%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGGTCATCTCACCTT 28
    ||||| ||||| ||||| ||||| |||||
Db 41 GACTCAGACCTTGTGCGATCGACGTT 16

RESULT 4
US-09-297-269-7/c
; Sequence 7, Application US/09297269
; Patent No. 6451557
; GENERAL INFORMATION:
; APPLICANT: VAUGHAN, Paul R.
; APPLICANT: GALANIS, Maria
; APPLICANT: RAMSHAW, John A.M.
; APPLICANT: WERKMEISTER, Jerome A.
; TITLE OF INVENTION: A METHOD FOR PRODUCING, IN YEAST, A HYDROXYLATED TRIPLE
; TITLE OF INVENTION: HELICAL PROTEIN, AND YEAST HOST CELLS USEFUL IN SAID
; TITLE OF INVENTION: METHOD (As Amended)
; FILE REFERENCE: Q54094
; CURRENT APPLICATION NUMBER: US/09/297,269
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: P03310
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: P04306
; EARLIER FILING DATE: 1996-12-19
; EARLIER APPLICATION NUMBER: PCT/AU97/00721
; EARLIER FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 24
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-297-269-7

Query Match          50.7%; Score 15.2; DB 4; Length 24;
Best Local Similarity 85.0%; Pred. No. 8.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 TCCTTGGTCATCTCACCTTC 29
    ||||| ||||| ||||| ||||| |||||
Db 20 TCCTTGGTGACCTCCCTTC 1

RESULT 5
US-09-671-317-930/c
; Sequence 930, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilva
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
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; SOFTWARE: Patent.pm
; SEQ ID NO 930
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 21
; OTHER INFORMATION: 12-442-133 : insertion C
US-09-671-317-930

Query Match          50.7%; Score 15.2; DB 4; Length 47;
Best Local Similarity 85.0%; Pred. No. 9.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 TCCTTGGTCATCTCACCTTC 29
    ||||| ||||| ||||| ||||| |||||
Db 21 TCCCTGATCATTCACCTTC 2

RESULT 6
US-08-944-410-53/c
; Sequence 53, Application US/08944410
; Patent No. 6607878
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-53

Query Match          49.3%; Score 14.8; DB 4; Length 46;
Best Local Similarity 73.1%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGGTCATCTCACCTT 28
    ||||| ||||| ||||| ||||| |||||
Db 41 GACTCAGACCTTGTGCGAGCTGACGTT 16

RESULT 7
US-08-944-410-54/c
; Sequence 54, Application US/08944410
; Patent No. 6607878
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-54

Query Match          49.3%; Score 14.8; DB 4; Length 46;
Best Local Similarity 73.1%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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QY 3 GACTCAGTCCTGGTCATCTCACCTT 28
|||||
Db 41 GACTCAGCTTGTGCACTGACGTT 16

RESULT 8

US-08-944-410-55/c
; Sequence 55, Application US/08944410
; Patent No. 6607878
; GENERAL INFORMATION:
; APPLICANT: SORGE, JOSEPH A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-55

Query Match 49.3%; Score 14.8; DB 4; Length 46;
Best Local Similarity 73.1%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTGGTCATCTCACCTT 28
|||||
Db 41 GACTCAGCTTGTGCACTGACGTT 16

RESULT 9

US-09-422-978-1893
; Sequence 1893, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: COHEN, DANIEL
; APPLICANT: CHUMAKOV, ILIYA
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1893
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-7144-261 : polymorphic base C or T
US-09-422-978-1893

Query Match 49.3%; Score 14.8; DB 4; Length 47;
Best Local Similarity 67.9%; Pred. No. 1.4e+03;
Matches 19; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTGGTCATCTCACCTTCT 30
|||||
Db 14 GTCTCAGTCYGTGGACCCCACTTCT 41

RESULT 10

US-09-916-510A-20
; Sequence 20, Application US/09916510A
; Patent No. 6544507
; GENERAL INFORMATION:
; APPLICANT: IGGO, RICHARD D.
; APPLICANT: BRUNORI, MICHELE A.
; TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
; FILE REFERENCE: 604-596
; CURRENT APPLICATION NUMBER: US/09/916,510A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: GB 9906815.7
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-916-510A-20

Query Match 48.7%; Score 14.6; DB 4; Length 36;
Best Local Similarity 69.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTGGTCATCTCACCTTC 29
|||||
Db 2 TGGCCCGCTATTGGTCATCTGACCTTC 30

RESULT 11

US-09-530-139-28/c
; Sequence 28, Application US/09530139
; Patent No. 6670453
; GENERAL INFORMATION:
; APPLICANT: FRENKEN, LEON GERARDUS
; APPLICANT: HOWELL, STEVEN
; APPLICANT: LEDEBOER, ADRIANUS MARINUS
; APPLICANT: VAN DER LOOT, CORNELIS PAUL
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
; FILE REFERENCE: 60113/268075/ASH
; CURRENT APPLICATION NUMBER: US/09/530,139
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/EP98/06991
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: EP 97308538.4
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-530-139-28

Query Match 48.7%; Score 14.6; DB 4; Length 42;
Best Local Similarity 69.0%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 GGACTCAGTCCTGGTCATCTCACCTTCT 30
|||||
Db 41 GGACCCAGGTCCACGCTCTCTCACCCTCT 13

RESULT 12

US-09-710-200-40/c
; Sequence 40, Application US/09710200
; Patent No. 6379897
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.

```
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Wang, Ling
; APPLICANT: Xu, Xiao
; APPLICANT: Heller, Michael J.
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MICROARRAYS
; FILE REFERENCE: 256/262 Patrick S. Egleman
; CURRENT APPLICATION NUMBER: US/09/710,200
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(1)
; OTHER INFORMATION: Biotinylated
US-09-710-200-40

Query Match          48.7%; Score 14.6; DB 3; Length 49;
Best Local Similarity 69.0%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GCACTCAGTCCTTGTCATCTCACCTTCT 30
Db 43 GCACTCAGTCCTAGTCATCTCCCTAT 15

RESULT 13
US-09-975-408-40/c
; Sequence 40, Application US/09975408
; Patent No. 6492122
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Xu, Xiao
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MICROARRAYS
; FILE REFERENCE: 267/174 Patrick S. Egleman
; CURRENT APPLICATION NUMBER: US/09/975,408
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/710,200
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(1)
; OTHER INFORMATION: Biotinylated
US-09-975-408-40

Query Match          48.7%; Score 14.6; DB 4; Length 49;
Best Local Similarity 69.0%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GCACTCAGTCCTTGTCATCTCACCTTCT 30
Db 43 GCACTCAGTCCTAGTCATCTCCCTAT 15

RESULT 14
US-08-758-306-368/c
; Sequence 368, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
```

```
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF DISEASES ASSOCIATED WITH INTERLEUKIN-2 RECEPTOR GAMMA-CHAIN EXPRESSION
; TITLE OF INVENTION: ASSOCIATED WITH INTERLEUKIN-2 RECEPTOR GAMMA-CHAIN EXPRESSION
; TITLE OF INVENTION: ASSOCIATED WITH INTERLEUKIN-2 RECEPTOR GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 368:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The letter "N" stands for the stem II
; OTHER INFORMATION: region of a HH ribozyme.
US-08-758-306-368

Query Match          48.0%; Score 14.4; DB 1; Length 27;
Best Local Similarity 72.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GACTCAGTCCTTGTCATCTCACCT 27
Db 26 GTCTCATTCATCAGTCACCT 2

RESULT 15
US-09-029-941-6
; Sequence 6, Application US/09029941
; Patent No. 6657106
; GENERAL INFORMATION:
; APPLICANT: SMITH, JAMES ANDREW CHARLES
; TITLE OF INVENTION: REMOVAL OF METALS FROM CONTAMINATED SUBSTRATES BY PLANTS
; FILE REFERENCE: SMITH ET AL.
; CURRENT APPLICATION NUMBER: US/09/029,941
; CURRENT FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
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OTHER INFORMATION: Description of Unknown Organism:SYNTHETIC DNA
OTHER INFORMATION: PRIMER
US-09-029-941-6
Query Match 48.0%; Score 14.4; DB 4; Length 34;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 1 TGGACTCAGTCTCTGGTCA 19
Db 12 TGGACTTAGTCTCTGGCCA 30
RESULT 18
US-09-079-984A-13
; Sequence 13, Application US/09079984A
; Patent No. 6231850
; GENERAL INFORMATION:
; APPLICANT: Okano, Fumiyo, Satoh, Masahiro,
; APPLICANT: Yamada, Katsushige
; TITLE OF INVENTION: Canine interleukin 12, a production method
; TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
; TITLE OF INVENTION: method using it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miller & Christenbury Intellectual Property
; ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
; STREET: 1500 Market Street, 39th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,984A
; FILING DATE: 15-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Austin R. Miller
; REGISTRATION NUMBER: 16,602
; REFERENCE/DOCKET NUMBER: 1051-98
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-1810
; TELEFAX: (215) 568-6946
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other DNA; synthetic DNA
US-09-079-984A-13
Query Match 47.3%; Score 14.2; DB 3; Length 39;
Best Local Similarity 84.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 5 CTCAGTCTCTGGTCAATC 23
Db 17 CTCAGCAGTGGTCAATC 35
RESULT 19
US-09-390-729-13
; Sequence 13, Application US/09390729
; Patent No. 6562334
; GENERAL INFORMATION:
; APPLICANT: Okano, Fumiyo, Satoh, Masahiro,
; APPLICANT: Yamada, Katsushige
; TITLE OF INVENTION: Canine interleukin 12, a production method
; TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
; TITLE OF INVENTION: method using it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miller & Christenbury Intellectual Property

OTHER INFORMATION: Description of Unknown Organism:SYNTHETIC DNA
OTHER INFORMATION: PRIMER
US-09-029-941-6
Query Match 48.0%; Score 14.4; DB 4; Length 34;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 1 TGGACTCAGTCTCTGGTCA 24
Db 6 TGGACTCACTCCATCATCTCTCA 29
RESULT 16
US-09-297-269-6
; Sequence 6, Application US/09297269
; Patent No. 6451557
; GENERAL INFORMATION:
; APPLICANT: VAUGHAN, Paul R.
; APPLICANT: GALANIS, Maria
; APPLICANT: RAMSHAW, John A.M.
; TITLE OF INVENTION: A METHOD FOR PRODUCING, IN YEAST, A HYDROXYLATED TRIPLE
; TITLE OF INVENTION: HELICAL PROTEIN, AND YEAST HOST CELLS USEFUL IN SAID
; TITLE OF INVENTION: METHOD (As Amended)
; FILE REFERENCE: Q54094
; CURRENT APPLICATION NUMBER: US/09/297,269
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: P03310
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: P04306
; EARLIER FILING DATE: 1996-12-19
; EARLIER APPLICATION NUMBER: PCT/AU97/00721
; EARLIER FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 24
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-297-269-6
Query Match 47.3%; Score 14.2; DB 4; Length 24;
Best Local Similarity 84.2%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 10 TCCTTGGTCACTCTCCTT 28
Db 6 TCCTTGGTCACTCTCCTT 24
RESULT 17
US-09-132-619-18
; Sequence 18, Application US/09132619B
; Patent No. 5958697
; GENERAL INFORMATION:
; APPLICANT: Shan, Bei
; APPLICANT: Nitta, Masahiro
; TITLE OF INVENTION: CYP7 Promoter-Binding Factors
; FILE REFERENCE: T97-013
; CURRENT APPLICATION NUMBER: US/09/132,619B
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 60/067,708
; EARLIER FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 34
; TYPE: DNA
; ORGANISM: human
US-09-132-619-18
Query Match 47.3%; Score 14.2; DB 2; Length 34;

```
; ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
; STREET: 1600 Market Street, 39th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/390,729
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/079,984
; FILING DATE: 15-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Austin R. Miller
; REGISTRATION NUMBER: 16,602
; REFERENCE/DOCKET NUMBER: 1051-98
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-1810
; TELEFAX: (215) 568-6946
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other DNA; synthetic DNA
; US-09-390-729-13

Query Match 47.3%; Score 14.2; DB 4; Length 39;
Best Local Similarity 84.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTCAGTCCTTGGTCATCTC 23
Db 17 CTCAGCAGTGGTCATCTC 35

RESULT 20
US-08-221-816B-18/c
; Sequence 18, Application US/08221816B
; Patent No. 5738985
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Witherell, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; TITLE OF INVENTION: OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A

US-08-221-816B-18/c
; Sequence 18, Application US/08221816B
; Patent No. 5738985
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Witherell, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; TITLE OF INVENTION: OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
```

```
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; US-08-221-816B-18

Query Match 47.3%; Score 14.2; DB 1; Length 45;
Best Local Similarity 70.4%; Pred. No. 2.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4 ACTCAGTCCTTGGTCATCTCACCTTCT 30
Db 33 ACTCAGTCAGTGATTATCTACCTGCT 7

RESULT 21
US-10-112-547-18/c
; Sequence 18, Application US/10112547
; Patent No. 6579674
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Witherell, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; TITLE OF INVENTION: OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,547
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
; US-10-112-547-18
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Query Match      47.3%; Score 14.2; DB 4; Length 45;
Best Local Similarity 70.4%; Pred. No. 2.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCCTTGGTCATCTCACCCTTCT 30
   ||||| ||||| ||||| ||||| |||||
Db 33 ACTCAGTCAGTGATTATCTACCCCTGCT 7

RESULT 22
US-10-112-241-18/c
; Sequence 18, Application US/10112241
; Patent No. 6623961
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,241
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-112-241-18

Query Match      47.3%; Score 14.2; DB 4; Length 45;
Best Local Similarity 70.4%; Pred. No. 2.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCCTTGGTCATCTCACCCTTCT 30
   ||||| ||||| ||||| ||||| |||||
Db 33 ACTCAGTCAGTGATTATCTACCCCTGCT 7

RESULT 23
US-09-639-667-1/c
; Sequence 1, Application US/09639667
; Patent No. 6632800
```

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; GENERAL INFORMATION:
; APPLICANT: Russell, Stephen James
; APPLICANT: Peng, Kah Whye
; TITLE OF INVENTION: SYSTEM FOR MONITORING THE EXPRESSION OF
; TRANSGENES
; FILE REFERENCE: 07039-292001
; CURRENT APPLICATION NUMBER: US/09/639,667
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/149,168
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 45
; TYPE: RNA
; ORGANISM: Influenza virus
; US-09-639-667-1

Query Match      47.3%; Score 14.2; DB 4; Length 45;
Best Local Similarity 70.4%; Pred. No. 2.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCCTTGGTCATCTCACCCTTCT 30
   ||||| ||||| ||||| ||||| |||||
Db 33 ACTCAGTCAGTGATTATCTACCCCTGCT 7

RESULT 24
US-10-104-611-18/c
; Sequence 18, Application US/10104611
; Patent No. 6667152
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/104,611
; FILING DATE: 22-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-104-611-18

Query Match      47.3%; Score 14.2; DB 4; Length 45;
Best Local Similarity 70.4%; Pred. No. 2.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCTTGGTCATCTCACCTTCT 30
Db 33 ACTCAGTGAGTGATTTACTACCTGCT 7

RESULT 25
US-10-109-368-18/c
; Sequence 18, Application US/10109368
; Patent No. 6777179
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/109,368
; FILING DATE: 27-Mar-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-109-368-18

Query Match      47.3%; Score 14.2; DB 4; Length 45;
Best Local Similarity 70.4%; Pred. No. 2.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCTTGGTCATCTCACCTTCT 30
Db 33 ACTCAGTGAGTGATTTACTACCTGCT 7

RESULT 26
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```
US-09-338-907-269/c
; Sequence 269, Application US/09338907
; Patent No. 6265546
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CPICP
; CURRENT APPLICATION NUMBER: US/09/338,907
; CURRENT FILING DATE: 1999-06-23
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 09/218,207
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 269
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1..47
; OTHER INFORMATION: polymorphic fragment 4-26-60, variant version of SEQ ID192
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: base G ; A in SEQ ID192
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..23
; OTHER INFORMATION: potential microsequencing oligo 4-26-60.mis1
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 25..47
; OTHER INFORMATION: complement potential microsequencing oligo 4-26-60.mis2
US-09-338-907-269

Query Match      47.3%; Score 14.2; DB 3; Length 47;
Best Local Similarity 70.4%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCTTGGTCATCTCACCTTCT 30
Db 46 AGTCGCTCCTTGGCGCTGCTAACCGTCT 20

RESULT 27
US-09-218-207-269/c
; Sequence 269, Application US/09218207
; Patent No. 6346381
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; FILE REFERENCE: GENSET.018CPI
; CURRENT APPLICATION NUMBER: US/09/218,207
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 269
; LENGTH: 47
; TYPE: DNA
```

```

; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1..47
; OTHER INFORMATION: polymorphic fragment 4-26-60, variant version of SEQ ID192
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: base G ; A in SEQ ID192
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..23
; OTHER INFORMATION: potential microsequencing oligo 4-26-60.mis1
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 25..47
; OTHER INFORMATION: complement potential microsequencing oligo 4-26-60.mis2
; US-09-218-207-269

Query Match          47.3%; Score 14.2; DB 3; Length 47;
Best Local Similarity 70.4%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

;
; 4 ACTCAGTCCTTGGTCATCTCACCTTCT 30
; ||||| ||||| ||||| ||||| |||||
; 46 AGTCGCTCCTTGGCCTGCTAACCGTCT 20
;

RESULT 28
US-08-591-492-18/c
; Sequence 18, Application US/08591492
; Patent No. 5756086
; GENERAL INFORMATION:
; APPLICANT: McClelland, Alan C.
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Adenoviruses Having Modified
; TITLE OF INVENTION: Fiber Proteins
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,492
; FILING DATE: 06-FEB-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,078
; FILING DATE: 13-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 271010-295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: PCR DNA primer
; US-08-591-492-18

Query Match          47.3%; Score 14.2; DB 1; Length 48;
Best Local Similarity 70.4%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

;
; 1 TGGACTCAGTCCTTGGTCATCTCACCT 27
; ||||| ||||| ||||| ||||| |||||
; 30 TGGACCGACTCCATTCCTCCAACTCACCT 4

Query Match          47.3%; Score 14.2; DB 1; Length 48;
Best Local Similarity 70.4%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

;
; 1 TGGACTCAGTCCTTGGTCATCTCACCT 27
; ||||| ||||| ||||| ||||| |||||
; 19 TGGACCGACTCCATTCCTCCAACTCACCT 45

RESULT 30
US-08-859-998-670
; Sequence 670, Application US/08859998
; Patent No. 594076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert
; US-08-591-492-18
```

;; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;; TITLE OF INVENTION: EXPRESSION
;; NUMBER OF SEQUENCES: 1375
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson, P.C.
;; STREET: 2200 Sand Hill Road, Suite 100
;; CITY: Menlo Park
;; STATE: CA
;; COUNTRY: US
;; ZIP: 94025
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows95
;; SOFTWARE: FastSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/859,998
;; FILING DATE: 21-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Field, Bret E.
;; REGISTRATION NUMBER: 37,620
;; REFERENCE/DOCKET NUMBER: 09096/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-322-5070
;; TELEFAX: 415-854-0875
;; INFORMATION FOR SEQ ID NO: 670:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; OTHER INFORMATION: oligonucleotide primer
;; US-08-859-998-670

Query Match 46.7%; Score 14; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGTCCTTGGTCAT 20
Db 9 CAGTCCTTGGTCAT 22

RESULT 31
US-09-225-928-670
; Sequence 670, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; Jokhadze, George
; Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 670:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; US-08-859-998-670

;; APPLICATION NUMBER: US/09/225,928
;; FILING DATE: 05-Jan-1999
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/859,998
;; FILING DATE: 21-MAY-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Field, Bret E.
;; REGISTRATION NUMBER: 37,620
;; REFERENCE/DOCKET NUMBER: 09096/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-322-5070
;; TELEFAX: 415-854-0875
;; INFORMATION FOR SEQ ID NO: 670:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; OTHER INFORMATION: oligonucleotide primer
;; US-09-225-928-670

Query Match 46.7%; Score 14; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGTCCTTGGTCAT 20
Db 9 CAGTCCTTGGTCAT 22

RESULT 32
US-09-225-2018-670
; Sequence 670, Application US/09225201B
; Patent No. 6489455
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; Jokhadze, George
; Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 670:
; SEQUENCE CHARACTERISTICS:

LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 670:
US-09-225-201B-670
Query Match 46.7%; Score 14; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.9e+03; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CAGTCCTTGGTCAT 20
DB 9 CAGTCCTTGGTCAT 22
PCT-US94-08052-9
Sequence 9, Application PC/TUS9408052
GENERAL INFORMATION:
APPLICANT: Schering Corporation
TITLE OF INVENTION: Agonists and Antagonists
TITLE OF INVENTION: Of Human Interleukin-10
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: One Giralda Farms
CITY: Madison
STATE: New Jersey
COUNTRY: USA
ZIP: 07940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh 7.1
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08052
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/098,943
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul, G.
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-08052-9
Query Match 46.7%; Score 14; DB 5; Length 40;
Best Local Similarity 66.7%; Pred. No. 3.1e+03; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
DB 4 TGAATTCATCTCATGTGTCATGAGCTTCT 33
RESULT 34
US-08-401-068-9/c
Sequence 9, Application US/08401068
Patent No. 5859335
GENERAL INFORMATION:
APPLICANT: Patton, David
TITLE OF INVENTION: Enhanced Biotin Biosynthesis in Plant Tissue
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,068
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/351,970
FILING DATE: 08-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide primer for PCR of bioA gene"
HYPOTHETICAL: NO
US-08-401-068-9
Query Match 46.7%; Score 14; DB 2; Length 44;
Best Local Similarity 77.3%; Pred. No. 3.1e+03; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 9 GTCCTTGGTCATCTCACCTTCT 30
DB 29 GTCCTTGGTCATCTCACCTTCT 8
RESULT 35
US-08-846-338-9/c
Sequence 9, Application US/08846338
Patent No. 5869719
GENERAL INFORMATION:
APPLICANT: Patton, David
TITLE OF INVENTION: Transgenic Plants Having Increased Biotin Content
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5869719artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,338
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide primer for
HYPOTHETICAL: NO
US-08-846-338-9

Query Match 46.7%; Score 14; DB 2; Length 44;
Best Local Similarity 77.3%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 9 GTCCCTTGTCATCTCACCTTCT 30
Db 29 GTCCCTTGTCATCTCACCTTCT 8

RESULT 36
US-09-422-978-2989
Sequence 2989, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 2989
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-21448-361 : polymorphic base A or G
US-09-422-978-2989

Query Match 46.7%; Score 14; DB 4; Length 47;
Best Local Similarity 66.7%; Pred. No. 3.1e+03;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCCTTGTCATCTCACCTTCT 30
Db 15 TGCCCTCTGCGCTGTCACCCACCACTT 44

RESULT 37
US-09-006-636-6/c
Sequence 6, Application US/09006636
Patent No. 6005092
GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Shani, Ziv
TITLE OF INVENTION: ARABIDOPSIS THALIANA ENDO-1,4-BETA-
GLUCANASE GENE, PROMOTER AND PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,636
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 7809-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-006-636-6

Query Match 46.0%; Score 13.8; DB 3; Length 28;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 13 TTGGTCATCTCACCTTC 29
Db 27 TTGGTCATCTCACCTTC 11

RESULT 38
US-09-006-632-6/c
Sequence 6, Application US/09006632
Patent No. 6184440
GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Shani, Ziv
APPLICANT: Shpigel, Etai
TITLE OF INVENTION: TRANSGENIC PLANTS OF ALTERED
MORPHOLOGY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,632
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 7809-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

```

; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-006-632-6
Query Match 46.0%; Score 13.8; DB 3; Length 28;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TTGGTCATCTCACCTTC 29
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Db 27 TTGGTCCTATCACCTTC 11

RESULT 39
US-09-325-274-6/c
; Sequence 6, Application US/09325274
; Patent No. 6323023
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; APPLICANT: Shani, Ziv
; TITLE OF INVENTION: ARABIDOPSIS THALIANA ENDO-1,4-BETA-
; TITLE OF INVENTION: GLUCANASE GENE, PROMOTER AND PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,274
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/006,636
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Baldwin, Geraldine F.
; REGISTRATION NUMBER: 31,232
; REFERENCE/DOCKET NUMBER: 7809-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-325-274-6
Query Match 46.0%; Score 13.8; DB 3; Length 28;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TTGGTCATCTCACCTTC 29
| | | | | | | | | |
Db 27 TTGGTCCTATCACCTTC 11
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; US-09-416-756A-14
; Sequence 14, Application US/09416756A
; Patent No. 6171845
; GENERAL INFORMATION:
; APPLICANT: Degussa-Huls AG
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF PANTOTHENIC ACID BY
; TITLE OF INVENTION: AMPLIFICATION OF NUCLEOTIDE SEQUENCES WHICH CODE FOR
; TITLE OF INVENTION: KETOPANTOATE REDUCTASE
; FILE REFERENCE: Elischewski
; CURRENT APPLICATION NUMBER: US/09/416,756A
; CURRENT FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: DE 19846499.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PCR primer
US-09-416-756A-14
Query Match 46.0%; Score 13.8; DB 3; Length 36;
Best Local Similarity 72.0%; Pred. No. 3.7e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGGTCATCTCAC 25
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Db 12 TGCAGTCAGTCCTTTCTCCAGTCAC 36

Search completed: November 23, 2004, 22:26:22
Job time : 43.7191 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 18:47:33 ; Search time 140.674 Seconds
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Title: US-10-087-631B-4

Perfect score: 30

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Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications NA.*

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16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	30	100.0	30	15	US-10-419-022-4
3	30	100.0	30	16	US-10-337-190-2
4	19	63.3	31	15	US-10-147-679A-22
5	16.6	55.3	25	15	US-10-098-263B-99847
6	16.4	54.7	46	8	US-08-944-410-52
7	16.2	54.0	25	15	US-10-098-263B-123322
8	16	53.3	26	15	US-10-098-263B-101913
9	15.8	52.7	25	15	US-10-038-835-56
10	15.6	52.0	50	16	US-10-131-827-405
11	15.6	52.0	50	16	US-10-131-827-4918
12	15.4	51.3	25	15	US-10-098-263B-112496

c 13	15.2	50.7	22	10	US-09-912-976-93	Sequence 93, Appl
c 14	15.2	50.7	22	10	US-09-965-422-76	Sequence 76, Appl
c 15	15.2	50.7	22	10	US-09-965-422-82	Sequence 82, Appl
c 16	15.2	50.7	22	15	US-10-005-041A-202	Sequence 202, Appl
c 17	15.2	50.7	24	14	US-10-023-831A-7	Sequence 7, Appl
c 18	15.2	50.7	47	16	US-10-294-934-930	Sequence 930, Appl
c 19	15.2	50.7	47	16	US-10-335-181-13	Sequence 13, Appl
c 20	15	50.0	25	15	US-10-098-263B-99848	Sequence 99848, A
c 21	15	50.0	25	15	US-10-098-263B-106307	Sequence 106307, A
c 22	15	50.0	25	15	US-10-098-263B-106308	Sequence 106308, A
c 23	15	50.0	31	9	US-09-801-274-1484	Sequence 1484, Ap
c 24	15	50.0	31	9	US-10-131-827-4195	Sequence 4195, Ap
c 25	14.8	49.3	50	16	US-10-038-835-27	Sequence 27, Appl
c 26	14.8	49.3	25	18	US-10-427-696-311	Sequence 311, Appl
c 27	14.8	49.3	41	16	US-10-035-833A-347	Sequence 347, Appl
c 28	14.8	49.3	41	16	US-10-035-833A-6498	Sequence 6498, Ap
c 29	14.8	49.3	46	8	US-08-944-410-53	Sequence 53, Appl
c 30	14.8	49.3	46	8	US-08-944-410-54	Sequence 54, Appl
c 31	14.8	49.3	46	8	US-08-944-410-55	Sequence 55, Appl
c 32	14.8	49.3	47	16	US-10-349-143-1893	Sequence 1893, Ap
c 33	14.6	48.7	25	15	US-10-098-263B-102519	Sequence 102519, A
c 34	14.6	48.7	25	15	US-10-098-263B-123321	Sequence 123321, A
c 35	14.6	48.7	26	16	US-10-210-130-295	Sequence 295, Appl
c 36	14.6	48.7	36	9	US-09-916-510A-20	Sequence 20, Appl
c 37	14.6	48.7	36	16	US-10-376-630-20	Sequence 20, Appl
c 38	14.6	48.7	38	16	US-10-453-827-1043	Sequence 1043, Ap
c 39	14.6	48.7	38	16	US-10-453-827-1190	Sequence 1190, Ap
c 40	14.6	48.7	42	10	US-09-530-139-28	Sequence 28, Appl
c 41	14.6	48.7	49	9	US-09-975-408-40	Sequence 40, Appl
c 42	14.6	48.7	49	13	US-10-075-579-40	Sequence 40, Appl
c 43	14.6	48.7	50	16	US-10-416-122-11	Sequence 11, Appl
c 44	14.4	48.0	25	15	US-10-098-263B-66485	Sequence 66485, A
c 45	14.4	48.0	25	15	US-10-098-263B-101914	Sequence 101914, A
c 46	14.4	48.0	34	9	US-09-029-941-6	Sequence 6, Appl
c 47	14.4	48.0	45	10	US-09-791-153A-26	Sequence 26, Appl
c 48	14.4	48.0	47	16	US-10-333-429-6	Sequence 6, Appl
c 49	14.2	47.3	24	14	US-10-023-831A-6	Sequence 6, Appl
c 50	14.2	47.3	34	18	US-10-721-997A-1	Sequence 1, Appl
c 51	14.2	47.3	34	18	US-10-721-997A-2	Sequence 2, Appl
c 52	14.2	47.3	37	9	US-09-917-265-99	Sequence 99, Appl
c 53	14.2	47.3	45	13	US-10-104-611-18	Sequence 18, Appl
c 54	14.2	47.3	45	13	US-10-112-547-18	Sequence 18, Appl
c 55	14.2	47.3	45	13	US-10-112-241-18	Sequence 18, Appl
c 56	14.2	47.3	45	15	US-10-109-368-18	Sequence 18, Appl
c 57	14.2	47.3	45	18	US-10-641-834-1	Sequence 1, Appl
c 58	14.2	47.3	47	9	US-09-901-484A-269	Sequence 269, Appl
c 59	14.2	47.3	47	9	US-09-853-526-269	Sequence 269, Appl
c 60	14	46.7	19	15	US-10-038-835-25	Sequence 25, Appl
c 61	14	46.7	24	15	US-10-411-954-61	Sequence 61, Appl
c 62	14	46.7	24	15	US-10-411-954-293	Sequence 293, Appl
c 63	14	46.7	24	16	US-10-617-070-61	Sequence 61, Appl
c 64	14	46.7	24	16	US-10-617-070-293	Sequence 293, Appl
c 65	14	46.7	24	16	US-10-617-070-448	Sequence 448, Appl
c 66	14	46.7	25	15	US-10-098-263B-13236	Sequence 13236, A
c 67	14	46.7	25	15	US-10-098-263B-80490	Sequence 80490, A
c 68	14	46.7	25	15	US-10-098-263B-127582	Sequence 127582, A
c 69	14	46.7	41	16	US-10-035-833A-4865	Sequence 4865, Ap
c 70	14	46.7	47	16	US-10-349-143-2989	Sequence 2989, Ap
c 71	14	46.7	50	15	US-10-131-827-885	Sequence 885, Appl
c 72	13.8	46.0	24	15	US-10-032-585-4184	Sequence 4184, Ap
c 73	13.8	46.0	25	15	US-10-098-263B-96195	Sequence 96195, A
c 74	13.8	46.0	25	15	US-10-098-263B-112495	Sequence 112495, A
c 75	13.8	46.0	37	16	US-10-671-403-159	Sequence 159, Appl
c 76	13.8	46.0	37	16	US-10-671-419-159	Sequence 159, Appl
c 77	13.8	46.0	37	16	US-10-670-844-159	Sequence 159, Appl
c 78	13.8	46.0	37	16	US-10-671-134-159	Sequence 159, Appl
c 79	13.8	46.0	37	16	US-10-673-098-159	Sequence 159, Appl
c 80	13.8	46.0	37	16	US-10-672-638-159	Sequence 159, Appl
c 81	13.8	46.0	37	16	US-10-673-127-159	Sequence 159, Appl
c 82	13.8	46.0	37	17	US-10-670-817-159	Sequence 159, Appl
c 83	13.8	46.0	37	17	US-10-673-119-159	Sequence 159, Appl
c 84	13.8	46.0	37	18	US-10-671-207-159	Sequence 159, Appl
c 85	13.8	46.0	50	16	US-10-131-827-4500	Sequence 4500, Ap

c 86	13.6	45.3	20	17	US-10-480-276-18	Sequence 18, Appl	c 159	13.2	44.0	23	15	US-10-094-466-113	Sequence 113, App
c 87	13.6	45.3	21	18	US-10-786-720-8259	Sequence 8259, Ap	c 160	13.2	44.0	25	15	US-10-098-263B-346	Sequence 346, App
c 88	13.6	45.3	21	18	US-10-786-720-10491	Sequence 10491, A	c 161	13.2	44.0	25	15	US-10-098-263B-29149	Sequence 29149, A
c 89	13.6	45.3	24	10	US-09-940-185-2392	Sequence 2392, Ap	c 162	13.2	44.0	25	15	US-10-098-263B-29150	Sequence 29150, A
c 90	13.6	45.3	25	15	US-10-098-263B-242	Sequence 242, App	c 163	13.2	44.0	25	15	US-10-098-263B-110822	Sequence 110822, A
c 91	13.6	45.3	25	15	US-10-098-263B-12999	Sequence 12999, A	c 164	13.2	44.0	25	17	US-10-717-597-952	Sequence 952, App
c 92	13.6	45.3	25	15	US-10-098-263B-42188	Sequence 42188, A	c 165	13.2	44.0	25	17	US-10-775-1619-581	Sequence 581, App
c 93	13.6	45.3	25	15	US-10-098-263B-73505	Sequence 73505, A	c 166	13.2	44.0	26	15	US-10-243-581B-7	Sequence 7, Appli
c 94	13.6	45.3	25	15	US-10-098-263B-93212	Sequence 93212, A	c 167	13.2	44.0	26	17	US-10-741-601-26211	Sequence 26211, A
c 95	13.6	45.3	29	16	US-10-093-463-204	Sequence 204, App	c 168	13.2	44.0	34	9	US-09-086-118-19	Sequence 19, Appl
c 96	13.6	45.3	29	16	US-10-072-012-1238	Sequence 1238, Ap	c 169	13.2	44.0	34	15	US-10-387-806-19	Sequence 19, Appl
c 97	13.6	45.3	31	10	US-09-961-077-437	Sequence 437, App	c 170	13.2	44.0	36	9	US-09-765-272-291	Sequence 291, App
c 98	13.6	45.3	31	17	US-10-772-656-69	Sequence 69, Appl	c 171	13.2	44.0	37	13	US-10-027-632-178427	Sequence 178427, App
c 99	13.6	45.3	39	10	US-09-093-972C-989	Sequence 989, App	c 172	13.2	44.0	37	15	US-10-027-632-178427	Sequence 87, Appl
c 100	13.6	45.3	43	16	US-10-260-238-6023	Sequence 6023, Ap	c 173	13.2	44.0	37	16	US-10-612-779-87	Sequence 49, Appl
c 101	13.4	44.7	17	14	US-10-060-756A-1888	Sequence 1888, Ap	c 174	13.2	44.0	46	8	US-08-944-410-49	Sequence 50, Appl
c 102	13.4	44.7	17	14	US-10-060-756A-1889	Sequence 1889, Ap	c 175	13.2	44.0	46	8	US-08-944-410-50	Sequence 51, Appl
c 103	13.4	44.7	17	14	US-10-060-756A-1890	Sequence 1890, Ap	c 176	13.2	44.0	46	8	US-08-944-410-56	Sequence 56, Appl
c 104	13.4	44.7	20	9	US-09-754-167-22	Sequence 22, Appl	c 177	13.2	44.0	46	8	US-08-944-410-57	Sequence 57, Appl
c 105	13.4	44.7	20	12	US-09-745-167A-22	Sequence 22, Appl	c 178	13.2	44.0	46	8	US-08-944-410-57	Sequence 57, Appl
c 106	13.4	44.7	21	18	US-10-786-720-6553	Sequence 6553, Ap	c 179	13.2	44.0	47	15	US-10-367-438-42	Sequence 42, Appl
c 107	13.4	44.7	21	18	US-10-786-720-6554	Sequence 6554, Ap	c 180	13.2	44.0	47	15	US-10-367-438-42	Sequence 1615, Ap
c 108	13.4	44.7	21	18	US-10-786-720-6555	Sequence 6555, Ap	c 181	13.2	44.0	47	16	US-10-349-143-1615	Sequence 2521, Ap
c 109	13.4	44.7	21	18	US-10-786-720-7888	Sequence 7888, Ap	c 182	13.2	44.0	47	16	US-10-349-143-2521	Sequence 802, Ap
c 110	13.4	44.7	21	18	US-10-786-720-8257	Sequence 8257, Ap	c 183	13.2	44.0	47	16	US-10-294-934-802	Sequence 945, App
c 111	13.4	44.7	21	18	US-10-786-720-8258	Sequence 8258, Ap	c 184	13.2	44.0	50	16	US-10-131-827-1516	Sequence 1516, Ap
c 112	13.4	44.7	21	18	US-10-786-720-8260	Sequence 8260, Ap	c 185	13.2	44.0	50	16	US-10-131-827-1516	Sequence 2, Appli
c 113	13.4	44.7	21	18	US-10-786-720-8261	Sequence 8261, Ap	c 186	13.2	44.0	20	10	US-09-998-009-2	Sequence 62, Appl
c 114	13.4	44.7	21	18	US-10-786-720-8262	Sequence 8262, Ap	c 187	13.2	44.0	22	9	US-09-814-777A-62	Sequence 66, Appl
c 115	13.4	44.7	21	18	US-10-786-720-8845	Sequence 8845, Ap	c 188	13.2	44.0	22	14	US-09-814-777A-66	Sequence 2, Appli
c 116	13.4	44.7	21	18	US-10-786-720-8846	Sequence 8846, Ap	c 189	13.2	44.0	22	14	US-10-137-290-2	Sequence 12, Appl
c 117	13.4	44.7	21	18	US-10-786-720-8847	Sequence 8847, Ap	c 190	13.2	44.0	22	15	US-10-141-541-12	Sequence 12, Appl
c 118	13.4	44.7	21	18	US-10-786-720-10138	Sequence 10138, A	c 191	13.2	44.0	22	15	US-10-388-263-158	Sequence 158, App
c 119	13.4	44.7	21	18	US-10-786-720-10489	Sequence 10489, A	c 192	13.2	44.0	25	15	US-10-098-263B-41815	Sequence 41815, A
c 120	13.4	44.7	21	18	US-10-786-720-10490	Sequence 10490, A	c 193	13.2	44.0	25	15	US-10-098-263B-42654	Sequence 42654, A
c 121	13.4	44.7	21	18	US-10-786-720-10492	Sequence 10492, A	c 194	13.2	44.0	25	15	US-10-098-263B-81526	Sequence 81526, A
c 122	13.4	44.7	21	18	US-10-786-720-10493	Sequence 10493, A	c 195	13.2	44.0	25	15	US-10-098-263B-93072	Sequence 93072, A
c 123	13.4	44.7	25	14	US-10-786-720-10494	Sequence 10494, A	c 196	13.2	44.0	25	15	US-10-098-263B-102520	Sequence 102520, A
c 124	13.4	44.7	25	14	US-10-060-756A-3885	Sequence 3885, Ap	c 197	13.2	44.0	25	15	US-10-098-263B-117000	Sequence 117000, A
c 125	13.4	44.7	25	14	US-10-060-756A-3886	Sequence 3886, Ap	c 198	13.2	44.0	25	15	US-10-061-201-2402	Sequence 2402, Ap
c 126	13.4	44.7	25	14	US-10-060-756A-3887	Sequence 3887, Ap	c 199	13.2	44.0	25	15	US-10-061-201-2403	Sequence 2403, Ap
c 127	13.4	44.7	25	14	US-10-060-756A-3888	Sequence 3888, Ap	c 200	13.2	44.0	25	15	US-10-061-201-2404	Sequence 2404, Ap
c 128	13.4	44.7	25	14	US-10-060-756A-3889	Sequence 3889, Ap	c 201	13.2	44.0	25	15	US-10-061-201-2405	Sequence 2405, Ap
c 129	13.4	44.7	25	14	US-10-060-756A-3890	Sequence 3890, Ap	c 202	13.2	44.0	25	15	US-10-061-201-2406	Sequence 2406, Ap
c 130	13.4	44.7	25	14	US-10-060-756A-3891	Sequence 3891, Ap	c 203	13.2	44.0	29	16	US-09-940-227-61	Sequence 61, Appl
c 131	13.4	44.7	25	14	US-10-060-756A-3892	Sequence 3892, Ap	c 204	13.2	44.0	30	13	US-10-451-942-21	Sequence 21, Appl
c 132	13.4	44.7	25	14	US-10-060-756A-3893	Sequence 3893, Ap	c 205	13.2	44.0	30	14	US-10-139-262-37	Sequence 37, Appl
c 133	13.4	44.7	25	14	US-10-060-756A-3894	Sequence 3894, Ap	c 206	13.2	44.0	31	10	US-10-255-969-37	Sequence 37, Appl
c 134	13.4	44.7	25	14	US-10-060-756A-3895	Sequence 3895, Ap	c 207	13.2	44.0	31	10	US-09-912-263-269	Sequence 269, App
c 135	13.4	44.7	25	14	US-10-215-112-3767	Sequence 3767, Ap	c 208	13.2	44.0	32	9	US-09-334-477-45	Sequence 45, Appl
c 136	13.4	44.7	25	14	US-10-215-112-4702	Sequence 4702, Ap	c 209	13.2	44.0	32	15	US-10-327-592-1	Sequence 1, Appli
c 137	13.4	44.7	25	15	US-10-098-263B-94375	Sequence 94375, A	c 210	13.2	44.0	33	17	US-10-679-620-49	Sequence 49, Appl
c 138	13.4	44.7	27	16	US-10-401-520-113	Sequence 113, App	c 211	13.2	44.0	34	17	US-10-475-970-57	Sequence 57, Appl
c 139	13.4	44.7	27	16	US-10-401-520-130	Sequence 130, App	c 212	13.2	44.0	35	15	US-10-280-261-7	Sequence 7, Appli
c 140	13.4	44.7	30	15	US-10-197-844-3	Sequence 3, Appli	c 213	13.2	44.0	36	9	US-09-932-2548-2	Sequence 2, Appli
c 141	13.4	44.7	31	9	US-09-801-274-1749	Sequence 1749, Ap	c 214	13.2	44.0	36	14	US-10-118-495-17	Sequence 17, Appl
c 142	13.4	44.7	32	14	US-10-118-783-8	Sequence 8, Appli	c 215	13.2	44.0	36	14	US-10-118-495-18	Sequence 18, Appl
c 143	13.4	44.7	36	15	US-10-182-269A-2	Sequence 2, Appli	c 216	13.2	44.0	36	16	US-10-620-914-17	Sequence 17, Appl
c 144	13.4	44.7	37	14	US-10-187-339-3	Sequence 3, Appli	c 217	13.2	44.0	39	9	US-10-620-914-18	Sequence 18, Appl
c 145	13.4	44.7	39	16	US-10-453-827-311	Sequence 311, App	c 218	13.2	44.0	41	15	US-09-749-831-33	Sequence 33, Appl
c 146	13.4	44.7	41	16	US-10-035-833A-1851	Sequence 1851, Ap	c 219	13.2	44.0	41	15	US-10-005-956-246	Sequence 246, App
c 147	13.4	44.7	41	16	US-10-035-833A-4446	Sequence 4446, Ap	c 220	13.2	44.0	41	16	US-10-035-833A-6033	Sequence 6033, Ap
c 148	13.4	44.7	42	8	US-08-944-410-80	Sequence 80, Appl	c 221	13.2	44.0	46	15	US-10-270-071-49	Sequence 49, Appl
c 149	13.4	44.7	44	16	US-10-377-134-24	Sequence 24, Appl	c 222	13.2	44.0	46	15	US-10-411-954-65	Sequence 65, Appl
c 150	13.4	44.7	44	16	US-10-377-134-36	Sequence 36, Appl	c 223	13.2	44.0	46	16	US-10-617-070-65	Sequence 65, Appl
c 151	13.4	44.7	47	16	US-10-349-143-1446	Sequence 1446, Ap	c 224	13.2	44.0	46	16	US-10-617-070-297	Sequence 297, App
c 152	13.4	44.7	49	9	US-09-771-425-16	Sequence 16, Appl	c 225	13.2	44.0	46	16	US-10-617-070-452	Sequence 452, App
c 153	13.4	44.7	50	16	US-10-131-827-520	Sequence 520, App	c 226	13.2	44.0	47	15	US-10-617-070-452	Sequence 452, App
c 154	13.2	44.0	19	16	US-10-206-705-77	Sequence 77, Appl	c 227	13.2	44.0	47	15	US-10-411-954-296	Sequence 296, App
c 155	13.2	44.0	19	16	US-10-206-705-262	Sequence 262, App	c 228	13.2	44.0	47	16	US-10-349-143-2988	Sequence 2988, Ap
c 156	13.2	44.0	20	16	US-09-865-866-93	Sequence 93, Appl	c 229	13.2	44.0	47	16	US-10-617-070-64	Sequence 64, Appl
c 157	13.2	44.0	20	16	US-10-444-206-336	Sequence 336, App	c 230	13.2	44.0	47	16	US-10-617-070-296	Sequence 296, App
c 158	13.2	44.0	22	13	US-10-021-509-14	Sequence 14, Appl	c 231	13.2	44.0	47	16	US-10-617-070-451	Sequence 451, App

C 232	13	43.3	48	10	US-09-405-032-70	Sequence 70, Appl	C 305	12.8	42.7	47	16	US-10-349-143-2336	Sequence 2336, Ap
C 233	13	43.3	48	13	US-10-027-632-52816	Sequence 52816, A	C 306	12.8	42.7	47	16	US-10-294-934-734	Sequence 734, App
C 234	13	43.3	48	13	US-10-027-632-52816	Sequence 52816, A	C 307	12.8	42.7	47	16	US-10-333-429-115	Sequence 115, App
C 235	13	43.3	48	16	US-10-179-940-165	Sequence 165, App	C 308	12.8	42.7	50	13	US-10-006-009-21	Sequence 21, Appl
C 236	13	43.3	48	16	US-10-179-940-169	Sequence 169, App	C 309	12.8	42.7	50	16	US-10-131-827-6610	Sequence 6610, Ap
C 237	13	43.3	50	9	US-09-880-732-15	Sequence 15, Appl	C 310	12.8	42.7	50	16	US-10-131-827-7000	Sequence 7000, Ap
C 238	13	43.3	50	10	US-09-993-346-393	Sequence 393, App	C 311	12.6	42.0	20	8	US-08-424-550B-711	Sequence 711, App
C 239	13	43.3	50	10	US-10-322-360-70	Sequence 70, Appl	C 312	12.6	42.0	20	15	US-10-071-179-96	Sequence 96, Appl
C 240	13	43.3	50	15	US-10-322-360-71	Sequence 71, Appl	C 313	12.6	42.0	20	15	US-10-126-704-96	Sequence 96, Appl
C 241	13	43.3	50	15	US-10-322-360-123	Sequence 123, App	C 314	12.6	42.0	21	16	US-10-307-817-657	Sequence 657, App
C 242	13	43.3	50	16	US-10-131-827-4275	Sequence 4275, Ap	C 315	12.6	42.0	21	18	US-10-786-720-289	Sequence 289, App
C 243	12.8	42.7	17	10	US-09-818-875-3530	Sequence 3530, Ap	C 316	12.6	42.0	21	18	US-10-786-720-291	Sequence 291, App
C 244	12.8	42.7	17	10	US-09-818-875-3531	Sequence 3531, Ap	C 317	12.6	42.0	21	18	US-10-786-720-13491	Sequence 13491, A
C 245	12.8	42.7	17	15	US-10-209-787-3530	Sequence 3530, Ap	C 318	12.6	42.0	23	9	US-09-863-086-57	Sequence 57, Appl
C 246	12.8	42.7	17	15	US-10-209-787-3531	Sequence 3531, Ap	C 319	12.6	42.0	23	9	US-09-863-086-58	Sequence 58, Appl
C 247	12.8	42.7	17	16	US-10-261-185-3530	Sequence 3530, Ap	C 320	12.6	42.0	23	9	US-09-863-086-59	Sequence 59, Appl
C 248	12.8	42.7	17	16	US-10-261-185-3531	Sequence 3531, Ap	C 321	12.6	42.0	23	9	US-09-863-086-60	Sequence 60, Appl
C 249	12.8	42.7	17	17	US-10-681-074-3530	Sequence 3530, Ap	C 322	12.6	42.0	23	16	US-10-672-238-57	Sequence 57, Appl
C 250	12.8	42.7	17	17	US-10-681-074-3531	Sequence 3531, Ap	C 323	12.6	42.0	23	16	US-10-672-238-58	Sequence 58, Appl
C 251	12.8	42.7	18	16	US-10-349-143-6022	Sequence 6022, Ap	C 324	12.6	42.0	23	16	US-10-672-238-59	Sequence 59, Appl
C 252	12.8	42.7	20	9	US-09-986-621-15	Sequence 15, Appl	C 325	12.6	42.0	23	16	US-10-672-238-60	Sequence 60, Appl
C 253	12.8	42.7	20	10	US-09-986-625-15	Sequence 15, Appl	C 326	12.6	42.0	24	10	US-09-826-509-135	Sequence 135, App
C 254	12.8	42.7	20	15	US-10-020-478-41	Sequence 41, Appl	C 327	12.6	42.0	25	9	US-09-866-108-3476	Sequence 3476, Ap
C 255	12.8	42.7	20	15	US-10-292-951-15	Sequence 15, Appl	C 328	12.6	42.0	25	9	US-09-866-108-3477	Sequence 3477, Ap
C 256	12.8	42.7	20	15	US-10-382-844-15	Sequence 15, Appl	C 329	12.6	42.0	25	9	US-09-866-108-3478	Sequence 3478, Ap
C 257	12.8	42.7	21	9	US-09-986-621-24	Sequence 24, Appl	C 330	12.6	42.0	25	9	US-09-866-108-3479	Sequence 3479, Ap
C 258	12.8	42.7	21	10	US-09-986-625-24	Sequence 24, Appl	C 331	12.6	42.0	25	9	US-09-866-108-3480	Sequence 3480, Ap
C 259	12.8	42.7	21	15	US-10-292-951-24	Sequence 24, Appl	C 332	12.6	42.0	25	9	US-09-866-108-3481	Sequence 3481, Ap
C 260	12.8	42.7	21	15	US-10-382-844-24	Sequence 24, Appl	C 333	12.6	42.0	25	9	US-09-866-108-3482	Sequence 3482, Ap
C 261	12.8	42.7	21	16	US-10-349-143-10245	Sequence 10245, A	C 334	12.6	42.0	25	9	US-09-866-108-14154	Sequence 14154, A
C 262	12.8	42.7	21	18	US-10-604-944-363	Sequence 363, App	C 335	12.6	42.0	25	9	US-09-866-108-14155	Sequence 14155, A
C 263	12.8	42.7	22	17	US-10-239-504-35	Sequence 35, Appl	C 336	12.6	42.0	25	9	US-09-866-108-14156	Sequence 14156, A
C 264	12.8	42.7	24	9	US-09-986-621-27	Sequence 27, Appl	C 337	12.6	42.0	25	9	US-09-866-108-14157	Sequence 14157, A
C 265	12.8	42.7	24	10	US-09-986-625-27	Sequence 27, Appl	C 338	12.6	42.0	25	9	US-09-866-108-14158	Sequence 14158, A
C 266	12.8	42.7	24	15	US-10-292-951-27	Sequence 27, Appl	C 339	12.6	42.0	25	9	US-09-866-108-14159	Sequence 14159, A
C 267	12.8	42.7	24	15	US-10-382-844-27	Sequence 27, Appl	C 340	12.6	42.0	25	9	US-09-866-108-14160	Sequence 14160, A
C 268	12.8	42.7	25	14	US-10-215-112-12589	Sequence 12589, A	C 341	12.6	42.0	25	15	US-10-098-263B-17296	Sequence 17296, A
C 269	12.8	42.7	25	15	US-10-098-263B-8329	Sequence 8329, Ap	C 342	12.6	42.0	25	15	US-10-098-263B-30917	Sequence 30917, A
C 270	12.8	42.7	25	15	US-10-098-263B-24435	Sequence 24435, A	C 343	12.6	42.0	25	15	US-10-098-263B-42104	Sequence 42104, A
C 271	12.8	42.7	25	15	US-10-098-263B-27425	Sequence 27425, A	C 344	12.6	42.0	25	15	US-10-098-263B-45997	Sequence 45997, A
C 272	12.8	42.7	25	15	US-10-098-263B-38774	Sequence 38774, A	C 345	12.6	42.0	25	15	US-10-098-263B-52825	Sequence 52825, A
C 273	12.8	42.7	25	15	US-10-098-263B-54872	Sequence 54872, A	C 346	12.6	42.0	25	15	US-10-098-263B-83862	Sequence 83862, A
C 274	12.8	42.7	25	15	US-10-098-263B-66486	Sequence 66486, A	C 347	12.6	42.0	25	15	US-10-098-263B-92556	Sequence 92556, A
C 275	12.8	42.7	25	15	US-10-098-263B-74154	Sequence 74154, A	C 348	12.6	42.0	25	15	US-10-098-263B-95863	Sequence 95863, A
C 276	12.8	42.7	25	15	US-10-098-263B-83753	Sequence 83753, A	C 349	12.6	42.0	25	15	US-10-098-263B-105744	Sequence 105744, A
C 277	12.8	42.7	25	15	US-10-098-263B-84248	Sequence 84248, A	C 350	12.6	42.0	25	15	US-10-098-263B-130559	Sequence 130559, A
C 278	12.8	42.7	25	15	US-10-098-263B-93410	Sequence 93410, A	C 351	12.6	42.0	25	15	US-10-098-263B-130560	Sequence 130560, A
C 279	12.8	42.7	25	15	US-10-098-263B-94900	Sequence 94900, A	C 352	12.6	42.0	25	17	US-10-723-361-3476	Sequence 3476, Ap
C 280	12.8	42.7	25	15	US-10-098-263B-96834	Sequence 96834, A	C 353	12.6	42.0	25	17	US-10-723-361-3477	Sequence 3477, Ap
C 281	12.8	42.7	25	15	US-10-098-263B-106361	Sequence 106361, A	C 354	12.6	42.0	25	17	US-10-723-361-3478	Sequence 3478, Ap
C 282	12.8	42.7	25	15	US-10-098-263B-113131	Sequence 113131, A	C 355	12.6	42.0	25	17	US-10-723-361-3479	Sequence 3479, Ap
C 283	12.8	42.7	25	15	US-10-098-263B-113132	Sequence 113132, A	C 356	12.6	42.0	25	17	US-10-723-361-3480	Sequence 3480, Ap
C 284	12.8	42.7	25	15	US-10-098-263B-122677	Sequence 122677, A	C 357	12.6	42.0	25	17	US-10-723-361-3481	Sequence 3481, Ap
C 285	12.8	42.7	25	15	US-10-098-263B-122678	Sequence 122678, A	C 358	12.6	42.0	25	17	US-10-723-361-3482	Sequence 3482, Ap
C 286	12.8	42.7	25	15	US-10-098-263B-125797	Sequence 125797, A	C 359	12.6	42.0	25	17	US-10-723-361-14154	Sequence 14154, A
C 287	12.8	42.7	25	15	US-10-098-263B-125798	Sequence 125798, A	C 360	12.6	42.0	25	17	US-10-723-361-14155	Sequence 14155, A
C 288	12.8	42.7	25	15	US-10-061-201-4103	Sequence 4103, Ap	C 361	12.6	42.0	25	17	US-10-723-361-14156	Sequence 14156, A
C 289	12.8	42.7	25	15	US-10-061-201-4104	Sequence 4104, Ap	C 362	12.6	42.0	25	17	US-10-723-361-14157	Sequence 14157, A
C 290	12.8	42.7	26	16	US-10-085-198-444	Sequence 444, App	C 363	12.6	42.0	25	17	US-10-723-361-14158	Sequence 14158, A
C 291	12.8	42.7	27	16	US-10-041-615-140	Sequence 140, App	C 364	12.6	42.0	25	17	US-10-723-361-14159	Sequence 14159, A
C 292	12.8	42.7	28	15	US-10-302-840A-8	Sequence 8, Appl	C 365	12.6	42.0	25	17	US-10-723-361-14160	Sequence 14160, A
C 293	12.8	42.7	29	9	US-09-729-674-242	Sequence 242, App	C 366	12.6	42.0	26	16	US-10-601-913-17	Sequence 17, Appl
C 294	12.8	42.7	29	15	US-10-204-884-74	Sequence 74, Appl	C 367	12.6	42.0	26	16	US-10-601-913-18	Sequence 18, Appl
C 295	12.8	42.7	31	9	US-09-801-274-605	Sequence 605, App	C 368	12.6	42.0	26	16	US-10-601-913-19	Sequence 19, Appl
C 296	12.8	42.7	34	9	US-09-943-692-54	Sequence 54, Appl	C 369	12.6	42.0	26	16	US-10-601-913-20	Sequence 20, Appl
C 297	12.8	42.7	38	13	US-10-114-030-1	Sequence 1, Appl	C 370	12.6	42.0	27	18	US-10-758-307-312	Sequence 312, App
C 298	12.8	42.7	41	16	US-10-035-833A-1345	Sequence 1345, Ap	C 371	12.6	42.0	28	9	US-09-917-265-85	Sequence 85, Appl
C 299	12.8	42.7	41	16	US-10-035-833A-2033	Sequence 2033, Ap	C 372	12.6	42.0	29	10	US-09-915-815-18	Sequence 18, Appl
C 300	12.8	42.7	41	16	US-10-035-833A-4139	Sequence 4139, Ap	C 373	12.6	42.0	30	10	US-09-359-595-23	Sequence 23, Appl
C 301	12.8	42.7	41	16	US-10-035-833A-7280	Sequence 7280, Ap	C 374	12.6	42.0	30	10	US-09-876-252-123	Sequence 123, App
C 302	12.8	42.7	43	10	US-09-971-372A-14	Sequence 14, Appl	C 375	12.6	42.0	30	10	US-09-876-252-124	Sequence 124, App
C 303	12.8	42.7	43	16	US-10-387-387-2	Sequence 2, Appl	C 376	12.6	42.0	30	15	US-10-417-820A-123	Sequence 123, App
C 304	12.8	42.7	47	16	US-10-349-143-1522	Sequence 1522, Ap	C 377	12.6	42.0	30	15	US-10-417-820A-124	Sequence 124, App

378	12.6	42.0	30	17	US-10-723-955-123	Sequence 123, App	C 451	12.4	41.3	25	15	US-10-098-263B-113954	Sequence 103954,
C 379	12.6	42.0	30	17	US-10-723-955-124	Sequence 124, App	C 452	12.4	41.3	25	15	US-10-098-263B-111664	Sequence 111664,
380	12.6	42.0	31	9	US-09-801-274-992	Sequence 992, App	C 453	12.4	41.3	25	15	US-10-098-263B-124876	Sequence 124876,
381	12.6	42.0	32	16	US-10-312-273-407	Sequence 407, App	C 454	12.4	41.3	25	15	US-10-098-263B-127581	Sequence 127581,
382	12.6	42.0	33	14	US-10-269-557-84	Sequence 84, Appl	C 455	12.4	41.3	25	15	US-10-098-263B-128603	Sequence 128603,
383	12.6	42.0	33	18	US-10-784-880-161	Sequence 161, App	C 456	12.4	41.3	25	15	US-10-230-026-83	Sequence 83, Appl
384	12.6	42.0	35	14	US-10-127-746-3	Sequence 3, Appl	C 457	12.4	41.3	25	15	US-10-061-201-4101	Sequence 4101, Ap
385	12.6	42.0	35	15	US-10-150-165-3	Sequence 3, Appl	C 458	12.4	41.3	25	15	US-10-061-201-4102	Sequence 4102, Ap
C 386	12.6	42.0	36	15	US-10-067-449-17	Sequence 17, Appl	C 459	12.4	41.3	25	15	US-10-440-066-4	Sequence 4, Appl
387	12.6	42.0	37	9	US-09-917-265-87	Sequence 87, Appl	C 460	12.4	41.3	25	17	US-10-717-597-1738	Sequence 1738, Ap
388	12.6	42.0	37	9	US-09-976-736-70	Sequence 70, Appl	C 461	12.4	41.3	25	17	US-10-717-597-1739	Sequence 1739, Ap
C 389	12.6	42.0	41	9	US-09-747-774-71	Sequence 71, Appl	C 462	12.4	41.3	25	17	US-10-717-597-1740	Sequence 1740, Ap
C 390	12.6	42.0	41	9	US-09-309-196-63	Sequence 63, Appl	C 463	12.4	41.3	25	17	US-10-717-597-1741	Sequence 1741, Ap
C 391	12.6	42.0	41	10	US-09-953-354-71	Sequence 71, Appl	C 464	12.4	41.3	25	17	US-10-775-169-835	Sequence 835, App
C 392	12.6	42.0	41	15	US-10-263-341-63	Sequence 63, Appl	C 465	12.4	41.3	27	14	US-10-062-848-30	Sequence 30, Appl
C 393	12.6	42.0	41	16	US-10-035-833A-1565	Sequence 1565, Ap	C 466	12.4	41.3	27	14	US-10-062-848-31	Sequence 31, Appl
C 394	12.6	42.0	41	16	US-10-035-833A-4060	Sequence 4060, Ap	C 467	12.4	41.3	27	17	US-10-776-104-30	Sequence 30, Appl
C 395	12.6	42.0	41	16	US-10-035-833A-7096	Sequence 7096, Ap	C 468	12.4	41.3	28	10	US-09-776-191-27	Sequence 27, Appl
C 396	12.6	42.0	41	18	US-10-600-003-63	Sequence 63, Appl	C 469	12.4	41.3	28	15	US-10-090-182A-133	Sequence 133, App
C 397	12.6	42.0	45	15	US-10-156-995-224	Sequence 224, App	C 470	12.4	41.3	29	15	US-10-090-182A-400	Sequence 400, App
C 398	12.6	42.0	47	9	US-09-901-484A-192	Sequence 192, App	C 471	12.4	41.3	29	15	US-10-336-638-798	Sequence 798, App
C 399	12.6	42.0	47	9	US-09-901-484A-193	Sequence 193, App	C 472	12.4	41.3	29	15	US-10-078-113-133	Sequence 133, App
C 400	12.6	42.0	47	9	US-09-853-526-192	Sequence 192, App	C 473	12.4	41.3	29	15	US-10-078-113-400	Sequence 400, App
C 401	12.6	42.0	47	9	US-09-853-526-193	Sequence 193, App	C 474	12.4	41.3	29	16	US-10-179-940-133	Sequence 133, App
C 402	12.6	42.0	47	15	US-10-076-802-63	Sequence 63, Appl	C 475	12.4	41.3	31	9	US-09-801-274-406	Sequence 406, App
C 403	12.6	42.0	47	15	US-10-170-097-803	Sequence 803, App	C 476	12.4	41.3	32	16	US-10-312-273-403	Sequence 403, App
C 404	12.6	42.0	47	15	US-10-170-097-981	Sequence 981, App	C 477	12.4	41.3	33	10	US-09-894-799-16	Sequence 16, Appl
C 405	12.6	42.0	47	15	US-10-367-169-63	Sequence 63, Appl	C 478	12.4	41.3	33	16	US-10-387-943-41	Sequence 41, Appl
C 406	12.6	42.0	47	16	US-10-349-143-1198	Sequence 1198, Ap	C 479	12.4	41.3	33	16	US-10-648-984-16	Sequence 16, Appl
C 407	12.6	42.0	47	16	US-10-349-143-1547	Sequence 1547, Ap	C 480	12.4	41.3	36	18	US-10-770-668-54	Sequence 54, Appl
C 408	12.6	42.0	47	16	US-10-349-143-2807	Sequence 2807, Ap	C 481	12.4	41.3	38	16	US-10-622-240-12	Sequence 12, Appl
C 409	12.6	42.0	47	16	US-10-349-143-3752	Sequence 3752, Ap	C 482	12.4	41.3	41	16	US-10-035-833A-14	Sequence 14, Appl
C 410	12.6	42.0	48	10	US-09-918-156-72	Sequence 72, Appl	C 483	12.4	41.3	41	16	US-10-035-833A-1669	Sequence 1669, Ap
C 411	12.6	42.0	48	16	US-10-179-940-166	Sequence 166, App	C 484	12.4	41.3	41	16	US-10-035-833A-1742	Sequence 1742, Ap
C 412	12.6	42.0	48	16	US-10-179-940-170	Sequence 170, App	C 485	12.4	41.3	41	16	US-10-035-833A-3889	Sequence 3889, Ap
C 413	12.6	42.0	48	18	US-10-843-720-72	Sequence 72, Appl	C 486	12.4	41.3	41	16	US-10-035-833A-5936	Sequence 5936, Ap
C 414	12.6	42.0	48	18	US-10-852-283-72	Sequence 72, Appl	C 487	12.4	41.3	42	16	US-09-276-455-5	Sequence 5, Appl
C 415	12.6	42.0	50	16	US-10-131-827-3448	Sequence 3448, Ap	C 488	12.4	41.3	42	16	US-10-361-208-34	Sequence 34, Appl
C 416	12.6	42.0	50	16	US-10-131-827-8136	Sequence 8136, Ap	C 489	12.4	41.3	42	16	US-10-361-208-35	Sequence 35, Appl
C 417	12.4	41.3	17	14	US-10-060-756A-1887	Sequence 1887, Ap	C 490	12.4	41.3	42	16	US-10-361-208-47	Sequence 47, Appl
C 418	12.4	41.3	17	14	US-10-060-756A-1891	Sequence 1891, Ap	C 491	12.4	41.3	42	16	US-10-361-208-48	Sequence 48, Appl
C 419	12.4	41.3	17	15	US-10-338-777-247	Sequence 247, App	C 492	12.4	41.3	42	16	US-10-601-610-11	Sequence 11, Appl
C 420	12.4	41.3	20	9	US-09-752-639-123	Sequence 123, App	C 493	12.4	41.3	46	16	US-10-071-179-46	Sequence 46, Appl
C 421	12.4	41.3	20	9	US-09-984-198-123	Sequence 123, App	C 494	12.4	41.3	46	15	US-10-126-704-46	Sequence 46, Appl
C 422	12.4	41.3	20	16	US-10-289-762-4748	Sequence 4748, Ap	C 495	12.4	41.3	47	15	US-10-349-143-1776	Sequence 1776, Ap
C 423	12.4	41.3	21	16	US-10-188-186-178	Sequence 178, App	C 496	12.4	41.3	47	16	US-10-349-143-1988	Sequence 1988, Ap
C 424	12.4	41.3	21	18	US-10-786-720-6232	Sequence 6232, App	C 497	12.4	41.3	47	16	US-09-864-785-3416	Sequence 3416, Ap
C 425	12.4	41.3	21	18	US-10-786-720-7890	Sequence 7890, Ap	C 498	12.4	41.3	47	16	US-10-103-597A-16	Sequence 16, Appl
C 426	12.4	41.3	21	18	US-10-786-720-10140	Sequence 10140, A	C 499	12.4	41.3	49	14	US-10-188-444-16	Sequence 16, Appl
C 427	12.4	41.3	21	18	US-10-786-720-13415	Sequence 13415, A	C 500	12.4	41.3	49	15	US-10-131-827-537	Sequence 537, App
C 428	12.4	41.3	22	16	US-10-114-270-338	Sequence 338, App	C 501	12.4	41.3	50	16	US-10-131-827-2103	Sequence 2103, Ap
C 429	12.4	41.3	22	16	US-10-092-900A-523	Sequence 523, App	C 502	12.4	41.3	50	16	US-10-131-827-3321	Sequence 3321, Ap
C 430	12.4	41.3	25	14	US-10-060-756A-3884	Sequence 3884, App	C 503	12.4	41.3	50	16	US-10-131-827-3526	Sequence 3526, Ap
C 431	12.4	41.3	25	14	US-10-060-756A-3896	Sequence 3896, App	C 504	12.4	41.3	50	16	US-10-131-827-4056	Sequence 4056, Ap
C 432	12.4	41.3	25	15	US-10-098-263B-767	Sequence 767, App	C 505	12.4	41.3	50	16	US-10-131-827-4706	Sequence 4706, Ap
C 433	12.4	41.3	25	15	US-10-098-263B-6401	Sequence 6401, App	C 506	12.4	41.3	50	16	US-10-131-827-4933	Sequence 4933, Ap
C 434	12.4	41.3	25	15	US-10-098-263B-7774	Sequence 7774, App	C 507	12.4	41.3	50	16	US-10-131-827-5055	Sequence 5055, Ap
C 435	12.4	41.3	25	15	US-10-098-263B-11738	Sequence 11738, A	C 508	12.4	41.3	50	16	US-09-866-108-547	Sequence 547, App
C 436	12.4	41.3	25	15	US-10-098-263B-12335	Sequence 12335, A	C 509	12.2	40.7	17	10	US-09-818-875-3526	Sequence 3526, Ap
C 437	12.4	41.3	25	15	US-10-098-263B-36574	Sequence 36574, A	C 510	12.2	40.7	17	10	US-09-818-875-3527	Sequence 3527, Ap
C 438	12.4	41.3	25	15	US-10-098-263B-46701	Sequence 46701, A	C 511	12.2	40.7	17	10	US-09-818-875-3534	Sequence 3534, Ap
C 439	12.4	41.3	25	15	US-10-098-263B-49081	Sequence 49081, A	C 512	12.2	40.7	17	10	US-09-818-875-3535	Sequence 3535, Ap
C 440	12.4	41.3	25	15	US-10-098-263B-58754	Sequence 58754, A	C 513	12.2	40.7	17	15	US-10-209-787-3526	Sequence 3526, Ap
C 441	12.4	41.3	25	15	US-10-098-263B-64671	Sequence 64671, A	C 514	12.2	40.7	17	15	US-10-209-787-3527	Sequence 3527, Ap
C 442	12.4	41.3	25	15	US-10-098-263B-66672	Sequence 66672, A	C 515	12.2	40.7	17	15	US-10-209-787-3534	Sequence 3534, Ap
C 443	12.4	41.3	25	15	US-10-098-263B-80489	Sequence 80489, A	C 516	12.2	40.7	17	15	US-10-209-787-3535	Sequence 3535, Ap
C 444	12.4	41.3	25	15	US-10-098-263B-86326	Sequence 86326, A	C 517	12.2	40.7	17	16	US-10-261-185-3526	Sequence 3526, Ap
C 445	12.4	41.3	25	15	US-10-098-263B-86815	Sequence 86815, A	C 518	12.2	40.7	17	16	US-10-261-185-3527	Sequence 3527, Ap
C 446	12.4	41.3	25	15	US-10-098-263B-88209	Sequence 88209, A	C 519	12.2	40.7	17	16	US-10-261-185-3534	Sequence 3534, Ap
C 447	12.4	41.3	25	15	US-10-098-263B-88210	Sequence 88210, A	C 520	12.2	40.7	17	16	US-10-261-185-3535	Sequence 3535, Ap
C 448	12.4	41.3	25	15	US-10-098-263B-97500	Sequence 97500, A	C 521	12.2	40.7	17	16	US-10-676-154-109	Sequence 109, App
C 449	12.4	41.3	25	15	US-10-098-263B-99849	Sequence 99849, A	C 522	12.2	40.7	17	16	US-10-723-361-547	Sequence 547, App
C 450	12.4	41.3	25	15	US-10-098-263B-99850	Sequence 99850, A	C 523	12.2	40.7	17	17		

C 524	12.2	40.7	17	17	US-10-681-074-3526	Sequence 3526, Ap	597	12.2	40.7	26	9	US-09-766-095-4	Sequence 4, Appli
C 525	12.2	40.7	17	17	US-10-681-074-3527	Sequence 3527, Ap	C 598	12.2	40.7	26	9	US-09-766-095-56	Sequence 56, Appl
C 526	12.2	40.7	17	17	US-10-681-074-3528	Sequence 3528, Ap	C 599	12.2	40.7	26	9	US-09-766-095-70	Sequence 70, Appl
C 527	12.2	40.7	17	17	US-10-681-074-3529	Sequence 3529, Ap	C 600	12.2	40.7	26	15	US-09-766-095-84	Sequence 84, Appl
C 528	12.2	40.7	19	15	US-10-225-023-297	Sequence 297, App	C 601	12.2	40.7	26	15	US-10-244-490-10	Sequence 10, Appl
C 529	12.2	40.7	19	15	US-10-225-023-301	Sequence 301, App	C 602	12.2	40.7	27	15	US-10-214-419-50	Sequence 50, Appl
C 530	12.2	40.7	19	15	US-10-225-023-303	Sequence 303, App	C 603	12.2	40.7	27	15	US-09-091-134-7	Sequence 7, Appli
C 531	12.2	40.7	19	15	US-10-225-023-1035	Sequence 1035, App	C 604	12.2	40.7	28	16	US-10-615-518-7	Sequence 7, Appli
C 532	12.2	40.7	19	15	US-10-225-023-1039	Sequence 1039, App	C 605	12.2	40.7	28	17	US-10-772-272A-1	Sequence 1, Appli
C 533	12.2	40.7	19	15	US-10-225-023-1351	Sequence 1351, App	C 606	12.2	40.7	29	10	US-09-749-873-67	Sequence 67, Appl
C 534	12.2	40.7	20	9	US-09-929-486-3	Sequence 3, Appli	C 607	12.2	40.7	29	10	US-09-749-873-83	Sequence 83, Appl
C 535	12.2	40.7	20	10	US-09-973-853-1	Sequence 1, Appli	C 608	12.2	40.7	30	9	US-09-761-413-11	Sequence 11, Appl
C 536	12.2	40.7	20	15	US-10-259-903-3	Sequence 3, Appli	C 609	12.2	40.7	30	15	US-10-341-836-11	Sequence 11, Appl
C 537	12.2	40.7	20	15	US-10-259-903-4	Sequence 4, Appli	C 610	12.2	40.7	30	15	US-10-310-734-73	Sequence 73, Appl
C 538	12.2	40.7	20	15	US-10-144-140-59	Sequence 59, Appl	C 611	12.2	40.7	30	15	US-10-310-734-74	Sequence 74, Appl
C 539	12.2	40.7	20	16	US-10-318-970-20	Sequence 20, Appl	C 612	12.2	40.7	31	9	US-09-801-274-1004	Sequence 1004, Ap
C 540	12.2	40.7	20	16	US-10-399-083-1	Sequence 1, Appli	C 613	12.2	40.7	31	10	US-09-912-263-123	Sequence 123, App
C 541	12.2	40.7	20	16	US-10-398-988-1	Sequence 1, Appli	C 614	12.2	40.7	33	15	US-10-338-411-42	Sequence 42, Appl
C 542	12.2	40.7	21	9	US-09-301-978C-7	Sequence 7, Appli	C 615	12.2	40.7	33	16	US-10-389-640-42	Sequence 42, Appl
C 543	12.2	40.7	21	13	US-10-090-378-7	Sequence 7, Appli	C 616	12.2	40.7	33	16	US-10-800-197-44	Sequence 44, Appl
C 544	12.2	40.7	21	18	US-10-786-720-12010	Sequence 12010, A	C 617	12.2	40.7	33	18	US-10-800-197-45	Sequence 45, Appl
C 545	12.2	40.7	21	18	US-10-786-720-12011	Sequence 12011, A	C 618	12.2	40.7	35	10	US-09-765-061B-56	Sequence 56, Appl
C 546	12.2	40.7	21	18	US-10-786-720-12012	Sequence 12012, A	C 619	12.2	40.7	35	10	US-09-948-747-21	Sequence 21, Appl
C 547	12.2	40.7	21	18	US-10-786-720-13492	Sequence 13492, A	C 620	12.2	40.7	35	18	US-10-719-895-40	Sequence 40, Appl
C 548	12.2	40.7	23	10	US-09-903-190-32	Sequence 32, Appl	C 621	12.2	40.7	36	9	US-09-971-309-81	Sequence 81, Appl
C 549	12.2	40.7	23	15	US-10-127-816-34	Sequence 34, Appl	C 622	12.2	40.7	36	15	US-10-202-896-32	Sequence 32, Appl
C 550	12.2	40.7	23	15	US-10-127-816-51	Sequence 51, Appl	C 623	12.2	40.7	41	15	US-10-224-683-14	Sequence 14, Appl
C 551	12.2	40.7	23	15	US-10-319-763-32	Sequence 32, Appl	C 624	12.2	40.7	41	16	US-10-035-833A-1009	Sequence 1009, Ap
C 552	12.2	40.7	23	15	US-10-315-664-18	Sequence 18, Appl	C 625	12.2	40.7	41	16	US-10-035-833A-3367	Sequence 3367, Ap
C 553	12.2	40.7	25	9	US-09-866-108-3483	Sequence 3483, Ap	C 626	12.2	40.7	41	16	US-10-035-833A-5321	Sequence 5321, Ap
C 554	12.2	40.7	25	9	US-09-866-108-3484	Sequence 3484, Ap	C 627	12.2	40.7	47	16	US-10-349-143-105	Sequence 105, App
C 555	12.2	40.7	25	10	US-09-770-107-48	Sequence 48, Appl	C 628	12.2	40.7	47	16	US-10-349-143-1042	Sequence 1042, Ap
C 556	12.2	40.7	25	10	US-09-848-107-18	Sequence 18, Appl	C 629	12.2	40.7	47	16	US-10-349-143-1459	Sequence 1459, Ap
C 557	12.2	40.7	25	10	US-09-848-107-19	Sequence 19, Appl	C 630	12.2	40.7	48	16	US-10-440-932-1	Sequence 1, Appli
C 558	12.2	40.7	25	14	US-10-109-498-13	Sequence 13, Appl	C 631	12.2	40.7	49	10	US-09-993-346-118	Sequence 118, App
C 559	12.2	40.7	25	14	US-10-109-498-14	Sequence 14, Appl	C 632	12.2	40.7	50	16	US-10-131-827-2927	Sequence 2927, Ap
C 560	12.2	40.7	25	14	US-10-215-112-4029	Sequence 4029, Ap	C 633	12.2	40.7	50	16	US-10-131-827-4858	Sequence 4858, Ap
C 561	12.2	40.7	25	15	US-10-255-032-2	Sequence 2, Appli	C 634	12.2	40.7	50	18	US-10-690-487-235	Sequence 235, App
C 562	12.2	40.7	25	15	US-10-255-032-3	Sequence 3, Appli	C 635	12	40.0	20	9	US-09-825-414-73	Sequence 73, Appl
C 563	12.2	40.7	25	15	US-10-098-263B-4369	Sequence 4369, Ap	C 636	12	40.0	20	14	US-10-010-802-331	Sequence 331, App
C 564	12.2	40.7	25	15	US-10-098-263B-12536	Sequence 12536, A	C 637	12	40.0	20	15	US-10-227-596-2	Sequence 2, Appli
C 565	12.2	40.7	25	15	US-10-098-263B-39284	Sequence 39284, A	C 638	12	40.0	20	15	US-10-164-863-9	Sequence 9, Appli
C 566	12.2	40.7	25	15	US-10-098-263B-41117	Sequence 41117, A	C 639	12	40.0	20	16	US-10-185-035-46	Sequence 46, Appl
C 567	12.2	40.7	25	15	US-10-098-263B-44049	Sequence 44049, A	C 640	12	40.0	20	16	US-10-185-035-107	Sequence 107, App
C 568	12.2	40.7	25	15	US-10-098-263B-48032	Sequence 48032, A	C 641	12	40.0	20	16	US-10-289-762-2977	Sequence 2977, Ap
C 569	12.2	40.7	25	15	US-10-098-263B-48568	Sequence 48568, A	C 642	12	40.0	20	17	US-10-342-311-2	Sequence 2, Appli
C 570	12.2	40.7	25	15	US-10-098-263B-51018	Sequence 51018, A	C 643	12	40.0	20	17	US-10-731-739-320	Sequence 320, App
C 571	12.2	40.7	25	15	US-10-098-263B-52725	Sequence 52725, A	C 644	12	40.0	20	18	US-10-477-238A-320	Sequence 320, App
C 572	12.2	40.7	25	15	US-10-098-263B-62212	Sequence 62212, A	C 645	12	40.0	21	18	US-10-786-720-7600	Sequence 7600, Ap
C 573	12.2	40.7	25	15	US-10-098-263B-65528	Sequence 65528, A	C 646	12	40.0	21	18	US-10-786-720-7602	Sequence 7602, Ap
C 574	12.2	40.7	25	15	US-10-098-263B-65922	Sequence 65922, A	C 647	12	40.0	21	18	US-10-786-720-9850	Sequence 9850, Ap
C 575	12.2	40.7	25	15	US-10-098-263B-75388	Sequence 75387, A	C 648	12	40.0	21	18	US-10-786-720-9852	Sequence 9852, Ap
C 576	12.2	40.7	25	15	US-10-098-263B-75388	Sequence 75388, A	C 649	12	40.0	21	18	US-10-786-720-13354	Sequence 13354, A
C 577	12.2	40.7	25	15	US-10-098-263B-78002	Sequence 78002, A	C 650	12	40.0	21	18	US-10-786-720-13355	Sequence 13355, A
C 578	12.2	40.7	25	15	US-10-098-263B-78572	Sequence 78572, A	C 651	12	40.0	21	18	US-10-786-720-13356	Sequence 13356, A
C 579	12.2	40.7	25	15	US-10-098-263B-80598	Sequence 80598, A	C 652	12	40.0	21	18	US-10-786-720-13357	Sequence 13357, A
C 580	12.2	40.7	25	15	US-10-098-263B-84944	Sequence 84944, A	C 653	12	40.0	21	18	US-10-786-720-13358	Sequence 13358, A
C 581	12.2	40.7	25	15	US-10-098-263B-87704	Sequence 87704, A	C 654	12	40.0	21	18	US-10-786-720-13359	Sequence 13359, A
C 582	12.2	40.7	25	15	US-10-098-263B-92657	Sequence 92657, A	C 655	12	40.0	21	18	US-10-786-720-13414	Sequence 13414, A
C 583	12.2	40.7	25	15	US-10-098-263B-96196	Sequence 96196, A	C 656	12	40.0	21	18	US-10-786-720-13416	Sequence 13416, A
C 584	12.2	40.7	25	15	US-10-098-263B-105046	Sequence 105046, A	C 657	12	40.0	21	18	US-10-786-720-13489	Sequence 13489, A
C 585	12.2	40.7	25	15	US-10-098-263B-106787	Sequence 106787, A	C 658	12	40.0	21	18	US-10-786-720-13490	Sequence 13490, A
C 586	12.2	40.7	25	15	US-10-098-263B-107251	Sequence 107251, A	C 659	12	40.0	22	15	US-10-032-585-5004	Sequence 5004, Ap
C 587	12.2	40.7	25	15	US-10-098-263B-114086	Sequence 114086, A	C 660	12	40.0	24	9	US-09-886-900-10	Sequence 10, Appl
C 588	12.2	40.7	25	15	US-10-098-263B-115799	Sequence 115799, A	C 661	12	40.0	24	10	US-09-940-185-3845	Sequence 3845, Ap
C 589	12.2	40.7	25	15	US-10-098-263B-125811	Sequence 125811, A	C 662	12	40.0	24	15	US-10-096-578-81	Sequence 81, Appl
C 590	12.2	40.7	25	17	US-10-717-597-4815	Sequence 4815, Ap	C 663	12	40.0	24	15	US-10-032-585-4814	Sequence 4814, Ap
C 591	12.2	40.7	25	17	US-10-717-597-4815	Sequence 4816, Ap	C 664	12	40.0	24	15	US-10-032-585-4879	Sequence 4879, Ap
C 592	12.2	40.7	25	17	US-10-723-361-3483	Sequence 3483, Ap	C 665	12	40.0	24	16	US-10-617-038-112	Sequence 112, App
C 593	12.2	40.7	25	17	US-10-723-361-3483	Sequence 3484, Ap	C 666	12	40.0	25	10	US-09-974-546-35	Sequence 35, Appl
C 594	12.2	40.7	25	17	US-10-723-361-3484	Sequence 3484, Ap	C 667	12	40.0	25	14	US-10-215-112-4039	Sequence 4039, Ap
C 595	12.2	40.7	25	18	US-10-669-537-3	Sequence 3, Appli	C 668	12	40.0	25	14	US-10-215-112-4040	Sequence 4040, Ap
C 596	12.2	40.7	25	18	US-10-669-537-3	Sequence 3, Appli	C 669	12	40.0	25	14	US-10-215-112-8243	Sequence 8243, Ap

c 670	12	40.0	25	14	US-10-215-112-8369	Sequence 8369, Ap	c 743	12	40.0	41	15	US-10-286-549A-34	Sequence 34, Appl
c 671	12	40.0	25	15	US-10-098-263B-241	Sequence 241, App	c 744	12	40.0	41	16	US-10-035-833A-431	Sequence 431, App
c 672	12	40.0	25	15	US-10-098-263B-3113	Sequence 3113, Ap	c 745	12	40.0	41	16	US-10-035-833A-2485	Sequence 2485, Ap
c 673	12	40.0	25	15	US-10-098-263B-4070	Sequence 4070, Ap	c 746	12	40.0	41	16	US-10-035-833A-2550	Sequence 2550, Ap
c 674	12	40.0	25	15	US-10-098-263B-5301	Sequence 5301, Ap	c 747	12	40.0	41	16	US-10-035-833A-3057	Sequence 3057, Ap
c 675	12	40.0	25	15	US-10-098-263B-9639	Sequence 9639, Ap	c 748	12	40.0	41	16	US-10-035-833A-5270	Sequence 5270, Ap
c 676	12	40.0	25	15	US-10-098-263B-10275	Sequence 10275, A	c 749	12	40.0	41	16	US-10-035-833A-5270	Sequence 5270, Ap
c 677	12	40.0	25	15	US-10-098-263B-13000	Sequence 13000, A	c 750	12	40.0	41	16	US-10-035-833A-5567	Sequence 5567, Ap
c 678	12	40.0	25	15	US-10-098-263B-17500	Sequence 17500, A	c 751	12	40.0	41	16	US-10-035-833A-6584	Sequence 6584, Ap
c 679	12	40.0	25	15	US-10-098-263B-27036	Sequence 27036, A	c 752	12	40.0	42	13	US-10-057-558-28	Sequence 28, Appl
c 680	12	40.0	25	15	US-10-098-263B-27984	Sequence 27984, A	c 753	12	40.0	42	18	US-10-858-775-28	Sequence 28, Appl
c 681	12	40.0	25	15	US-10-098-263B-28537	Sequence 28537, A	c 754	12	40.0	43	9	US-09-423-800-15	Sequence 15, Appl
c 682	12	40.0	25	15	US-10-098-263B-28537	Sequence 28537, A	c 755	12	40.0	43	14	US-10-182-018-15	Sequence 15, Appl
c 683	12	40.0	25	15	US-10-098-263B-34105	Sequence 34105, A	c 756	12	40.0	43	15	US-10-169-003-15	Sequence 15, Appl
c 684	12	40.0	25	15	US-10-098-263B-41114	Sequence 41114, A	c 757	12	40.0	43	15	US-10-337-981-15	Sequence 15, Appl
c 685	12	40.0	25	15	US-10-098-263B-42187	Sequence 42187, A	c 758	12	40.0	43	16	US-10-344-733-15	Sequence 15, Appl
c 686	12	40.0	25	15	US-10-098-263B-43957	Sequence 43957, A	c 759	12	40.0	44	10	US-09-510-378-117	Sequence 117, Appl
c 687	12	40.0	25	15	US-10-098-263B-55555	Sequence 55555, A	c 760	12	40.0	45	9	US-09-850-964-6	Sequence 6, Appl
c 688	12	40.0	25	15	US-10-098-263B-61693	Sequence 61693, A	c 761	12	40.0	47	9	US-09-765-272-391	Sequence 391, Appl
c 689	12	40.0	25	15	US-10-098-263B-61693	Sequence 61693, A	c 762	12	40.0	47	10	US-09-993-346-15	Sequence 15, Appl
c 690	12	40.0	25	15	US-10-098-263B-62681	Sequence 62681, A	c 763	12	40.0	47	15	US-10-076-802-59	Sequence 59, Appl
c 691	12	40.0	25	15	US-10-098-263B-68272	Sequence 68272, A	c 764	12	40.0	47	15	US-10-211-160-26	Sequence 26, Appl
c 692	12	40.0	25	15	US-10-098-263B-72261	Sequence 72261, A	c 765	12	40.0	47	15	US-10-051-681A-26	Sequence 26, Appl
c 693	12	40.0	25	15	US-10-098-263B-73506	Sequence 73506, A	c 766	12	40.0	47	15	US-10-170-077-775	Sequence 775, Appl
c 694	12	40.0	25	15	US-10-098-263B-76831	Sequence 76831, A	c 767	12	40.0	47	15	US-10-367-169-59	Sequence 59, Appl
c 695	12	40.0	25	15	US-10-098-263B-78612	Sequence 78612, A	c 768	12	40.0	47	16	US-10-349-143-1243	Sequence 575, Appl
c 696	12	40.0	25	15	US-10-098-263B-89562	Sequence 89562, A	c 769	12	40.0	47	16	US-10-349-143-1243	Sequence 1243, Ap
c 697	12	40.0	25	15	US-10-098-263B-92792	Sequence 92792, A	c 770	12	40.0	47	16	US-10-349-143-2137	Sequence 2137, Ap
c 698	12	40.0	25	15	US-10-098-263B-96712	Sequence 96712, A	c 771	12	40.0	47	16	US-10-349-143-2424	Sequence 2424, Ap
c 699	12	40.0	25	15	US-10-098-263B-96712	Sequence 96712, A	c 772	12	40.0	47	16	US-10-333-429-105	Sequence 105, Appl
c 700	12	40.0	25	15	US-10-098-263B-103945	Sequence 103945, A	c 773	12	40.0	47	16	US-10-617-070-487	Sequence 487, Appl
c 701	12	40.0	25	15	US-10-098-263B-103946	Sequence 103946, A	c 774	12	40.0	47	17	US-10-467-639-52	Sequence 52, Appl
c 702	12	40.0	25	15	US-10-098-263B-105592	Sequence 105592, A	c 775	12	40.0	47	17	US-10-467-639-58	Sequence 88, Appl
c 703	12	40.0	25	15	US-10-098-263B-111285	Sequence 111285, A	c 776	12	40.0	48	10	US-09-927-046-5317	Sequence 5317, Ap
c 704	12	40.0	25	15	US-10-098-263B-123180	Sequence 123180, A	c 777	12	40.0	48	10	US-09-792-818-1981	Sequence 1981, Ap
c 705	12	40.0	25	15	US-10-098-263B-125761	Sequence 125761, A	c 778	12	40.0	48	10	US-09-792-818-2137	Sequence 2137, Ap
c 706	12	40.0	25	15	US-10-098-263B-130501	Sequence 130501, A	c 779	12	40.0	48	16	US-10-617-070-488	Sequence 488, Appl
c 707	12	40.0	25	15	US-10-061-201-2401	Sequence 2401, Ap	c 780	12	40.0	49	15	US-10-026-925-34	Sequence 34, Appl
c 708	12	40.0	25	15	US-10-061-201-2407	Sequence 2407, Ap	c 781	12	40.0	49	15	US-10-174-992-8	Sequence 8, Appl
c 709	12	40.0	25	17	US-10-717-597-4237	Sequence 4237, Ap	c 782	12	40.0	49	18	US-10-666-806A-2	Sequence 2, Appl
c 710	12	40.0	27	10	US-09-833-039-17	Sequence 17, Appl	c 783	12	40.0	50	16	US-10-131-827-3392	Sequence 3392, Ap
c 711	12	40.0	27	18	US-10-177-277-17	Sequence 17, Appl	c 784	12	40.0	50	16	US-10-131-827-3393	Sequence 3393, Ap
c 712	12	40.0	27	18	US-10-851-884-25	Sequence 25, Appl	c 785	12	40.0	50	16	US-10-131-827-3452	Sequence 3452, Ap
c 713	12	40.0	28	9	US-09-795-006A-8	Sequence 8, Appl	c 786	12	40.0	50	16	US-10-131-827-4732	Sequence 4732, Ap
c 714	12	40.0	28	16	US-10-321-039-161	Sequence 161, App	c 787	12	40.0	50	16	US-10-131-827-4778	Sequence 4778, Ap
c 715	12	40.0	29	15	US-10-336-638-551	Sequence 551, App	c 788	12	40.0	50	16	US-10-131-827-7239	Sequence 7239, Ap
c 716	12	40.0	30	9	US-09-327-933A-19	Sequence 19, Appl	c 789	11.8	39.3	17	9	US-09-735-787-33	Sequence 33, Appl
c 717	12	40.0	30	9	US-09-888-938-9	Sequence 9, Appl	c 790	11.8	39.3	17	10	US-09-740-332-1113	Sequence 1113, Ap
c 718	12	40.0	30	11	US-09-852-238A-12	Sequence 12, Appl	c 791	11.8	39.3	17	10	US-09-817-879-1113	Sequence 1113, Ap
c 719	12	40.0	30	14	US-10-093-958-12	Sequence 11, Appl	c 792	11.8	39.3	17	15	US-10-138-870-33	Sequence 33, Appl
c 720	12	40.0	30	14	US-10-093-958-12	Sequence 12, Appl	c 793	11.8	39.3	17	17	US-10-669-841-3706	Sequence 3706, Ap
c 721	12	40.0	31	16	US-10-138-674-19449	Sequence 19449, A	c 794	11.8	39.3	19	10	US-09-864-636A-1950	Sequence 1950, Ap
c 722	12	40.0	31	17	US-10-287-949A-19449	Sequence 19449, A	c 795	11.8	39.3	19	11	US-09-864-426A-1950	Sequence 1950, Ap
c 723	12	40.0	31	18	US-10-712-633-5246	Sequence 5246, Ap	c 796	11.8	39.3	19	15	US-10-084-839-1950	Sequence 6, Appl
c 724	12	40.0	32	15	US-10-293-239-39	Sequence 39, Appl	c 797	11.8	39.3	19	16	US-10-669-724-6	Sequence 184, App
c 725	12	40.0	33	15	US-10-116-299A-2	Sequence 2, Appl	c 798	11.8	39.3	19	16	US-10-252-155-184	Sequence 266, App
c 726	12	40.0	33	16	US-10-374-953-2	Sequence 2, Appl	c 799	11.8	39.3	20	10	US-09-382-860-266	Sequence 266, App
c 727	12	40.0	33	16	US-10-465-789A-64	Sequence 64, Appl	c 800	11.8	39.3	20	15	US-10-032-585-4319	Sequence 4319, Ap
c 728	12	40.0	34	14	US-10-229-747-5	Sequence 5, Appl	c 801	11.8	39.3	20	15	US-10-093-463-338	Sequence 338, App
c 729	12	40.0	35	9	US-09-753-126-60	Sequence 60, Appl	c 802	11.8	39.3	20	17	US-10-303-541-61	Sequence 24, Appl
c 730	12	40.0	35	16	US-10-330-697-60	Sequence 60, Appl	c 803	11.8	39.3	20	17	US-10-303-541-61	Sequence 61, Appl
c 731	12	40.0	36	14	US-10-083-168-25	Sequence 25, Appl	c 804	11.8	39.3	20	17	US-10-671-395-1643	Sequence 1643, Ap
c 732	12	40.0	37	9	US-09-795-006A-17	Sequence 17, Appl	c 805	11.8	39.3	20	17	US-10-671-395-1708	Sequence 1708, Ap
c 733	12	40.0	37	10	US-09-791-301-213	Sequence 213, App	c 806	11.8	39.3	20	17	US-10-671-395-1709	Sequence 1709, Ap
c 734	12	40.0	38	9	US-09-768-779A-15	Sequence 15, Appl	c 807	11.8	39.3	20	17	US-10-671-395-1727	Sequence 1727, Ap
c 735	12	40.0	38	15	US-10-291-480-15	Sequence 15, Appl	c 808	11.8	39.3	20	17	US-10-671-395-1737	Sequence 1737, Ap
c 736	12	40.0	38	18	US-10-721-997A-13	Sequence 13, Appl	c 809	11.8	39.3	20	17	US-10-671-395-1743	Sequence 1743, Ap
c 737	12	40.0	38	18	US-10-721-997A-14	Sequence 14, Appl	c 810	11.8	39.3	21	9	US-09-972-467-7	Sequence 7, Appl
c 738	12	40.0	39	15	US-09-826-509-295	Sequence 295, App	c 811	11.8	39.3	22	9	US-09-817-014-73	Sequence 73, Appl
c 739	12	40.0	39	15	US-10-219-227-16	Sequence 16, Appl	c 812	11.8	39.3	22	9	US-09-755-665-113	Sequence 113, App
c 740	12	40.0	39	17	US-10-327-598-845	Sequence 845, App	c 813	11.8	39.3	22	9	US-09-755-665-114	Sequence 114, App
c 741	12	40.0	41	10	US-09-826-509-294	Sequence 294, App	c 814	11.8	39.3	22	14	US-10-074-246-26	Sequence 26, Appl
c 742	12	40.0	41	15	US-10-319-227A-34	Sequence 34, Appl	c 815	11.8	39.3	22	15	US-10-056-229-73	Sequence 73, Appl

816	11.8	39.3	22	16	US-10-309-230-187	Sequence 187, App	889	11.8	39.3	28	15	US-10-016-496-17	Sequence 17, Appl
817	11.8	39.3	22	17	US-10-629-248-113	Sequence 113, App	890	11.8	39.3	28	15	US-10-411-076-27	Sequence 27, Appl
818	11.8	39.3	22	17	US-10-629-248-114	Sequence 114, App	891	11.8	39.3	28	15	US-10-411-076-29	Sequence 29, Appl
819	11.8	39.3	23	14	US-10-269-557-58	Sequence 58, Appl	892	11.8	39.3	28	15	US-10-410-872-22	Sequence 22, Appl
820	11.8	39.3	23	14	US-10-296-995-89	Sequence 89, Appl	893	11.8	39.3	28	15	US-10-410-885-15	Sequence 15, Appl
821	11.8	39.3	23	16	US-10-374-077-13	Sequence 13, Appl	894	11.8	39.3	28	17	US-10-675-738B-8	Sequence 8, Appl
822	11.8	39.3	23	16	US-10-398-757-16	Sequence 16, Appl	895	11.8	39.3	28	17	US-10-675-738B-8	Sequence 8, Appl
823	11.8	39.3	24	9	US-09-904-389-6	Sequence 6, Appl	896	11.8	39.3	30	9	US-10-622-869A-23	Sequence 23, Appl
824	11.8	39.3	24	10	US-09-468-147-63	Sequence 63, Appl	897	11.8	39.3	30	9	US-09-297-910-4	Sequence 4, Appl
825	11.8	39.3	24	15	US-10-319-745-63	Sequence 63, Appl	898	11.8	39.3	30	15	US-10-364-649-48	Sequence 48, Appl
826	11.8	39.3	24	16	US-10-072-012-926	Sequence 926, App	899	11.8	39.3	31	9	US-10-692-605-46	Sequence 46, Appl
827	11.8	39.3	24	16	US-10-072-012-928	Sequence 928, App	900	11.8	39.3	31	9	US-09-801-274-797	Sequence 797, App
828	11.8	39.3	25	9	US-09-866-108-4370	Sequence 4370, App	901	11.8	39.3	31	15	US-10-235-079B-81	Sequence 81, Appl
829	11.8	39.3	25	9	US-09-866-108-4371	Sequence 4371, App	902	11.8	39.3	31	16	US-10-239-656-88	Sequence 88, Appl
830	11.8	39.3	25	9	US-09-866-108-4372	Sequence 4372, App	903	11.8	39.3	32	8	US-08-911-824-88	Sequence 88, Appl
831	11.8	39.3	25	14	US-10-074-246-49	Sequence 49, Appl	904	11.8	39.3	33	10	US-09-864-636A-246	Sequence 246, App
832	11.8	39.3	25	14	US-10-215-112-3893	Sequence 3893, App	905	11.8	39.3	33	10	US-09-758-282-45	Sequence 45, Appl
833	11.8	39.3	25	14	US-10-215-112-4826	Sequence 4826, App	906	11.8	39.3	33	11	US-09-864-426A-246	Sequence 246, App
834	11.8	39.3	25	14	US-10-215-112-6375	Sequence 6375, App	907	11.8	39.3	33	15	US-10-084-839-246	Sequence 246, App
835	11.8	39.3	25	14	US-10-098-263B-2946	Sequence 2946, App	908	11.8	39.3	34	10	US-09-949-427-108	Sequence 108, App
836	11.8	39.3	25	15	US-10-098-263B-5698	Sequence 5698, App	909	11.8	39.3	34	16	US-10-332-155-5	Sequence 5, Appl
837	11.8	39.3	25	15	US-10-098-263B-8967	Sequence 8967, App	910	11.8	39.3	35	10	US-09-854-867-520	Sequence 520, App
838	11.8	39.3	25	15	US-10-098-263B-10291	Sequence 10291, A	911	11.8	39.3	35	15	US-10-317-832-226	Sequence 226, App
839	11.8	39.3	25	15	US-10-098-263B-13913	Sequence 13913, A	912	11.8	39.3	35	18	US-10-733-878-226	Sequence 226, App
840	11.8	39.3	25	15	US-10-098-263B-21484	Sequence 21484, A	913	11.8	39.3	36	15	US-10-084-814-31	Sequence 31, Appl
841	11.8	39.3	25	15	US-10-098-263B-33057	Sequence 33057, A	914	11.8	39.3	36	16	US-10-462-128-31	Sequence 31, Appl
842	11.8	39.3	25	15	US-10-098-263B-33057	Sequence 33057, A	915	11.8	39.3	38	10	US-09-825-805-1263	Sequence 1263, Ap
843	11.8	39.3	25	15	US-10-098-263B-35698	Sequence 35698, A	916	11.8	39.3	38	10	US-09-780-533A-4604	Sequence 4604, Ap
844	11.8	39.3	25	15	US-10-098-263B-36516	Sequence 36516, A	917	11.8	39.3	38	10	US-09-877-478-4236	Sequence 4236, Ap
845	11.8	39.3	25	15	US-10-098-263B-38809	Sequence 38809, A	918	11.8	39.3	38	10	US-09-877-478-4236	Sequence 4236, Ap
846	11.8	39.3	25	15	US-10-098-263B-38810	Sequence 38810, A	919	11.8	39.3	38	16	US-10-342-902-4236	Sequence 4236, Ap
847	11.8	39.3	25	15	US-10-098-263B-39770	Sequence 39770, A	920	11.8	39.3	38	16	US-10-342-902-4236	Sequence 4236, Ap
848	11.8	39.3	25	15	US-10-098-263B-41897	Sequence 41897, A	921	11.8	39.3	38	17	US-10-669-841-9127	Sequence 9127, Ap
849	11.8	39.3	25	15	US-10-098-263B-42032	Sequence 42032, A	922	11.8	39.3	38	17	US-10-669-841-9239	Sequence 9239, Ap
850	11.8	39.3	25	15	US-10-098-263B-46867	Sequence 46867, A	923	11.8	39.3	39	10	US-09-093-972C-990	Sequence 990, App
851	11.8	39.3	25	15	US-10-098-263B-62572	Sequence 62572, A	924	11.8	39.3	39	15	US-10-178-673-16	Sequence 16, Appl
852	11.8	39.3	25	15	US-10-098-263B-68004	Sequence 68004, A	925	11.8	39.3	39	16	US-10-453-827-447	Sequence 447, App
853	11.8	39.3	25	15	US-10-098-263B-71643	Sequence 71643, A	926	11.8	39.3	39	16	US-10-453-827-448	Sequence 448, App
854	11.8	39.3	25	15	US-10-098-263B-72259	Sequence 72259, A	927	11.8	39.3	40	9	US-09-989-723-25	Sequence 25, Appl
855	11.8	39.3	25	15	US-10-098-263B-73526	Sequence 73526, A	928	11.8	39.3	40	9	US-09-989-723-25	Sequence 25, Appl
856	11.8	39.3	25	15	US-10-098-263B-73526	Sequence 73526, A	929	11.8	39.3	40	9	US-09-989-723-25	Sequence 25, Appl
857	11.8	39.3	25	15	US-10-098-263B-78527	Sequence 78527, A	930	11.8	39.3	40	9	US-09-989-723-25	Sequence 25, Appl
858	11.8	39.3	25	15	US-10-098-263B-94376	Sequence 94376, A	931	11.8	39.3	40	9	US-09-989-723-25	Sequence 25, Appl
859	11.8	39.3	25	15	US-10-098-263B-97982	Sequence 97982, A	932	11.8	39.3	40	9	US-09-989-723-25	Sequence 25, Appl
860	11.8	39.3	25	15	US-10-098-263B-101430	Sequence 100245, A	933	11.8	39.3	40	9	US-09-991-073-25	Sequence 25, Appl
861	11.8	39.3	25	15	US-10-098-263B-101430	Sequence 101430, A	934	11.8	39.3	40	9	US-09-991-073-25	Sequence 25, Appl
862	11.8	39.3	25	15	US-10-098-263B-108180	Sequence 108180, A	935	11.8	39.3	40	9	US-09-991-163-25	Sequence 25, Appl
863	11.8	39.3	25	15	US-10-098-263B-108180	Sequence 108180, A	936	11.8	39.3	40	9	US-09-993-604-25	Sequence 25, Appl
864	11.8	39.3	25	15	US-10-098-263B-112728	Sequence 112728, A	937	11.8	39.3	40	9	US-09-990-456-25	Sequence 25, Appl
865	11.8	39.3	25	15	US-10-098-263B-119984	Sequence 119984, A	938	11.8	39.3	40	9	US-09-989-721-25	Sequence 25, Appl
866	11.8	39.3	25	15	US-10-098-263B-120547	Sequence 120547, A	939	11.8	39.3	40	9	US-09-992-598-25	Sequence 25, Appl
867	11.8	39.3	25	15	US-10-098-263B-120548	Sequence 120548, A	940	11.8	39.3	40	9	US-09-989-293A-25	Sequence 25, Appl
868	11.8	39.3	25	15	US-10-098-263B-121342	Sequence 121342, A	941	11.8	39.3	40	9	US-09-989-735-25	Sequence 25, Appl
869	11.8	39.3	25	15	US-10-098-263B-124191	Sequence 124191, A	942	11.8	39.3	40	9	US-09-990-444-25	Sequence 25, Appl
870	11.8	39.3	25	15	US-10-098-263B-128190	Sequence 128190, A	943	11.8	39.3	40	9	US-09-991-181-25	Sequence 25, Appl
871	11.8	39.3	25	15	US-10-098-263B-130350	Sequence 130350, A	944	11.8	39.3	40	9	US-09-989-730-25	Sequence 25, Appl
872	11.8	39.3	25	15	US-10-061-201-4105	Sequence 4105, Ap	945	11.8	39.3	40	9	US-09-990-436-25	Sequence 25, Appl
873	11.8	39.3	25	17	US-10-717-597-3165	Sequence 3165, Ap	946	11.8	39.3	40	9	US-09-993-687-25	Sequence 25, Appl
874	11.8	39.3	25	17	US-10-723-361-4970	Sequence 4970, Ap	947	11.8	39.3	40	10	US-09-989-734-25	Sequence 25, Appl
875	11.8	39.3	25	17	US-10-723-361-4971	Sequence 4971, Ap	948	11.8	39.3	40	10	US-09-997-653-25	Sequence 25, Appl
876	11.8	39.3	25	17	US-10-723-361-4972	Sequence 4972, Ap	949	11.8	39.3	40	10	US-09-989-724-25	Sequence 25, Appl
877	11.8	39.3	25	17	US-10-775-169-4880	Sequence 4880, Ap	950	11.8	39.3	40	10	US-09-989-724-25	Sequence 25, Appl
878	11.8	39.3	25	17	US-10-775-169-5133	Sequence 5133, Ap	951	11.8	39.3	40	10	US-09-990-441-25	Sequence 25, Appl
879	11.8	39.3	26	9	US-09-802-669-89	Sequence 89, Appl	952	11.8	39.3	40	10	US-09-993-667-25	Sequence 25, Appl
880	11.8	39.3	26	16	US-10-619-220-89	Sequence 89, Appl	953	11.8	39.3	40	10	US-09-997-428-25	Sequence 25, Appl
881	11.8	39.3	27	10	US-09-961-077-908	Sequence 908, App	954	11.8	39.3	40	10	US-09-997-666-25	Sequence 25, Appl
882	11.8	39.3	28	9	US-09-975-553-22	Sequence 22, Appl	955	11.8	39.3	40	10	US-09-990-438-25	Sequence 25, Appl
883	11.8	39.3	28	14	US-10-125-792-13	Sequence 13, Appl	956	11.8	39.3	40	10	US-09-990-562-25	Sequence 25, Appl
884	11.8	39.3	28	14	US-10-125-778-13	Sequence 13, Appl	957	11.8	39.3	40	10	US-09-990-711-25	Sequence 25, Appl
885	11.8	39.3	28	14	US-10-270-795-22	Sequence 22, Appl	958	11.8	39.3	40	10	US-09-989-726-25	Sequence 25, Appl
886	11.8	39.3	28	15	US-10-270-876-22	Sequence 22, Appl	959	11.8	39.3	40	10	US-09-998-156-25	Sequence 25, Appl
887	11.8	39.3	28	15	US-10-268-051-12	Sequence 12, Appl	960	11.8	39.3	40	10	US-09-990-437-25	Sequence 25, Appl
888	11.8	39.3	28	15	US-10-125-772-13	Sequence 13, Appl	961	11.8	39.3	40	10	US-09-991-157-25	Sequence 25, Appl

RESUL 4
US-10-147-679A-22

Matches	19;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
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Db	3	GACTCAGTCCTTGGTCGTCCTC	25						
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US-08-944-410-52/c									
; Sequence 52, Application US/08944410									
; Publication No. US20030050453A1									
; GENERAL INFORMATION:									
; APPLICANT: Sorge, Joseph A.									
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES									
; FILE REFERENCE: 04121.0018-00000									
; CURRENT APPLICATION NUMBER: US/08/944,410									
; CURRENT FILING DATE: 1997-10-06									
; NUMBER OF SEQ ID NOS: 113									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 52									
; LENGTH: 46									
; TYPE: DNA									
; ORGANISM: Artificial									
; FEATURE:									
; OTHER INFORMATION: Synthetic primer									
US-08-944-410-52									
Query Match 54.7%; Score 16.4; DB 8; Length 46;									
Best Local Similarity 76.9%; Pred. No. 1.6e+03;									
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
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Db	41	GACTCAGACCTTGTGCATCTGACGTT	16						
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US-10-098-263B-123322									
; Sequence 123322, Application US/10098263B									
; Publication No. US20030104410A1									
; GENERAL INFORMATION:									
; APPLICANT: Mittman, Michael									
; TITLE OF INVENTION: Human Microarray									
; FILE REFERENCE: 3118.1									
; CURRENT APPLICATION NUMBER: US/10/098,263B									
; CURRENT FILING DATE: 2003-01-08									
; PRIOR APPLICATION NUMBER: 60/276,759									
; PRIOR FILING DATE: 2001-03-16									
; NUMBER OF SEQ ID NOS: 131066									
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1									
; SEQ ID NO 123322									
; LENGTH: 25									
; TYPE: DNA									
; ORGANISM: Homo sapien									
US-10-098-263B-123322									
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Best Local Similarity 85.7%; Pred. No. 1.9e+03;									
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Db	5	CAGTCCTTGGTCATCTCAC	25						
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; Sequence 101913, Application US/10098263B									
; Publication No. US20030104410A1									
; GENERAL INFORMATION:									
; APPLICANT: Mittman, Michael									
; TITLE OF INVENTION: Human Microarray									
; FILE REFERENCE: 3118.1									

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; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 101913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-101913

Query Match      53.3%; Score 16; DB 15; Length 25;
Best Local Similarity 79.2%; Pred. No. 2.3e+03;
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Db 25 TGGGCTCAGTCATGGTTCTTCTCA 2

RESULT 9
US-10-038-835-56/c
; Sequence 56, Application US/10038835
; Publication No. US20030130497A1
; GENERAL INFORMATION:
; APPLICANT: Bai, Yue-Luen
; TITLE OF INVENTION: DETECTION OF RESPIRATORY VIRUSES
; FILE REFERENCE: 12674-006001
; CURRENT APPLICATION NUMBER: US/10/038,835
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Human adenovirus
US-10-038-835-56

Query Match      52.7%; Score 15.8; DB 15; Length 26;
Best Local Similarity 81.0%; Pred. No. 2.8e+03;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGACTCAGTCCTTGGTCATCT 22
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Db 22 GGAACCACTCTTGGTCATGT 2

RESULT 10
US-10-131-827-405
; Sequence 405, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 8090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 405
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-405

Query Match      52.0%; Score 15.6; DB 16; Length 50;
Best Local Similarity 70.0%; Pred. No. 3.7e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
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Db 13 TGCACCCAGTCTCTCTTATCTCACTTAT 42

RESULT 11
US-10-131-827-4918
; Sequence 4918, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4918
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4918

Query Match      52.0%; Score 15.6; DB 16; Length 50;
Best Local Similarity 70.0%; Pred. No. 3.7e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 13 TGCACCCAGTCTCTCTTATCTCACTTAT 42

RESULT 12
US-10-098-263B-112496
; Sequence 112496, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 112496
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-112496

Query Match      51.3%; Score 15.4; DB 15; Length 25;
Best Local Similarity 76.0%; Pred. No. 4.3e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGACTCAGTCCTTGGTCATCTCACC 26
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Db 1 GGACTTCGACATTGGTAATCCACC 25
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RESULT 13

US-09-912-976-93/c
; Sequence 93, Application US/09912976
; Publication No. US20030212255A1
; GENERAL INFORMATION:

; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mezes, Peter
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Mishra, Vishnu

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-070
; CURRENT APPLICATION NUMBER: US/09/912,976

; CURRENT FILING DATE: 2001-07-05

; PRIOR APPLICATION NUMBER: 60/221,336

; PRIOR FILING DATE: 2000-07-26

; PRIOR APPLICATION NUMBER: 60/238,333

; PRIOR FILING DATE: 2000-10-05

; PRIOR APPLICATION NUMBER: 60/260,675

; PRIOR FILING DATE: 2001-01-10

; PRIOR APPLICATION NUMBER: 60/271,025

; PRIOR FILING DATE: 2001-02-22

; PRIOR APPLICATION NUMBER: 60/278,164

; PRIOR FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: 60/280,876

; PRIOR FILING DATE: 2001-04-02

; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 93

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Ag1279/Ag2590

; OTHER INFORMATION: PCR Primer Sequence

US-09-912-976-93

Query Match 50.7%; Score 15.2; DB 10; Length 22;

Best Local Similarity 85.0%; Pred. No. 5.2e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 10 TCCTTGGTCATCTCACCTTC 29
||||| ||||| |||||

Db 21 TCCTTTCTCATCTCTCCTTC 2

RESULT 14

US-09-965-422-76/c

; Sequence 76, Application US/09965422

; Publication No. US20030216545A1

; GENERAL INFORMATION:

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Casman, Stacie

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Dickson, Kevin

; APPLICANT: Vernet, Corine

; APPLICANT: Spaderna, Steven K

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Gerlach, Valerie

; APPLICANT: Ellerman, Karen

; APPLICANT: Edinger, Shlomit

; APPLICANT: MacDougall, John R

; APPLICANT: Smithson, Glennda

; APPLICANT: Li, Li

; APPLICANT: Malyankar, Urial M

; APPLICANT: Taylor, Sarah

; APPLICANT: Taylor, Sarah

; APPLICANT: Gunther, Erik

; APPLICANT: Tchernev, Velizar T

; TITLE OF INVENTION: No. US20030216545A1el Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21401-132

; CURRENT APPLICATION NUMBER: US/09/965,422

; CURRENT FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: 60/236,286

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: 60/236,284

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: 60/237,581

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/238,735

; PRIOR FILING DATE: 2000-10-06

; PRIOR APPLICATION NUMBER: 60/240,736

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/260,019

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 60/260,338

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/262,156

; PRIOR FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: 60/262,498

; PRIOR FILING DATE: 2001-01-18

; PRIOR APPLICATION NUMBER: 60/263,133

; PRIOR FILING DATE: 2001-01-19

; PRIOR APPLICATION NUMBER: 60/263,691

; PRIOR FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: 60/266,109

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 60/271,634

; PRIOR FILING DATE: 2001-02-26

; NUMBER OF SEQ ID NOS: 127

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 76

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer

; OTHER INFORMATION: Sequence

US-09-965-422-76

Query Match 50.7%; Score 15.2; DB 10; Length 22;

Best Local Similarity 85.0%; Pred. No. 5.2e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 10 TCCTTGGTCATCTCACCTTC 29
||||| ||||| |||||

Db 21 TCCTTTCTCATCTCTCCTTC 2

RESULT 15

US-09-965-422-82/c

; Sequence 82, Application US/09965422

; Publication No. US20030216545A1

; GENERAL INFORMATION:

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Casman, Stacie

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Dickson, Kevin

; APPLICANT: Vernet, Corine

; APPLICANT: Spaderna, Steven K

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Gerlach, Valerie

; APPLICANT: Ellerman, Karen

; APPLICANT: Edinger, Shlomit

; APPLICANT: MacDougall, John R

; APPLICANT: Smithson, Glennda

; APPLICANT: Li, Li

; APPLICANT: Malyankar, Urial M

; APPLICANT: Taylor, Sarah

```
; APPLICANT: Gunther, Erik
; APPLICANT: Tchernev, Velizar T
; TITLE OF INVENTION: No. US20030216545A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21401-132
; CURRENT APPLICATION NUMBER: US/09/965,422
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,286
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/236,284
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,581
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,735
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/240,736
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/260,019
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,338
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/262,156
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/262,498
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/263,133
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,691
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/266,109
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/271,634
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
; OTHER INFORMATION: Sequence
US-09-965-422-82

Query Match 50.7%; Score 15.2; DB 10; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TCCTTGGTCATCTCACCTTC 29
Db 21 TCCTTTCATCTCTCCTTC 2

RESULT 16
US-10-005-041A-202/c
; Sequence 202, Application US/10005041A
; Publication No. US2003023231A1
; GENERAL INFORMATION:
; APPLICANT: Casman, Stacie J
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shinkets, Richard A
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gilbert, Jennifer A
; APPLICANT: Mayotte, Jane E
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Mishra, Vishnu
; APPLICANT: Vernet, Corine AM
; APPLICANT: Dickinson, Kevin S
; APPLICANT: Ballinger, Robert A
; APPLICANT: Wolenc, Adam R
; APPLICANT: Edinger, Shlomit R
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda

Query Match 50.7%; Score 15.2; DB 10; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TCCTTGGTCATCTCACCTTC 29
Db 21 TCCTTTCATCTCTCCTTC 2
```

```
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Gerlach, Valerie
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-215
; CURRENT APPLICATION NUMBER: US/10/005,041A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/251,459
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/259,007
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 202
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
; OTHER INFORMATION: Sequence
US-10-005-041A-202

Query Match 50.7%; Score 15.2; DB 15; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TCCTTGGTCATCTCACCTTC 29
Db 21 TCCTTTCATCTCTCCTTC 2

RESULT 17
US-10-023-831A-7/c
; Sequence 7, Application US/10023831A
; Publication No. US20030064436A1
; GENERAL INFORMATION:
; APPLICANT: VAUGHAN, Paul R.
; APPLICANT: GALANIS, Maria
; APPLICANT: RAMSHAW, John A.M.
; APPLICANT: WERKWEISTER, Jerome A.
; TITLE OF INVENTION: METHOD FOR PRODUCING, IN YEAST, A HYDROXYLATED TRIPLE HELICAL PRO
; TITLE OF INVENTION: AND YEAST HOST CELLS USEFUL IN SAID METHOD
; FILE REFERENCE: Q67867
; CURRENT APPLICATION NUMBER: US/10/023,831A
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 09/297,269
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: P03310
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: P04306
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: PCT/AU97/00721
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-023-831A-7

Query Match 50.7%; Score 15.2; DB 14; Length 24;
Best Local Similarity 85.0%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TCCTTGGTCATCTCACCTTC 29
Db 20 TCCTTGGTGACCTCCCTTC 1
```

```

RESULT 20
US-10-098-263B-99848
; Sequence 99848, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131086
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 99848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-99848

Query Match          50.0%; Score 15; DB 15; Length 25;
Best Local Similarity 78.3%; Pred. No. 6.4e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GACTCAGTCCTTGGTCATCTCAC 25
    ||||| ||||| ||||| |||||
Db 3 GACTCAGTCCTAGGTCGCTCTC 25

RESULT 21
US-10-098-263B-106307
; Sequence 106307, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131086
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 106307
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-106307

Query Match          50.0%; Score 15; DB 15; Length 25;
Best Local Similarity 78.3%; Pred. No. 6.4e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCCTTGGTCATCTC 23
    ||||| | ||||| |||||
Db 3 TGGACCCCTCTTCTGGTCTCTC 25

RESULT 22
US-10-098-263B-106308
; Sequence 106308, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131086
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 106308

```

```

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-098-263B-106308

Query Match
Best Local Similarity 50.0%; Score 15; DB 15; Length 25;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGGTCATCTC 23
Db 3 TGGACCTCTACTTGGTCATCTC 25

RESULT 23
US-09-801-274-1484/c
; Sequence 1484, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.209-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1484
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-1484

Query Match
Best Local Similarity 50.0%; Score 15; DB 9; Length 31;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGGTCATCTCAC 25
Db 31 TGGACTAGCCTTTGKCCATCGCCC 7

RESULT 24
US-10-131-827-4195
; Sequence 4195, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4195
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4195

Query Match
Best Local Similarity 50.0%; Score 15; DB 16; Length 50;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CTCAGTCCTTGGTCATCTCACCT 27
Db 4 CTCAGTCCTTGGTCATCTCACCT 26

RESULT 25
US-10-038-835-27
; Sequence 27, Application US/10038835
; Publication No. US20030130497A1
; GENERAL INFORMATION:
; APPLICANT: Bai, Yue-Luen
; APPLICANT: Terng, Harn-Jing
; TITLE OF INVENTION: DETECTION OF RESPIRATORY VIRUSES
; FILE REFERENCE: 12674-006001
; CURRENT APPLICATION NUMBER: US/10/038,835
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human adenovirus type 1
US-10-038-835-27

Query Match
Best Local Similarity 49.3%; Score 14.8; DB 15; Length 20;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGGTCATCT 22
Db 1 GAACCACTCTTGGTCATGT 20

RESULT 26
US-10-427-696-311/c
; Sequence 311, Application US/10427696
; Publication No. US20040220750A1
; GENERAL INFORMATION:
; APPLICANT: Hinds, David
; APPLICANT: Stokowski, Renee
; TITLE OF INVENTION: Method for identifying matched groups
; FILE REFERENCE: PERLP024
; CURRENT APPLICATION NUMBER: US/10/427,696
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 311
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Human
US-10-427-696-311

Query Match
Best Local Similarity 49.3%; Score 14.8; DB 18; Length 25;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTCAGTCCTTGGTCATCTCA 24
Db 21 CTCATCTCTTGGTCATCTGA 2

RESULT 27
US-10-035-833A-347
; Sequence 347, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
```

; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 347
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-347

Query Match 49.3%; Score 14.8; DB 16; Length 41;
Best Local Similarity 80.0%; Pred. No. 8.2e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTCAGTCCTTGGTCATCTCA 24
| | | | | : | | | | | | | | | |
Db 13 CTCAAATTCYGTGTCATCTGA 32

RESULT 28
US-10-035-833A-6498
; Sequence 6498, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6498
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-6498

Query Match 49.3%; Score 14.8; DB 16; Length 41;
Best Local Similarity 80.0%; Pred. No. 8.2e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTCAGTCCTTGGTCATCTCA 24
| | | | | : | | | | | | | | | |
Db 13 CTCAAATTCYGTGTCATCTGA 32

RESULT 29
US-08-944-410-53/c
; Sequence 53, Application US/08944410
; Publication No. US20030050453A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.

; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-53

Query Match 49.3%; Score 14.8; DB 8; Length 46;

Best Local Similarity 73.1%; Pred. No. 8.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 3 GACTCAGTCCTTGGTCATCTCACCTT 28
| | | | | : | | | | | | | | | |
Db 41 GACTCAGACCTTGTGCGACTGACGTT 16

RESULT 30
US-08-944-410-54/c
; Sequence 54, Application US/08944410
; Publication No. US20030050453A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-54

Query Match 49.3%; Score 14.8; DB 8; Length 46;
Best Local Similarity 73.1%; Pred. No. 8.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GACTCAGTCCTTGGTCATCTCACCTT 28
| | | | | : | | | | | | | | | |
Db 41 GACTCAGACCTTGTGCGACTGACGTT 16

RESULT 31
US-08-944-410-55/c
; Sequence 55, Application US/08944410
; Publication No. US20030050453A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-55

Query Match 49.3%; Score 14.8; DB 8; Length 46;
Best Local Similarity 73.1%; Pred. No. 8.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GACTCAGTCCTTGGTCATCTCACCTT 28
| | | | | : | | | | | | | | | |
Db 41 GACTCAGACCTTGTGCGAACTGACGTT 16

RESULT 32
US-10-349-143-1893
; Sequence 1893, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta

```
; APPLICANT: Chumakov, Ilva
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSER.020Cp1
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1893
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-7144-261 : polymorphic base C or T
US-10-349-143-1893

Query Match      49.3%; Score 14.8; DB 16; Length 47;
Best Local Similarity 67.9%; Pred. No. 8.3e+03;
Matches 19; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTGGTCAATCTCACCTTCT 30
   ||||| : | | | | |
Db 14 GTCTCAGTTCYGTGGAACCCACCTTCT 41

RESULT 33
US-10-098-263B-102519
; Sequence 102519, Application US/10098263B
; Publication No. US2003010410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 102519
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-102519

Query Match      48.7%; Score 14.6; DB 15; Length 25;
Best Local Similarity 81.0%; Pred. No. 9.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 TCAGTCCTTGGTCAATCTCACCTCACC 26
   ||| ||||| ||||| |||||
Db 5 TCTGTCCTTGGTCCCTGACC 25

RESULT 34
US-10-098-263B-123321
; Sequence 123321, Application US/10098263B
; Publication No. US2003010410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
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; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 123321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-123321

Query Match      48.7%; Score 14.6; DB 15; Length 25;
Best Local Similarity 81.0%; Pred. No. 9.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CAGTCCTTGGTCAATCTCACCT 27
   ||||| ||||| |||||
Db 5 CAGTCCTGTCGAACCTCACTT 25

RESULT 35
US-10-210-130-295
; Sequence 295, Application US/10210130
; Publication No. US20040014053A1
; GENERAL INFORMATION:
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Patturajan, Meera
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shmukets, Richard A.
; APPLICANT: Li, Li
; APPLICANT: Berghs, Constance
; APPLICANT: Zhong, Mei
; APPLICANT: Casman, Stacie J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Smithson, Glennda
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Leite, Mario W.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Anderson, David W.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Khrantsov, Nikolai V.
; APPLICANT: Ort, Tatiana
; APPLICANT: Ellerman, Karen
; APPLICANT: Rastelli, Luca
; APPLICANT: Agee, Michele L.
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Chant, John S.
; APPLICANT: DiPippo, Vincent A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Giot, Loic
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Hjal, Tord
; APPLICANT: Liu, Xiaohong
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Catterton, Elina
; APPLICANT: Shenoy, Suresh G.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-416C (Cura-716 SMT)
; CURRENT APPLICATION NUMBER: US/10/210,130
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
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; PRIOR APPLICATION NUMBER: 60/316,508
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/354,655
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/383,887
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/323,936
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/381,039
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 295
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-10-210-130-295

Query Match      48.7%; Score 14.6; DB 16; Length 26;
Best Local Similarity 81.0%; Pred. No. 9.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 10 TCCTTGGTCATCTCACCTTCT 30
    ||||| ||||| ||||| |||||
Db 3 TCCTGGCTGACCTCACCTTCT 23

RESULT 36
US-09-916-510A-20
; Sequence 20, Application US/09916510A
; Patent No. US20020168349A1
; GENERAL INFORMATION:
; APPLICANT: IGGO, RICHARD D.
; TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
; FILE REFERENCE: 604-596
; CURRENT APPLICATION NUMBER: US/09/916,510A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: GB 9906815.7
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-916-510A-20

Query Match      48.7%; Score 14.6; DB 9; Length 36;
Best Local Similarity 69.0%; Pred. No. 1e+04;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCCTTGGTCATCTCACCTTC 29
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Db 2 TGGCGCCGCTATTGGTCATCTGCACTTC 30

RESULT 37
US-10-376-630-20
; Sequence 20, Application US/10376630
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; Publication No. US20040047836A1
; GENERAL INFORMATION:
; APPLICANT: BTG INTERNATIONAL LTD
; APPLICANT: IGGO DR, RICHARD D
; APPLICANT: BRUNORI DR, MICHELE A
; TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
; FILE REFERENCE: ADENOVIRUS
; CURRENT APPLICATION NUMBER: US/10/376,630
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: GB 9906815.7
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-376-630-20

Query Match      48.7%; Score 14.6; DB 16; Length 36;
Best Local Similarity 69.0%; Pred. No. 1e+04;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCCTTGGTCATCTCACCTTC 29
    ||||| ||||| ||||| |||||
Db 2 TGGCGCCGCTATTGGTCATCTGCACTTC 30

RESULT 38
US-10-453-827-1043/c
; Sequence 1043, Application US/10453827
; Publication No. US20040033582A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0211 NP
; CURRENT APPLICATION NUMBER: US/10/453,827
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: U.S. 60/384,980
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 1219
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1043
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-453-827-1043

Query Match      48.7%; Score 14.6; DB 16; Length 38;
Best Local Similarity 69.0%; Pred. No. 1e+04;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCCTTGGTCATCTCACCTTC 29
    ||||| ||||| ||||| |||||
Db 32 TTGCCCTGTCCTTGGTCATAGCTGTTTC 4

RESULT 39
US-10-453-827-1190/c
; Sequence 1190, Application US/10453827
; Publication No. US20040033582A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0211 NP
; CURRENT APPLICATION NUMBER: US/10/453,827
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: U.S. 60/384,980
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 1219
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 1190
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-453-827-1190

Query Match      48.7%; Score 14.6; DB 16; Length 38;
Best Local Similarity 69.0%; Pred. No. 1e+04;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      1 TGGACTCAGTCCTTGGTCATCTCACCTTC 29
Db      32 TTGCCCTCTCCTTGGTCATAGCTGTTTC 4

RESULT 40
US-09-530-139-28/c
; Sequence 28, Application US/09530139
; Publication No. US20030092892A1
; GENERAL INFORMATION:
; APPLICANT: FRENKEN, LEON GERARDUS
; APPLICANT: HOWELL, STEVEN
; APPLICANT: LEDEBOER, ADRIANUS MARINUS
; APPLICANT: VAN DER LOGT, CORNELIS PAUL
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
; FILE REFERENCE: 60113/268075/ASH
; CURRENT APPLICATION NUMBER: US/09/530,139
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/EP98/06991
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: EP 97308538.4
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-530-139-28

Query Match      48.7%; Score 14.6; DB 10; Length 42;
Best Local Similarity 69.0%; Pred. No. 1e+04;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      2 GGACTCAGTCCTTGGTCATCTCACCTTCT 30
Db      41 GGACCCAGGTCACCGTCTCCTCACCGTCT 13

Search completed: November 24, 2004, 03:42:25
Job time : 151.774 secs
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1438.31 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-4

Perfect score: 30

Sequence: 1 tggactcagtccttggtcattcaccattct 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: gb_estl.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	53.3	35	9	CL436787 PST3831-N
2	15.6	52.0	42	8	BH864588 SALK_0963
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4	14.2	47.3	41	9	CL212954 G028G03 G
5	14.2	47.3	49	2	B9770036 601680150
6	14.2	47.3	49	9	BX531144 Arabidops
7	14.2	47.3	50	1	AU105600 AU105600
8	13.8	46.0	42	9	AJ622668 Drosophil
9	13.8	46.0	46	1	AA954628 oes3e04.s
10	13.8	46.0	50	1	AU106264 AU106264
11	13.6	45.3	34	1	AZ259780 va87b10.r
12	13.6	45.3	41	8	AZ604835 IM0425E19
13	13.6	45.3	48	9	AL950922 Arabidops
14	13.4	44.7	44	1	AU264313 AU264313
15	13.4	44.7	50	1	AU107621 AU107621
16	13.4	44.7	50	1	AU107622 AU107622
17	13.4	44.7	50	1	AU107623 AU107623
18	13.2	44.0	37	4	BG260157 60371257
19	13.2	44.0	50	1	AU102328 AU102328
20	13	43.3	28	7	H26079 Y156d10.r1
21	13	43.3	28	9	CC795628 SALK_0876
22	13	43.3	47	8	AZ309567 IM0016F07
23	13	43.3	49	1	A1746816 u107907.Y
24	12.8	42.7	24	8	AZ607692 IM0430113

C 25	12.8	42.7	24	8	AZ662752
C 26	12.8	42.7	31	1	AI582089
C 27	12.8	42.7	34	9	DM545069
C 28	12.8	42.7	37	7	H13124
C 29	12.8	42.7	37	8	BH759504
C 30	12.8	42.7	43	7	CN762433
C 31	12.8	42.7	44	8	AZ479665
C 32	12.8	42.7	44	9	CL675662
C 33	12.8	42.7	45	8	AZ328994
C 34	12.8	42.7	48	8	BH791670
C 35	12.8	42.7	49	1	AV833344
C 36	12.6	42.0	24	9	AG198679
C 37	12.6	42.0	28	8	AZ309679
C 38	12.6	42.0	29	9	CC798624
C 39	12.6	42.0	32	9	AG198685
C 40	12.6	42.0	36	8	BH011404
C 41	12.6	42.0	41	8	BZ381303
C 42	12.6	42.0	45	8	BH848020
C 43	12.6	42.0	45	9	EX292770
C 44	12.6	42.0	46	4	BI488502
C 45	12.6	42.0	48	8	AZ408184
C 46	12.6	42.0	48	8	AZ504262
C 47	12.6	42.0	49	1	AI019053
C 48	12.4	41.3	26	8	AZ662138
C 49	12.4	41.3	34	1	AV844944
C 50	12.4	41.3	34	8	AZ600325
C 51	12.4	41.3	35	8	AZ664145
C 52	12.4	41.3	36	8	AZ482058
C 53	12.4	41.3	39	4	BI766377
C 54	12.4	41.3	43	1	AA947665
C 55	12.4	41.3	43	1	AI282013
C 56	12.4	41.3	45	9	AJ597160
C 57	12.4	41.3	46	1	AI036878
C 58	12.4	41.3	47	6	C20881
C 59	12.4	41.3	49	6	CD530579
C 60	12.4	41.3	49	9	EX659968
C 61	12.4	41.3	50	1	AU107220
C 62	12.4	41.3	50	1	AU107978
C 63	12.4	41.3	50	1	AU107979
C 64	12.2	40.7	27	8	AZ623080
C 65	12.2	40.7	28	8	AZ456389
C 66	12.2	40.7	30	8	AZ645878
C 67	12.2	40.7	32	8	AZ775049
C 68	12.2	40.7	32	8	BH911753
C 69	12.2	40.7	35	8	AZ801831
C 70	12.2	40.7	37	1	AA704663
C 71	12.2	40.7	37	4	BI834423
C 72	12.2	40.7	37	9	AG201843
C 73	12.2	40.7	38	9	CC795484
C 74	12.2	40.7	40	9	AL764467
C 75	12.2	40.7	41	8	AZ813179
C 76	12.2	40.7	41	9	CG399825
C 77	12.2	40.7	45	4	BI916371
C 78	12.2	40.7	45	8	AZ662522
C 79	12.2	40.7	46	1	AA641248
C 80	12.2	40.7	46	4	BI837191
C 81	12.2	40.7	46	8	BH628167
C 82	12.2	40.7	46	9	TA5A02P
C 83	12.2	40.7	48	1	AV847374
C 84	12.2	40.7	48	4	EG403326
C 85	12.2	40.7	48	8	AZ775146
C 86	12.2	40.7	48	8	BH850842
C 87	12.2	40.7	50	1	AU103005
C 88	12.2	40.7	50	1	AU103636
C 89	12.2	40.7	50	1	AU103999
C 90	12.2	40.7	50	1	AU104000
C 91	12.2	40.7	50	1	AU104001
C 92	12.2	40.7	50	1	AU104002
C 93	12.2	40.7	50	1	AU104003
C 94	12.2	40.7	50	1	AU104004
C 95	12.2	40.7	50	1	AU104005
C 96	12.2	40.7	50	1	AU104007
C 97	12.2	40.7	50	1	AU104008

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c 98 12.2 40.7 50 1  AUI104009  AUI104009  AUI104009  171  11.6  38.7  42  8  BH740786  KG02679-3
c 99 12.2 40.7 50 1  AUI106265  AUI106265  AUI106265  C 172  11.6  38.7  42  8  BH850477  SALK 0713
c 100 12.2 40.7 50 6  CF329688  NACL--05-  CF329688  C 173  11.6  38.7  42  8  BH911378  SALK_0681
c 101 12.2 40.7 50 8  AZ480460  IM0302E05  AZ480460  C 174  11.6  38.7  42  9  CL459539  XQ0498 Sa
c 102 12.2 40.7 50 8  BZ766933  SALK_1380  BZ766933  C 175  11.6  38.7  42  9  CL528326  ASV22B12.
c 103 12.2 40.0 24 9  CL670084  PRI0161a  CL670084  C 176  11.6  38.7  43  7  NS7043  YW85C11.r1
c 104 12.2 40.0 31 8  AZ368771  IM0119E01  AZ368771  C 177  11.6  38.7  43  7  NS7043  YW85C11.r1
c 105 12.2 40.0 33 9  CR358676  Arabidops  CR358676  C 178  11.6  38.7  44  1  A1118713  ucl11g11.r
c 106 12.2 40.0 33 9  CR866586  SALK_1487  CR866586  C 179  11.6  38.7  44  8  BH911599  SALK_0696
c 107 12.2 40.0 34 9  CG723116  111974G1  CG723116  C 180  11.6  38.7  44  8  BH911599  SALK_0696
c 108 12.2 40.0 36 3  CNS0916S  Single re  BX063536  C 181  11.6  38.7  45  8  BZ664959  SALK_1103
c 109 12.2 40.0 37 4  AA889301  ak13f03.s  AA889301  C 182  11.6  38.7  46  1  A1035942  uC49f12.r
c 110 12.2 40.0 37 4  BM400180  5009-0-68  BM400180  C 183  11.6  38.7  46  6  CA908621  PCS02482
c 111 12.2 40.0 39 1  AV955711  AV955711  AV955711  C 184  11.6  38.7  46  8  A2489801  1M0322M20
c 112 12.2 40.0 39 3  CNS09H9S  Single re  BX058460  C 185  11.6  38.7  46  8  A2659931  1M0337L12
c 113 12.2 40.0 39 8  BZ594107  SALK_0828  BZ594107  C 186  11.6  38.7  47  8  A2805275  2M0066P01
c 114 12.2 40.0 42 1  AUI009032  AUI009032  AUI009032  C 187  11.6  38.7  47  8  BH791124  SALK 0587
c 115 12.2 40.0 43 1  AA829397  od06d01.s  AA829397  C 188  11.6  38.7  47  8  BH791157  SALK 0588
c 116 12.2 40.0 43 1  A1363387  AUI363387  AUI363387  C 189  11.6  38.7  47  9  AG204311  Pan trogl
c 117 12.2 40.0 43 1  AUI009031  AUI009031  AUI009031  C 190  11.6  38.7  47  9  AG216926  Drosophil
c 118 12.2 40.0 44 9  BX129899  Danilo rer  BX129899  C 191  11.6  38.7  48  4  EM041668  603614731
c 119 12.2 40.0 45 9  AL763705  Arabidops  AL763705  C 192  11.6  38.7  48  4  EM041668  603614731
c 120 12.2 40.0 46 1  A1539046  tp76g11.x  A1539046  C 193  11.6  38.7  48  9  CG427281  oIS0726-0
c 121 12.2 40.0 46 8  AZ429958  IM0214M07  AZ429958  C 194  11.6  38.7  49  1  AA922891  oIS1h05.s
c 122 12.2 40.0 48 9  BZ286631  Arabidops  BZ286631  C 195  11.6  38.7  49  4  BM280302  3'EST-NC
c 123 12.2 40.0 49 8  AZ814214  2M0081N13  AZ814214  C 196  11.6  38.7  49  7  N40856  YW83d11.r1
c 124 12.2 40.0 49 9  CG718294  1119052D0  CG718294  C 197  11.6  38.7  49  8  BH608677  7L11 L1L18
c 125 12.2 40.0 49 9  CG722873  1119073G1  CG722873  C 198  11.6  38.7  49  8  BH901307  SALK_0743
c 126 12.2 40.0 50 1  AUI05857  AUI05857  AUI05857  C 199  11.6  38.7  49  8  BH901307  SALK_0743
c 127 12.2 40.0 50 1  AUI07935  AUI07935  AUI07935  C 200  11.6  38.7  50  1  AUI02326  AUI02326
c 128 12.2 40.0 50 2  BF571906  602078216  BF571906  C 201  11.6  38.7  50  1  AUI02329  AUI02329
c 129 11.8 39.3 28 8  AZ309062  IM0012B14  AZ309062  C 202  11.6  38.7  50  1  AUI03621  AUI03621
c 130 11.8 39.3 32 8  AZ303920  1M0003F19  AZ303920  C 203  11.6  38.7  50  2  A459434  sh24c05.Y
c 131 11.8 39.3 32 8  BZ594797  SALK_0852  BZ594797  C 204  11.6  38.7  50  5  BX722422  BX722422
c 132 11.8 38.3 34 1  A1662334  uj69c01.Y  A1662334  C 205  11.6  38.7  50  6  CB219956  1AB002B12
c 133 11.8 39.3 36 9  CG466758  oIS0638-0  CG466758  C 206  11.6  38.7  50  6  CB219956  1AB002B12
c 134 11.8 39.3 41 8  AZ441689  IM0233K24  AZ441689  C 207  11.6  38.7  50  6  CB275037  ku61e09.Y
c 135 11.8 39.3 42 5  BQ5885504  E012306-0  BQ5885504  C 208  11.6  38.7  50  8  BH856729  SALK 0792
c 136 11.8 39.3 42 5  BQ5885504  E012306-0  BQ5885504  C 209  11.4  38.0  29  9  AG188890  Pan trogl
c 137 11.8 39.3 44 6  CF298055  7LEAF--01  CF298055  C 210  11.4  38.0  30  8  BH740820  XG04070-5
c 138 11.8 38.3 44 8  AZ778971  2M0014M09  AZ778971  C 211  11.4  38.0  30  8  BH740820  XG04070-5
c 139 11.8 39.3 45 9  DR6119S  Danilo rer  AL746188  C 212  11.4  38.0  30  8  BH789905  SALK_0483
c 140 11.8 39.3 46 1  A1146894  oy23g04.s  A1146894  C 213  11.4  38.0  32  6  CD531546  11D06 Ara
c 141 11.8 39.3 46 1  A1569880  tr57a07.x  A1569880  C 214  11.4  38.0  36  9  TA124B04P  AA822396 vx44c11.r
c 142 11.8 39.3 46 6  CA967893  CcLX05a15  CA967893  C 215  11.4  38.0  37  1  AA882396  vx44c11.r
c 143 11.8 39.3 46 9  TA57A07P  T_brucei  AL456782  C 216  11.4  38.0  39  9  AL756928  Arabidops
c 144 11.8 38.3 47 8  BH631605  100708SG0  BH631605  C 217  11.4  38.0  40  8  CC040316  3591_1_13
c 145 11.8 39.3 48 1  AA930873  vz71e07.s  AA930873  C 218  11.4  38.0  40  9  CL436831  PST3920-N
c 146 11.8 39.3 48 1  A1172854  ucl10c07.r  A1172854  C 219  11.4  38.0  43  9  CL528741  ASV7B09.r
c 147 11.8 39.3 48 1  AA386692  vb55c05.r  AA386692  C 220  11.4  38.0  44  8  AZ862141  2M0169M04
c 148 11.8 39.3 48 8  AZ805363  2M0066B13  AZ805363  C 221  11.4  38.0  44  8  B07611  CDC104 Cri
c 149 11.8 39.3 48 8  AZ831191  2M0110L13  AZ831191  C 222  11.4  38.0  45  8  A2487209  1M0316B12
c 150 11.8 39.3 48 8  BH608655  609 LL18N  BH608655  C 223  11.4  38.0  46  1  AA940161  ua23c07.r
c 151 11.8 39.3 49 1  A1282035  qq8e06.x  A1282035  C 224  11.4  38.0  46  8  BZ763623  SALK 1197
c 152 11.8 39.3 49 1  AA515410  nf69a09.s  AA515410  C 225  11.4  38.0  46  8  A2321341  1M0041B20
c 153 11.8 39.3 50 1  AUI03979  AUI03979  AUI03979  C 226  11.4  38.0  47  8  A2778132  2M0011N08
c 154 11.8 39.3 50 1  AUI06735  AUI06735  AUI06735  C 227  11.4  38.0  47  8  BH801184  1008126A0
c 155 11.6 38.7 24 8  A2626098  1M0466109  A2626098  C 228  11.4  38.0  47  8  BH847193  SALK_0445
c 156 11.6 38.7 27 4  EG927411  HNC1-1-G9  EG927411  C 229  11.4  38.0  47  8  CC039002  3591_1_99
c 157 11.6 38.7 29 8  BZ592652  SALK_0283  BZ592652  C 230  11.4  38.0  48  8  A2621115  1M0454F07
c 158 11.6 38.7 31 1  A1382798  tc08f05.x  A1382798  C 231  11.4  38.0  48  8  BH901106  KG09864-5
c 159 11.6 38.7 32 9  AL764287  Arabidops  AL764287  C 232  11.4  38.0  48  8  BH902185  SALK 0914
c 160 11.6 38.7 34 4  BM397004  5009-0-28  BM397004  C 233  11.4  38.0  48  1  A1036013  vZ68a10.r
c 161 11.6 38.7 35 9  CL234779  0383051-0  CL234779  C 234  11.4  38.0  49  1  AA146697  z03a10.s
c 162 11.6 38.7 36 8  AZ759424  1M0551H17  AZ759424  C 235  11.4  38.0  49  1  AA146697  z03a10.s
c 163 11.6 38.7 36 8  AZ8099373  2M0073A20  AZ8099373  C 236  11.4  38.0  49  7  T68434  YC42d01.e1
c 164 11.6 38.7 37 1  A1002874  ank23d08.s  A1002874  C 237  11.4  38.0  49  8  CC045158  3591_1_17
c 165 11.6 38.7 38 8  BH853522  SALK_0770  BH853522  C 238  11.4  38.0  50  1  AUI02629  AUI02629
c 166 11.6 38.7 38 8  BZ355823  SALK_1275  BZ355823  C 239  11.4  38.0  50  1  AUI03222  AUI03222
c 167 11.6 38.7 39 8  BZ357473  SALK_1307  BZ357473  C 240  11.4  38.0  50  1  AUI03491  AUI03491
c 168 11.6 38.7 39 8  BZ649373  SALK_1275  BZ649373  C 241  11.4  38.0  50  1  AUI04542  AUI04542
c 169 11.6 38.7 40 1  A1882509  ub97a09.r  A1882509  C 242  11.4  38.0  50  1  AUI04786  AUI04786
c 170 11.6 38.7 40 2  BF683654  602139883  BF683654  C 243  11.4  38.0  50  1  AUI04787  AUI04787

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C 244	11.4	38.0	50	1	AUI04788	AUI04788	AUI04788	C 317	11.2	37.3	50	1	AUI06721	AUI06721
C 245	11.4	38.0	50	1	AUI04789	AUI04789	AUI04789	C 318	11.2	37.3	50	1	AUI07040	AUI07040
C 246	11.4	38.0	50	1	AUI04790	AUI04790	AUI04790	C 319	11.2	37.3	50	1	AA411320	AA411320
C 247	11.4	38.0	50	1	AUI04791	AUI04791	AUI04791	C 320	11.2	37.3	50	1	AA411320	AA411320
C 248	11.4	38.0	50	1	AUI04792	AUI04792	AUI04792	C 321	11.2	37.3	50	6	CG222716	CG222716
C 249	11.4	38.0	50	1	AUI04793	AUI04793	AUI04793	C 322	11.2	37.3	50	6	BF222649	BF222649
C 250	11.4	38.0	50	1	AUI04794	AUI04794	AUI04794	C 323	11.2	37.3	50	9	CR357976	CR357976
C 251	11.4	38.0	50	1	AUI04795	AUI04795	AUI04795	C 324	11.2	37.3	50	9	CR357976	CR357976
C 252	11.4	38.0	50	1	AUI04796	AUI04796	AUI04796	C 325	11.2	37.3	50	9	TA100C01Q	TA100C01Q
C 253	11.4	38.0	50	1	AUI04797	AUI04797	AUI04797	C 326	11.2	37.3	50	9	AJ589502	AJ589502
C 254	11.4	38.0	50	1	AUI04798	AUI04798	AUI04798	C 327	11.2	37.3	50	9	AJ589502	AJ589502
C 255	11.4	38.0	50	1	AUI04799	AUI04799	AUI04799	C 328	11.2	37.3	50	9	AJ589502	AJ589502
C 256	11.4	38.0	50	1	AUI04800	AUI04800	AUI04800	C 329	11.2	37.3	50	9	AJ589502	AJ589502
C 257	11.4	38.0	50	1	AUI04801	AUI04801	AUI04801	C 330	11.2	37.3	50	9	AJ589502	AJ589502
C 258	11.4	38.0	50	1	AUI04802	AUI04802	AUI04802	C 331	11.2	37.3	50	9	AJ589502	AJ589502
C 259	11.4	38.0	50	1	AUI04803	AUI04803	AUI04803	C 332	11.2	37.3	50	9	AJ589502	AJ589502
C 260	11.4	38.0	50	1	AUI05007	AUI05007	AUI05007	C 333	11.2	37.3	50	9	AJ589502	AJ589502
C 261	11.4	38.0	50	1	AUI05008	AUI05008	AUI05008	C 334	11.2	37.3	50	9	AJ589502	AJ589502
C 262	11.4	38.0	50	1	AUI05010	AUI05010	AUI05010	C 335	11.2	37.3	50	9	AJ589502	AJ589502
C 263	11.4	38.0	50	1	AUI06303	AUI06303	AUI06303	C 336	11.2	37.3	50	9	AJ589502	AJ589502
C 264	11.4	38.0	50	9	CG801160	CG801160	CG801160	C 337	11.2	37.3	50	9	AJ589502	AJ589502
C 265	11.2	37.3	21	8	AZ336281	AZ336281	AZ336281	C 338	11.2	37.3	50	9	AJ589502	AJ589502
C 266	11.2	37.3	23	8	AZ501330	AZ501330	AZ501330	C 339	11.2	37.3	50	9	AJ589502	AJ589502
C 267	11.2	37.3	27	8	AZ345930	AZ345930	AZ345930	C 340	11.2	37.3	50	9	AJ589502	AJ589502
C 268	11.2	37.3	27	8	AZ347008	AZ347008	AZ347008	C 341	11.2	37.3	50	9	AJ589502	AJ589502
C 269	11.2	37.3	27	8	AZ580733	AZ580733	AZ580733	C 342	11.2	37.3	50	9	AJ589502	AJ589502
C 270	11.2	37.3	29	8	AZ771858	AZ771858	AZ771858	C 343	11.2	37.3	50	9	AJ589502	AJ589502
C 271	11.2	37.3	29	9	TA84F02Q	TA84F02Q	TA84F02Q	C 344	11.2	37.3	50	9	AJ589502	AJ589502
C 272	11.2	37.3	31	1	AI313645	AI313645	AI313645	C 345	11.2	37.3	50	9	AJ589502	AJ589502
C 273	11.2	37.3	32	9	AG193703	AG193703	AG193703	C 346	11.2	37.3	50	9	AJ589502	AJ589502
C 274	11.2	37.3	35	8	BH908490	BH908490	BH908490	C 347	11.2	37.3	50	9	AJ589502	AJ589502
C 275	11.2	37.3	35	8	TH352802Q	TH352802Q	TH352802Q	C 348	11.2	37.3	50	9	AJ589502	AJ589502
C 276	11.2	37.3	39	1	AJ673474	AJ673474	AJ673474	C 349	11.2	37.3	50	9	AJ589502	AJ589502
C 277	11.2	37.3	39	1	AZ308522	AZ308522	AZ308522	C 350	11.2	37.3	50	9	AJ589502	AJ589502
C 278	11.2	37.3	39	9	TA306D11P	TA306D11P	TA306D11P	C 351	11.2	37.3	50	9	AJ589502	AJ589502
C 279	11.2	37.3	40	1	AA767606	AA767606	AA767606	C 352	11.2	37.3	50	9	AJ589502	AJ589502
C 280	11.2	37.3	40	1	AA860078	AA860078	AA860078	C 353	11.2	37.3	50	9	AJ589502	AJ589502
C 281	11.2	37.3	40	1	AA417630	AA417630	AA417630	C 354	11.2	37.3	50	9	AJ589502	AJ589502
C 282	11.2	37.3	40	7	N91653	N91653	N91653	C 355	11.2	37.3	50	9	AJ589502	AJ589502
C 283	11.2	37.3	40	8	AZ859943	AZ859943	AZ859943	C 356	11.2	37.3	50	9	AJ589502	AJ589502
C 284	11.2	37.3	40	9	BX659989	BX659989	BX659989	C 357	11.2	37.3	50	9	AJ589502	AJ589502
C 285	11.2	37.3	41	8	AZ361377	AZ361377	AZ361377	C 358	11.2	37.3	50	9	AJ589502	AJ589502
C 286	11.2	37.3	41	9	AJ601244	AJ601244	AJ601244	C 359	11.2	37.3	50	9	AJ589502	AJ589502
C 287	11.2	37.3	43	7	CO782826	CO782826	CO782826	C 360	11.2	37.3	50	9	AJ589502	AJ589502
C 288	11.2	37.3	43	8	BH851172	BH851172	BH851172	C 361	11.2	37.3	50	9	AJ589502	AJ589502
C 289	11.2	37.3	44	1	AI185812	AI185812	AI185812	C 362	11.2	37.3	50	9	AJ589502	AJ589502
C 290	11.2	37.3	44	1	AU255883	AU255883	AU255883	C 363	11.2	37.3	50	9	AJ589502	AJ589502
C 291	11.2	37.3	44	8	BZ384329	BZ384329	BZ384329	C 364	11.2	37.3	50	9	AJ589502	AJ589502
C 292	11.2	37.3	45	8	BH171689	BH171689	BH171689	C 365	11.2	37.3	50	9	AJ589502	AJ589502
C 293	11.2	37.3	45	8	BZ352401	BZ352401	BZ352401	C 366	11.2	37.3	50	9	AJ589502	AJ589502
C 294	11.2	37.3	46	1	AI001117	AI001117	AI001117	C 367	11.2	37.3	50	9	AJ589502	AJ589502
C 295	11.2	37.3	46	1	AA447381	AA447381	AA447381	C 368	11.2	37.3	50	9	AJ589502	AJ589502
C 296	11.2	37.3	46	1	AA485011	AA485011	AA485011	C 369	11.2	37.3	50	9	AJ589502	AJ589502
C 297	11.2	37.3	46	9	AL765862	AL765862	AL765862	C 370	11.2	37.3	50	9	AJ589502	AJ589502
C 298	11.2	37.3	47	8	AQ074021	AQ074021	AQ074021	C 371	11.2	37.3	50	9	AJ589502	AJ589502
C 299	11.2	37.3	47	8	AZ783950	AZ783950	AZ783950	C 372	11.2	37.3	50	9	AJ589502	AJ589502
C 300	11.2	37.3	47	8	BH855918	BH855918	BH855918	C 373	11.2	37.3	50	9	AJ589502	AJ589502
C 301	11.2	37.3	47	9	CG799680	CG799680	CG799680	C 374	11.2	37.3	50	9	AJ589502	AJ589502
C 302	11.2	37.3	48	9	AL751670	AL751670	AL751670	C 375	11.2	37.3	50	9	AJ589502	AJ589502
C 303	11.2	37.3	49	1	AA659355	AA659355	AA659355	C 376	11.2	37.3	50	9	AJ589502	AJ589502
C 304	11.2	37.3	49	1	AI032978	AI032978	AI032978	C 377	11.2	37.3	50	9	AJ589502	AJ589502
C 305	11.2	37.3	49	7	CO780197	CO780197	CO780197	C 378	11.2	37.3	50	9	AJ589502	AJ589502
C 306	11.2	37.3	49	7	CO780197	CO780197	CO780197	C 379	11.2	37.3	50	9	AJ589502	AJ589502
C 307	11.2	37.3	49	8	AZ359000	AZ359000	AZ359000	C 380	11.2	37.3	50	9	AJ589502	AJ589502
C 308	11.2	37.3	49	8	AZ768953	AZ768953	AZ768953	C 381	11.2	37.3	50	9	AJ589502	AJ589502
C 309	11.2	37.3	49	8	BH902591	BH902591	BH902591	C 382	11.2	37.3	50	9	AJ589502	AJ589502
C 310	11.2	37.3	49	9	CG775874	CG775874	CG775874	C 383	11.2	37.3	50	9	AJ589502	AJ589502
C 311	11.2	37.3	50	1	AUI03196	AUI03196	AUI03196	C 384	11.2	37.3	50	9	AJ589502	AJ589502
C 312	11.2	37.3	50	1	AUI03197	AUI03197	AUI03197	C 385	11.2	37.3	50	9	AJ589502	AJ589502
C 313	11.2	37.3	50	1	AUI03199	AUI03199	AUI03199	C 386	11.2	37.3	50	9	AJ589502	AJ589502
C 314	11.2	37.3	50	1	AUI03202	AUI03202	AUI03202	C 387	11.2	37.3	50	9	AJ589502	AJ589502
C 315	11.2	37.3	50	1	AUI04744	AUI04744	AUI04744	C 388	11.2	37.3	50	9	AJ589502	AJ589502
C 316	11.2	37.3	50	1	AUI04745	AUI04745	AUI04745	C 389	11.2	37.3	50	9	AJ589502	AJ589502

C 390	11	36.7	50	1	AU103220	AU103220 AU103220	463	10.8	36.0	42	6	C00705	C00705 HUMGS000826
C 391	11	36.7	50	1	AU103221	AU103221 AU103221	464	10.8	36.0	42	7	CK577724	CK577724 IST WT5 1
C 392	11	36.7	50	1	AU103223	AU103223 AU103223	C 465	10.8	36.0	42	8	BH641345	BH641345 1008046H0
C 393	11	36.7	50	1	AU103635	AU103635 AU103635	C 466	10.8	36.0	42	9	CR395913	CR395913 Arabidops
C 394	11	36.7	50	1	AU103637	AU103637 AU103637	C 467	10.8	36.0	42	9	AG215405	AG215405 Arabidops
C 395	11	36.7	50	1	AU103638	AU103638 AU103638	C 468	10.8	36.0	42	1	AA838558	AA838558 oe39409.s
C 396	11	36.7	50	1	AU103640	AU103640 AU103640	C 469	10.8	36.0	43	1	AI1356829	AI1356829 qv23c11.x
C 397	11	36.7	50	1	AU104382	AU104382 AU104382	C 470	10.8	36.0	43	1	AA103211	AA103211 mo22807.r
C 398	11	36.7	50	1	AU104383	AU104383 AU104383	C 471	10.8	36.0	43	1	AI583773	AI583773 tt71404.x
C 399	11	36.7	50	1	AU104385	AU104385 AU104385	C 472	10.8	36.0	43	1	AA594823	AA594823 no20c10.s
C 400	11	36.7	50	1	AU106326	AU106326 AU106326	C 473	10.8	36.0	43	2	AW698575	AW698575 g377 glan
C 401	11	36.7	50	1	AU106715	AU106715 AU106715	C 474	10.8	36.0	43	6	CA969808	CA969808 CCLX06a24
C 402	11	36.7	50	1	AU106716	AU106716 AU106716	C 475	10.8	36.0	43	7	H57259	H57259 Yr10906.r1
C 403	11	36.7	50	1	AU106725	AU106725 AU106725	C 476	10.8	36.0	43	8	AZ443922	AZ443922 IM0238N08
C 404	11	36.7	50	1	AU106728	AU106728 AU106728	C 477	10.8	36.0	43	9	CG869477	CG869477 XP0160 Sa
C 405	11	36.7	50	1	AU106732	AU106732 AU106732	C 478	10.8	36.0	43	9	CL656268	CL656268 PRI0126a
C 406	11	36.7	50	1	AU107381	AU107381 AU107381	C 479	10.8	36.0	43	9	AG215223	AG215223 Drosophill
C 407	11	36.7	50	2	AW248365	AW248365 2820706.s	C 480	10.8	36.0	44	8	AQ025982	AQ025982 EP(210358
C 408	11	36.7	50	4	BM733456	BM733456 k13303.y	C 481	10.8	36.0	44	8	BZ290554	BZ290554 SALK_0901
C 409	11	36.7	50	4	BM733804	BM733804 k126c04.y	C 482	10.8	36.0	44	8	BZ767073	BZ767073 SALK_1383
C 410	11	36.7	50	7	R98157	R98157 yq66g08.r1	C 483	10.8	36.0	45	6	CD028928	CD028928 wgmV001xL
C 411	11	36.7	50	8	BH641149	BH641149 1008046A0	C 484	10.8	36.0	45	9	EX948434	EX948434 Arabidops
C 412	11	36.7	50	9	AL947641	AL947641 Arabidops	C 485	10.8	36.0	45	9	CR395481	CR395481 Arabidops
C 413	10.8	36.0	21	6	CF279674	CF279674 14ETL1-06	C 486	10.8	36.0	46	8	AZ476040	AZ476040 IM0239AG04
C 414	10.8	36.0	27	9	CL655506	CL655506 PRI0123c	C 487	10.8	36.0	46	8	BH901021	BH901021 KG08333-3
C 415	10.8	36.0	28	1	AI131886	AI131886 uc38h05.r	C 488	10.8	36.0	46	9	EX143450	EX143450 Danio rer
C 416	10.8	36.0	28	9	AJ598776	AJ598776 Arabidops	C 489	10.8	36.0	46	9	CG721749	CG721749 1119068G1
C 417	10.8	36.0	29	8	AZ633359	AZ633359 IM0488K02	C 490	10.8	36.0	46	9	CL655496	CL655496 PRI0123c
C 418	10.8	36.0	29	8	AZ775515	AZ775515 2M0008U12	C 491	10.8	36.0	47	2	AW059631	AW059631 RUTH.bssC
C 419	10.8	36.0	31	1	AA885849	AA885849 o336c01.s	C 492	10.8	36.0	47	2	CO787749	CO787749 NT0028.D0
C 420	10.8	36.0	31	1	AI001917	AI001917 o42d10.s	C 493	10.8	36.0	47	8	AZ403608	AZ403608 IM0003117
C 421	10.8	36.0	31	4	EG537808	EG537808 602566163	C 494	10.8	36.0	47	8	AZ403867	AZ403867 IM0171A16
C 422	10.8	36.0	31	4	BM392644	BM392644 50071-2-1	C 495	10.8	36.0	47	8	AZ974877	AZ974877 2M0249N10
C 423	10.8	36.0	31	4	BM393821	BM393821 50072-2-1	C 496	10.8	36.0	47	8	BZ380035	BZ380035 SALK_1144
C 424	10.8	36.0	31	8	AZ815323	AZ815323 2M0083B05	C 497	10.8	36.0	47	9	EX532135	EX532135 Arabidops
C 425	10.8	36.0	32	9	TA222D01P	TA222D01P T. brucei	C 498	10.8	36.0	47	9	CG869479	CG869479 XP0166 Sa
C 426	10.8	36.0	32	9	AJ600534	AJ600534 Arabidops	C 499	10.8	36.0	47	9	AG189046	AG189046 Pan trogl
C 427	10.8	36.0	34	1	AA148571	AA148571 z104b02.r	C 500	10.8	36.0	48	8	AZ412179	AZ412179 IM0185H06
C 428	10.8	36.0	34	9	TA368C01Q	TA368C01Q T. brucei	C 501	10.8	36.0	48	8	BH913087	BH913087 3526 1 38
C 429	10.8	36.0	34	9	CG711407	CG711407 1119021C0	C 502	10.8	36.0	48	9	CC799604	CC799604 01S0579-0
C 430	10.8	36.0	35	9	AL949791	AL949791 Arabidops	C 503	10.8	36.0	49	1	AI198147	AI198147 q151b10.x
C 431	10.8	36.0	35	9	DR421245	DR421245 Danio rer	C 504	10.8	36.0	49	1	AI340390	AI340390 tb40c01.x
C 432	10.8	36.0	35	9	TA275C03P	TA275C03P T. brucei	C 505	10.8	36.0	49	1	AI800933	AI800933 wgl14g11.x
C 433	10.8	36.0	35	9	CL438234	CL438234 PST7051-N	C 506	10.8	36.0	49	1	AI941380	AI941380 sg12e11.y
C 434	10.8	36.0	36	8	BH849834	BH849834 SALK_0703	C 507	10.8	36.0	49	1	AA413837	AA413837 vc67d05.s
C 435	10.8	36.0	36	9	AL941496	AL941496 Arabidops	C 508	10.8	36.0	49	2	BF970220	BF970220 602273453
C 436	10.8	36.0	37	1	AI900168	AI900168 sc01g10.y	C 509	10.8	36.0	49	7	CF350566	CF350566 r160d09.y
C 437	10.8	36.0	37	8	AQ073641	AQ073641 EF(212504	C 510	10.8	36.0	49	8	AZ807976	AZ807976 2M0071N10
C 438	10.8	36.0	37	8	BH417967	BH417967 W22-05 Mu	C 511	10.8	36.0	49	9	CR395482	CR395482 Arabidops
C 439	10.8	36.0	38	2	BF302851	BF302851 602032746	C 512	10.8	36.0	49	9	CG869475	CG869475 XP0156 Sa
C 440	10.8	36.0	38	8	AZ332275	AZ332275 IM0060M11	C 513	10.8	36.0	49	9	CG869476	CG869476 XP0159 Sa
C 441	10.8	36.0	38	9	EX662465	EX662465 Arabidops	C 514	10.8	36.0	50	1	AU103201	AU103201 AU103201
C 442	10.8	36.0	38	9	BM662465	BM662465 Arabidops	C 515	10.8	36.0	50	1	AU104145	AU104145 AU104145
C 443	10.8	36.0	38	9	DME547594	DME547594 Drosophill	C 516	10.8	36.0	50	1	AU104558	AU104558 AU104558
C 444	10.8	36.0	39	9	CG677721	CG677721 02F2009-0	C 517	10.8	36.0	50	1	AU104563	AU104563 AU104563
C 445	10.8	36.0	39	9	CL528564	CL528564 ASV20E06.	C 518	10.8	36.0	50	1	AU104567	AU104567 AU104567
C 446	10.8	36.0	40	1	AV833543	AV833543 ASB33543	C 519	10.8	36.0	50	1	AU105214	AU105214 AU105214
C 447	10.8	36.0	40	1	AA566138	AA566138 ESTK3037	C 520	10.8	36.0	50	1	AU105216	AU105216 AU105216
C 448	10.8	36.0	40	4	BJ082487	BJ082487 BJO82487	C 521	10.8	36.0	50	1	AU105219	AU105219 AU105219
C 449	10.8	36.0	40	8	AZ938886	AZ938886 2M0197F07	C 522	10.8	36.0	50	1	AU105221	AU105221 AU105221
C 450	10.8	36.0	40	8	CC199659	CC199659 XH683 Bay	C 523	10.8	36.0	50	1	AU105222	AU105222 AU105222
C 451	10.8	36.0	40	9	CR358612	CR358612 Arabidops	C 524	10.8	36.0	50	1	AU105223	AU105223 AU105223
C 452	10.8	36.0	40	9	TA187A02Q	TA187A02Q T. brucei	C 525	10.8	36.0	50	1	AU105224	AU105224 AU105224
C 453	10.8	36.0	40	9	CG892121	CG892121 01S0592-0	C 526	10.8	36.0	50	1	AU105225	AU105225 AU105225
C 454	10.8	36.0	40	9	CL639115	CL639115 G080F09 G	C 527	10.8	36.0	50	1	AU105226	AU105226 AU105226
C 455	10.8	36.0	41	1	AV967151	AV967151 AV967151	C 528	10.8	36.0	50	1	AU105228	AU105228 AU105228
C 456	10.8	36.0	41	5	BQ589105	BQ589105 E012580-0	C 529	10.8	36.0	50	1	AU105230	AU105230 AU105230
C 457	10.8	36.0	41	6	CD530780	CD530780 07007 Ara	C 530	10.8	36.0	50	1	AU105604	AU105604 AU105604
C 458	10.8	36.0	41	8	AZ793879	AZ793879 2M0047F19	C 531	10.8	36.0	50	1	AU107078	AU107078 AU107078
C 459	10.8	36.0	41	8	BH909688	BH909688 SALK_0554	C 532	10.8	36.0	50	1	AU107144	AU107144 AU107144
C 460	10.8	36.0	41	8	BZ358843	BZ358843 SALK_1333	C 533	10.8	36.0	50	1	AU107148	AU107148 AU107148
C 461	10.8	36.0	41	9	CL256600	CL256600 XP0167 Sa	C 534	10.8	36.0	50	1	AU107149	AU107149 AU107149
C 462	10.8	36.0	42	2	AW059799	AW059799 LE6e02.y9	C 535	10.8	36.0	50	1	AU107150	AU107150 AU107150

C 536	10.8	36.0	50	1	AU107151	AU107151	609	10.6	35.3	42	9	AL756014	Arabidops
C 537	10.8	36.0	50	2	AM459434	sh24c05.y	610	10.6	35.3	42	9	AL756480	Arabidops
C 538	10.8	36.0	50	6	CB275220	ku71c05.y	611	10.6	35.3	42	9	DME547352	Drosophill
C 539	10.8	36.0	50	6	CB858048	NISC_nal12	612	10.6	35.3	43	1	AA902242	Q107f02_s
C 540	10.8	36.0	50	8	AZ666374	1M0548C19	613	10.6	35.3	43	1	BG756501	602715642
C 541	10.8	36.0	50	8	BZ596617	SALK_0928	614	10.6	35.3	43	6	CD533224	30K5_Arab
C 542	10.8	36.0	50	9	CC885693	SALK_1477	615	10.6	35.3	43	8	AZ45872	2M0080L14
C 543	10.8	36.0	50	9	CG869478	XP0161.Sa	616	10.6	35.3	43	8	AZ809933	2M0074K07
C 544	10.8	36.0	50	9	CG869480	XP0168.Sa	617	10.6	35.3	43	8	AG026111	Homo_sapi
C 545	10.6	35.3	21	4	BM398975	5009-0-51	618	10.6	35.3	44	2	BE294167	601172934
C 546	10.6	35.3	21	8	AZ820318	2M0092L19	619	10.6	35.3	44	7	H94616	Vw56e06.sl
C 547	10.6	35.3	21	9	TA37H07P	AL453065	620	10.6	35.3	45	4	BM392671	50071-2-1
C 548	10.6	35.3	24	6	CD530829	08C09_Ara	621	10.6	35.3	45	4	BM392671	50071-2-1
C 549	10.6	35.3	25	1	AB57V062	BZ76062	622	10.6	35.3	45	6	CA794943	Cac_BL_19
C 550	10.6	35.3	25	8	BZ766895	SALK_1380	623	10.6	35.3	45	7	T17578	mps_v8_The
C 551	10.6	35.3	26	8	AZ792942	2M0045N21	624	10.6	35.3	45	8	BH633389	SALK_0462
C 552	10.6	35.3	26	8	CC455971	SALK_0912	625	10.6	35.3	45	8	BH748760	SALK_0466
C 553	10.6	35.3	27	8	BZ358060	SALK_1318	626	10.6	35.3	46	1	A1973945	sd14a09.y
C 554	10.6	35.3	27	8	BZ358396	SALK_1324	627	10.6	35.3	46	8	AZ434072	1M0220K13
C 555	10.6	35.3	28	7	W11835	mb20h01.r1	628	10.6	35.3	46	8	CC031287	3591_1_12
C 556	10.6	35.3	30	8	AZ969026	2M0241E12	629	10.6	35.3	46	9	CC887026	SALK_1493
C 557	10.6	35.3	30	8	CC455639	SALK_0851	630	10.6	35.3	46	9	CG778195	CG778195_1123026G0
C 558	10.6	35.3	30	9	AG192903	Pan_Trogl	631	10.6	35.3	47	1	AJ669335	AJ669335
C 559	10.6	35.3	31	1	AI097991	V982d09.r	632	10.6	35.3	47	2	B534847	601231985
C 560	10.6	35.3	31	1	AI174157	vz84e01.r	633	10.6	35.3	47	2	B534847	601231985
C 561	10.6	35.3	31	9	TA131A06P	AL464159.T_brucei	634	10.6	35.3	47	8	AZ760561	1M0554G23
C 562	10.6	35.3	32	2	BF568357	BF568357_602184546	635	10.6	35.3	47	8	AZ822668	2M0096B09
C 563	10.6	35.3	33	6	CO1097	CO1097_HUMGS000775	636	10.6	35.3	47	8	AZ828520	2M0105J05
C 564	10.6	35.3	33	8	AZ479535	1M0300B16	637	10.6	35.3	47	8	AZ835122	2M0129M08
C 565	10.6	35.3	33	8	AZ513143	1M0359E08	638	10.6	35.3	47	8	BZ385300	SALK_1370
C 566	10.6	35.3	33	8	TA1514085	AL473267.T_brucei	639	10.6	35.3	47	9	AG189368	Pan_Trogl
C 567	10.6	35.3	33	9	TA154808Q	AL497413.T_brucei	640	10.6	35.3	48	1	AV969497	AV969497
C 568	10.6	35.3	33	9	CT339610P	CT339610P	641	10.6	35.3	48	8	AZ320508	1M0040A07
C 569	10.6	35.3	33	9	CT97625	CT97625	642	10.6	35.3	48	8	AZ576656	AST-T14C0
C 570	10.6	35.3	34	1	AI721161	as73h12.x	643	10.6	35.3	48	8	AZ801292	2M0059M10
C 571	10.6	35.3	34	2	BE277165	601178504	644	10.6	35.3	48	8	BZ290571	SALK_0901
C 572	10.6	35.3	34	7	R84653	yo38c05.r1	645	10.6	35.3	49	1	AI147249	qb36908.x
C 573	10.6	35.3	34	8	BZ356400	SALK_1289	646	10.6	35.3	49	1	AI160561	qc87406.x
C 574	10.6	35.3	35	2	BE867678	601443224	647	10.6	35.3	49	1	AI1709135	as62901.x
C 575	10.6	35.3	35	8	AZ579575	1M0367M07	648	10.6	35.3	49	1	AI814770	wk65608.x
C 576	10.6	35.3	35	9	CC888512	SALK_1519	649	10.6	35.3	49	8	AZ605742	1M0427E13
C 577	10.6	35.3	36	1	AJ746775	AJ746775	650	10.6	35.3	49	8	AZ872239	2M0185C03
C 578	10.6	35.3	36	2	AW063331	TN0242_KR	651	10.6	35.3	49	9	CG869945	X50950_Sa
C 579	10.6	35.3	36	8	BZ381466	SALK_1167	652	10.6	35.3	49	9	CL307742	02S0135-1
C 580	10.6	35.3	36	9	TA126A03P	AL463811.T_brucei	653	10.6	35.3	50	1	AU103158	AU103158
C 581	10.6	35.3	37	6	CF297401	30DGS--08	654	10.6	35.3	50	1	AU103159	AU103159
C 582	10.6	35.3	37	8	AZ308362	1M0011F16	655	10.6	35.3	50	1	AU103614	AU103614
C 583	10.6	35.3	37	8	AZ832421	2M0112N13	656	10.6	35.3	50	1	AU104307	AU104307
C 584	10.6	35.3	38	1	AL637555	AL637555	657	10.6	35.3	50	1	AU104308	AU104308
C 585	10.6	35.3	38	7	D19136	MUSGS01352	658	10.6	35.3	50	1	AU104310	AU104310
C 586	10.6	35.3	38	8	AZ312598	1M028H06	659	10.6	35.3	50	1	AU104311	AU104311
C 587	10.6	35.3	38	8	AZ439902	2M0230C13	660	10.6	35.3	50	1	AU104549	AU104549
C 588	10.6	35.3	38	8	AZ806846	2M0069K10	661	10.6	35.3	50	1	AU105856	AU105856
C 589	10.6	35.3	38	8	BH751791	SALK_0506	662	10.6	35.3	50	1	AU106467	AU106467
C 590	10.6	35.3	39	4	BJ051176	BJ051176	663	10.6	35.3	50	1	AU106551	AU106551
C 591	10.6	35.3	39	8	AZ309582	1M0016K11	664	10.6	35.3	50	1	AU106554	AU106554
C 592	10.6	35.3	39	8	AZ856438	2M0160B23	665	10.6	35.3	50	1	AU106723	AU106723
C 593	10.6	35.3	39	8	BH847395	SALK_0531	666	10.6	35.3	50	1	AU107199	AU107199
C 594	10.6	35.3	39	8	BZ665246	SALK_1109	667	10.6	35.3	50	4	EG409021	gb85f04.y
C 595	10.6	35.3	39	9	CC800300	02S0088-0	668	10.6	35.3	50	5	BX629197	BX629197
C 596	10.6	35.3	39	9	CL685477	PR10141b	669	10.6	35.3	50	7	CO578886	ta159f10
C 597	10.6	35.3	40	1	AI692266	AI692266	670	10.6	35.3	50	8	AZ386495	ew02h09.x
C 598	10.6	35.3	40	1	AA589938	wc83d01.x	671	10.6	35.3	50	8	AZ756885	1M045E01
C 599	10.6	35.3	40	8	AZ458268	1M0262N11	672	10.6	35.3	50	8	AZ852818	2M0155K12
C 600	10.6	35.3	40	8	BH251215	SALK_0112	673	10.6	35.3	50	8	BH748752	SALK_0466
C 601	10.6	35.3	40	8	BZ768127	SALK_1398	674	10.6	35.3	50	9	CR207109	Forward s
C 602	10.6	35.3	41	6	CAB851520	D14F06_L0	675	10.6	35.3	50	9	CR230363	Reverse s
C 603	10.6	35.3	41	8	AZ630326	1M0483L11	676	10.6	35.3	50	9	AG211154	Oryza sat
C 604	10.6	35.3	41	8	BH802422	1008026B0	677	10.6	34.7	19	8	AZ991531	2M0275K15
C 605	10.6	35.3	42	1	AV839107	AV839107	678	10.4	34.7	22	1	AJ806746	AJ806746
C 606	10.6	35.3	42	8	AZ628072	1M0480A05	679	10.4	34.7	24	4	BM397115	5009-0-29
C 607	10.6	35.3	42	8	AZ645652	1M0511P07	680	10.4	34.7	24	4	BM399801	5009-0-61
C 608	10.6	35.3	42	8	BH752131	SALK_0518	681	10.4	34.7	24	9	CL694812	PR10165a

682	10.4	34.7	25	4	BM400178	5009-0-68	BM400178	5009-0-68	10.4	34.7	43	1	AA134736
683	10.4	34.7	25	8	AZ817392	2M0086E08	AZ817392	2M0086E08	10.4	34.7	43	1	AV955378
684	10.4	34.7	26	4	BM397261	5009-0-30	BM397261	5009-0-30	10.4	34.7	43	4	BM397324
685	10.4	34.7	27	5	EX565326	EX565326	EX565326	EX565326	10.4	34.7	43	6	CA969020
686	10.4	34.7	27	8	AZ433910	1M0220H06	AZ433910	1M0220H06	10.4	34.7	43	7	R73866
687	10.4	34.7	27	8	AZ599857	1M0416K19	AZ599857	1M0416K19	10.4	34.7	43	7	W60657
688	10.4	34.7	27	8	AZ623078	1M0460G19	AZ623078	1M0460G19	10.4	34.7	43	8	AZ320464
689	10.4	34.7	27	9	CL680176	PR10128A	CL680176	PR10128A	10.4	34.7	43	8	AZ320464
690	10.4	34.7	28	1	AA994218	cu49405.S	AA994218	cu49405.S	10.4	34.7	43	9	CC799108
691	10.4	34.7	28	2	AW250231	2822603.3	AW250231	2822603.3	10.4	34.7	43	9	CC894144
692	10.4	34.7	28	8	BZ592883	SALK_0476	BZ592883	SALK_0476	10.4	34.7	43	9	AG264217
693	10.4	34.7	31	6	CD028820	mgmy006XA	CD028820	mgmy006XA	10.4	34.7	44	6	CA794547
694	10.4	34.7	31	7	H04593	H04593 YJ49C03.S1	H04593	YJ49C03.S1	10.4	34.7	44	6	CA794547
695	10.4	34.7	32	8	AZ317543	1M0036F11	AZ317543	1M0036F11	10.4	34.7	44	6	CA794547
696	10.4	34.7	32	8	AJ598209	Arabidops	AJ598209	Arabidops	10.4	34.7	44	8	AZ590450
697	10.4	34.7	33	4	BM392440	50071-2-1	BM392440	50071-2-1	10.4	34.7	44	8	AZ590450
698	10.4	34.7	33	4	BM393652	50072-2-1	BM393652	50072-2-1	10.4	34.7	44	8	AZ804224
699	10.4	34.7	33	8	AZ834737	2M0117O06	AZ834737	2M0117O06	10.4	34.7	44	8	AZ804224
700	10.4	34.7	33	9	AL769444	Arabidops	AL769444	Arabidops	10.4	34.7	45	8	BH855546
701	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	45	8	BH855546
702	10.4	34.7	34	1	AU254211	AU254211	AU254211	AU254211	10.4	34.7	45	8	AQ025518
703	10.4	34.7	34	1	AU255089	AU255089	AU255089	AU255089	10.4	34.7	45	8	EP(X)1587
704	10.4	34.7	34	1	AZ807690	2M0070N09	AZ807690	2M0070N09	10.4	34.7	45	8	EP(X)1587
705	10.4	34.7	34	8	BZ287163	SALK_0205	BZ287163	SALK_0205	10.4	34.7	45	8	EP(X)1587
706	10.4	34.7	35	1	AU260296	AU260296	AU260296	AU260296	10.4	34.7	45	8	EP(X)1587
707	10.4	34.7	35	8	BZ380078	SALK_1145	BZ380078	SALK_1145	10.4	34.7	45	8	EP(X)1587
708	10.4	34.7	35	9	EX656919	Arabidops	EX656919	Arabidops	10.4	34.7	45	8	EP(X)1587
709	10.4	34.7	35	9	EX906212	Leishmani	EX906212	Leishmani	10.4	34.7	45	8	EP(X)1587
710	10.4	34.7	35	9	LBAF020G09	LBAF020G09	LBAF020G09	LBAF020G09	10.4	34.7	45	8	EP(X)1587
711	10.4	34.7	35	9	TAL127A02P	TAL127A02P	TAL127A02P	TAL127A02P	10.4	34.7	45	8	EP(X)1587
712	10.4	34.7	36	7	N50146	YJ12F02.S1	N50146	YJ12F02.S1	10.4	34.7	45	8	EP(X)1587
713	10.4	34.7	36	8	AZ316533	1M0034A13	AZ316533	1M0034A13	10.4	34.7	45	8	EP(X)1587
714	10.4	34.7	36	8	AZ810652	2M0076N17	AZ810652	2M0076N17	10.4	34.7	45	8	EP(X)1587
715	10.4	34.7	36	8	BH813986	SALK_0655	BH813986	SALK_0655	10.4	34.7	45	8	EP(X)1587
716	10.4	34.7	36	9	AL756094	Arabidops	AL756094	Arabidops	10.4	34.7	45	8	EP(X)1587
717	10.4	34.7	36	9	CL528565	ASV20E10.	CL528565	ASV20E10.	10.4	34.7	45	8	EP(X)1587
718	10.4	34.7	36	9	AG198637	Pan trogl	AG198637	Pan trogl	10.4	34.7	45	8	EP(X)1587
719	10.4	34.7	36	9	AI118892	uc15d07.r	AI118892	uc15d07.r	10.4	34.7	45	8	EP(X)1587
720	10.4	34.7	37	1	AA233522	zr30b02.r	AA233522	zr30b02.r	10.4	34.7	45	8	EP(X)1587
721	10.4	34.7	37	1	AZ333194	1M0062F12	AZ333194	1M0062F12	10.4	34.7	45	8	EP(X)1587
722	10.4	34.7	37	8	AL953020	Arabidops	AL953020	Arabidops	10.4	34.7	45	8	EP(X)1587
723	10.4	34.7	37	9	TA26H05Q	TA26H05Q	TA26H05Q	TA26H05Q	10.4	34.7	45	8	EP(X)1587
724	10.4	34.7	37	9	CL423546	01S0557-0	CL423546	01S0557-0	10.4	34.7	45	8	EP(X)1587
725	10.4	34.7	37	9	AZ769363	1M0569N20	AZ769363	1M0569N20	10.4	34.7	45	8	EP(X)1587
726	10.4	34.7	38	8	CG723684	1119077F0	CG723684	1119077F0	10.4	34.7	45	8	EP(X)1587
727	10.4	34.7	38	9	CG723684	1119077F0	CG723684	1119077F0	10.4	34.7	45	8	EP(X)1587
728	10.4	34.7	39	2	BF025819	601670253	BF025819	601670253	10.4	34.7	45	8	EP(X)1587
729	10.4	34.7	39	6	CA899378	PCEP03168	CA899378	PCEP03168	10.4	34.7	45	8	EP(X)1587
730	10.4	34.7	39	8	BH862154	SALK_0888	BH862154	SALK_0888	10.4	34.7	45	8	EP(X)1587
731	10.4	34.7	39	9	AL947170	Arabidops	AL947170	Arabidops	10.4	34.7	45	8	EP(X)1587
732	10.4	34.7	40	1	AB088498	AB088498	AB088498	AB088498	10.4	34.7	45	8	EP(X)1587
733	10.4	34.7	40	1	AI001131	ot-04h09.s	AI001131	ot-04h09.s	10.4	34.7	45	8	EP(X)1587
734	10.4	34.7	40	1	AJ789396	AJ789396	AJ789396	AJ789396	10.4	34.7	45	8	EP(X)1587
735	10.4	34.7	40	1	H95706	YJ95910.S1	H95706	YJ95910.S1	10.4	34.7	45	8	EP(X)1587
736	10.4	34.7	40	8	AQ073776	EP(3)3140	AQ073776	EP(3)3140	10.4	34.7	45	8	EP(X)1587
737	10.4	34.7	40	8	BZ762552	SALK_1053	BZ762552	SALK_1053	10.4	34.7	45	8	EP(X)1587
738	10.4	34.7	40	9	CC882924	02S0111-0	CC882924	02S0111-0	10.4	34.7	45	8	EP(X)1587
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740	10.4	34.7	41	2	AW248446	2820480.3	AW248446	2820480.3	10.4	34.7	45	8	EP(X)1587
741	10.4	34.7	41	2	D19129	MUGS01345	D19129	MUGS01345	10.4	34.7	45	8	EP(X)1587
742	10.4	34.7	41	8	AZ768121	1M0567N20	AZ768121	1M0567N20	10.4	34.7	45	8	EP(X)1587
743	10.4	34.7	41	8	BH852066	SALK_0741	BH852066	SALK_0741	10.4	34.7	45	8	EP(X)1587
744	10.4	34.7	41	8	BZ292530	SALK_1243	BZ292530	SALK_1243	10.4	34.7	45	8	EP(X)1587
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746	10.4	34.7	41	9	CG793034	SALK_0064	CG793034	SALK_0064	10.4	34.7	45	8	EP(X)1587
747	10.4	34.7	41	9	AG216170	Drosophila	AG216170	Drosophila	10.4	34.7	45	8	EP(X)1587
748	10.4	34.7	42	5	EX561080	EX561080	EX561080	EX561080	10.4	34.7	45	8	EP(X)1587
749	10.4	34.7	42	6	CF314464	HD--02-P2	CF314464	HD--02-P2	10.4	34.7	45	8	EP(X)1587
750	10.4	34.7	42	8	AZ315275	1M0032M19	AZ315275	1M0032M19	10.4	34.7	45	8	EP(X)1587
751	10.4	34.7	42	8	AZ489017	1M0319006	AZ489017	1M0319006	10.4	34.7	45	8	EP(X)1587
752	10.4	34.7	42	8	AZ615918	1M0445C02	AZ615918	1M0445C02	10.4	34.7	45	8	EP(X)1587
753	10.4	34.7	43	1	AA744543	ny79C03.S	AA744543	ny79C03.S	10.4	34.7	45	8	EP(X)1587
754	10.4	34.7	43	1	AA976535	Oq40d09.S	AA976535	Oq40d09.S	10.4	34.7	45	8	EP(X)1587

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C 830	10.4	34.7	50	7	CK584111	IST WIS 1	CK584111	C 903	10.2	34.0	37	2	BF792074	BF792074
C 831	10.4	34.7	50	8	AQ025065	EP(3) 0339	AQ025065	C 904	10.2	34.0	37	4	BG035903	BG035903
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C 834	10.4	34.7	50	8	AQ025065	EP(3) 0339	AQ025065	C 907	10.2	34.0	37	8	AQ025065	AQ025065
C 835	10.4	34.7	50	9	BX286949	ArabiDops	BX286949	C 908	10.2	34.0	37	8	AQ025065	AQ025065
C 836	10.4	34.7	50	9	BX286949	ArabiDops	BX286949	C 909	10.2	34.0	37	8	AQ025065	AQ025065
C 837	10.4	34.7	50	9	CR105282	Forward s	CR105282	C 910	10.2	34.0	38	8	AQ025065	AQ025065
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C 839	10.2	34.0	16	1	AI154875	u80f04.r	AI154875	C 912	10.2	34.0	38	8	AQ025065	AQ025065
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C 842	10.2	34.0	24	8	BZ767824	IM0567K22	BZ767824	C 915	10.2	34.0	39	4	BQ063882	BQ063882
C 843	10.2	34.0	24	8	BZ767824	IM0567K22	BZ767824	C 916	10.2	34.0	39	8	AQ025356	EP(X) 0773
C 844	10.2	34.0	24	8	BZ767824	IM0567K22	BZ767824	C 917	10.2	34.0	39	8	AQ025356	EP(X) 0773
C 845	10.2	34.0	25	8	BZ767824	IM0567K22	BZ767824	C 918	10.2	34.0	39	9	BX291484	ArabiDops
C 846	10.2	34.0	25	8	BZ767824	IM0567K22	BZ767824	C 919	10.2	34.0	39	9	BX291484	ArabiDops
C 847	10.2	34.0	25	9	AG190823	AG190823	AG190823	C 920	10.2	34.0	39	9	BX291484	ArabiDops
C 848	10.2	34.0	26	8	AZ345919	IM0080122	AZ345919	C 921	10.2	34.0	40	1	AA887375	QJ53908.x
C 849	10.2	34.0	27	8	AZ345919	IM0080122	AZ345919	C 922	10.2	34.0	40	1	AA887375	QJ53908.x
C 850	10.2	34.0	27	8	AZ345919	IM0080122	AZ345919	C 923	10.2	34.0	40	8	AQ025356	EP(X) 0773
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C 859	10.2	34.0	28	8	BZ595211	SALK 0863	BZ595211	C 932	10.2	34.0	42	6	CA966788	CLX06a23
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C 861	10.2	34.0	28	8	BZ595211	SALK 0863	BZ595211	C 934	10.2	34.0	42	6	CA966788	CLX06a23
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C 863	10.2	34.0	28	8	BZ595211	SALK 0863	BZ595211	C 936	10.2	34.0	42	8	AQ025356	EP(X) 0773
C 864	10.2	34.0	29	8	BZ767739	SALK_1392	BZ767739	C 937	10.2	34.0	42	8	AQ025356	EP(X) 0773
C 865	10.2	34.0	29	8	BZ767739	SALK_1392	BZ767739	C 938	10.2	34.0	42	8	AQ025356	EP(X) 0773
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C 867	10.2	34.0	31	1	AI037963	ox53d09.x	AI037963	C 940	10.2	34.0	42	9	BX127928	Danio rer
C 868	10.2	34.0	31	1	AI037963	ox53d09.x	AI037963	C 941	10.2	34.0	42	9	BX127928	Danio rer
C 869	10.2	34.0	31	1	AI037963	ox53d09.x	AI037963	C 942	10.2	34.0	42	9	BX127928	Danio rer
C 870	10.2	34.0	31	1	AI037963	ox53d09.x	AI037963	C 943	10.2	34.0	43	1	AV962413	AV962413
C 871	10.2	34.0	31	1	AI037963	ox53d09.x	AI037963	C 944	10.2	34.0	43	1	AV962413	AV962413
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C 873	10.2	34.0	31	8	AZ625223	IM0271105	AZ625223	C 946	10.2	34.0	43	1	AA569427	nF22407.s
C 874	10.2	34.0	31	8	AZ625223	IM0271105	AZ625223	C 947	10.2	34.0	43	8	BZ380206	SALK_1147
C 875	10.2	34.0	31	8	AZ625223	IM0271105	AZ625223	C 948	10.2	34.0	43	9	AJ591396	ArabiDops
C 876	10.2	34.0	31	8	AZ625223	IM0271105	AZ625223	C 949	10.2	34.0	43	9	AJ591396	ArabiDops
C 877	10.2	34.0	31	9	CC887820	SALK_1508	CC887820	C 950	10.2	34.0	43	9	AG220919	Lotus cor
C 878	10.2	34.0	32	7	H63110	yr48b03.s1	H63110	C 951	10.2	34.0	44	9	AL753874	ArabiDops
C 879	10.2	34.0	32	8	AZ490918	IM0324M09	AZ490918	C 952	10.2	34.0	44	9	AL753874	ArabiDops
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C 881	10.2	34.0	32	8	AZ490918	IM0324M09	AZ490918	C 954	10.2	34.0	44	9	AL753874	ArabiDops
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C 883	10.2	34.0	32	8	AZ490918	IM0324M09	AZ490918	C 956	10.2	34.0	45	6	CA966788	CLX06a23
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C 887	10.2	34.0	32	9	CC887822	SALK_1508	CC887822	C 960	10.2	34.0	45	8	AQ025356	EP(X) 0773
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C 889	10.2	34.0	33	8	AZ617294	IM0448E04	AZ617294	C 962	10.2	34.0	45	9	AJ597990	ArabiDops
C 890	10.2	34.0	33	8	AZ617294	IM0448E04	AZ617294	C 963	10.2	34.0	45	9	AJ597990	ArabiDops
C 891	10.2	34.0	33	9	AL770136	ArabiDops	AL770136	C 964	10.2	34.0	45	9	CC886318	SALK_1484
C 892	10.2	34.0	34	1	AA114877	z103b12.r	AA114877	C 965	10.2	34.0	46	1	AA209176	zq65805.s
C 893	10.2	34.0	34	4	BM400034	5009-0-65	BM400034	C 966	10.2	34.0	46	1	AA209176	zq65805.s
C 894	10.2	34.0	34	7	H43178	yo02906.r1	H43178	C 967	10.2	34.0	46	1	AA209176	zq65805.s
C 895	10.2	34.0	34	8	AZ425761	IM0206F03	AZ425761	C 968	10.2	34.0	46	1	AA209176	zq65805.s
C 896	10.2	34.0	35	8	AZ822670	2M0096B11	AZ822670	C 969	10.2	34.0	46	6	CA587290	LBEL10p60
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C 898	10.2	34.0	36	2	BF969721	602272124	BF969721	C 971	10.2	34.0	46	7	CO577181	TVEST067G
C 899	10.2	34.0	36	8	AZ666765	IM0564K02	AZ666765	C 972	10.2	34.0	46	8	AZ666765	IM0564K02
C 900	10.2	34.0	36	9	AL757413	ArabiDops	AL757413	C 973	10.2	34.0	46	8	AZ666765	IM0564K02

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c 984 10.2 34.0 47 9 AJ592846
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c 999 10.2 34.0 49 5 AZ355782
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ALIGNMENTS

RESULT 1
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LOCUS PST3831-NL.Seq MICB1 Mus musculus genomic clone PST3831-NL.Seq,
DEFINITION genomic survey sequence.
ACCESSION CL436787.1 GI:45571935
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
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Query Match 52.0%; Score 15.6; DB 8; Length 42;
Best Local Similarity 81.8%; Pred. No. 6.6e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 GTCCTTGGTCATCTCACCTTCT 30
Db 42 GTCGCTCGTCATCTCGCTTCT 21

RESULT 3
AU106879 50 bp mRNA linear EST 28-JAN-2004
LOCUS AU106879 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION LNG00759, mRNA sequence.
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ORIGIN
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Best Local Similarity 79.2%; Pred. No. 4.4e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy 7 CAGTCCTTGGTCATCTCACCTTCT 30
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RESULT 2
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LOCUS SAUK_096301 Arabidopsis thaliana TDNA insertion lines Arabidopsis
DEFINITION thaliana genomic clone SAUK_096301, genomic survey sequence.
ACCESSION BH864588
VERSION
KEYWORDS
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 42)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J., and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL Arabidopsis Genome
COMMENT Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At5g64960.
Class: TDNA tagged.
Location/Qualifiers
1..42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotye="Col-0"
/db_xref="taxon:3702"
/clone="SAUK_096301"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

FEATURES
source
1..42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotye="Col-0"
/db_xref="taxon:3702"
/clone="SAUK_096301"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

ORIGIN
Query Match 52.0%; Score 15.6; DB 8; Length 42;
Best Local Similarity 81.8%; Pred. No. 6.6e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 GTCCTTGGTCATCTCACCTTCT 30
Db 42 GTCGCTCGTCATCTCGCTTCT 21

RESULT 3
AU106879 50 bp mRNA linear EST 28-JAN-2004
LOCUS AU106879 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION LNG00759, mRNA sequence.
```



```

ACCESSION   AU106879
VERSION     AU106879.1  GI:13556400
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE       Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL     EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE     21270072
PUBMED      11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and Characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).

FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match       49.3%; Score 14.8; DB 1; Length 50;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 5 CTCAGCTCTTGTCATCTCACCTTCT 30
    ||||| ||| ||||| |||||
Db 19 CTCAGCTCAGCGCAACCTCACCTTCT 44

RESULT 4
CL212954
LOCUS       CL212954
DEFINITION G028G03 GGTC Gene Trap Library GV07C05 Mus musculus cDNA clone
ACCESSION   G028G03
VERSION     G028G03
KEYWORDS    mRNA sequence.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 41)
AUTHORS     Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F.,
            Arnold,H.H., Schnutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.
TITLE       A large-scale, gene-driven mutagenesis approach for the functional
            analysis of the mouse genome
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
MEDLINE     22810117
PUBMED      12904583
COMMENT     On Jun 30, 2004 this sequence version replaced gi:40729855.
            Contact: GGTC
            German Genetrap Consortium (GGTC)
            Email: info@genetrap.de
            U3C80 gene trap. Sequence tag generated by 5'RACE. Additional
            sequence information can be found at:
            'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
            clone_id=G028G03'. ES cell line harboring insertion mutation of
            target gene is available at:
            'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm

1' Inhouse Sequence Identifier: 15667
Class: Gene trap.
Location/Qualifiers
     source           1..41
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 Sv"
                     /db_xref="taxon:10090"
                     /clone="G028G03"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"
                     /clone_lib="GGTC Gene Trap Library GV07C05"
                     /note="Vector: U3CEO"

ORIGIN
Query Match       47.3%; Score 14.2; DB 9; Length 41;
Best Local Similarity 70.4%; Pred. No. 2.5e+05;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4 ACTCAGTCTTGTCATCTCACCTTCT 30
    ||||| ||||| ||||| |||||
Db 8 ACTTAGTCGTTGCTCGTCTAGTCTTGT 34

RESULT 5
BE970036/c
LOCUS       BE970036
DEFINITION 601680150F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3950172 5',
            mRNA sequence.
ACCESSION   BE970036
VERSION     BE970036.1  GI:10582969
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 49)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
TITLE       Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LICM816 row: d column: 13
            High quality sequence stop: 49.
            Location/Qualifiers
     source           1..49
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3950172"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_78"
                     /note="Organ: pancreas; Vector: pDNR-LIB (Clontech);
            Site 1: Sfil (ggcgctcgcc); Site 2: Sfil
            (ggccattggcc); 5' and 3' adaptors were used in cloning
            as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3'
            and 3' adaptor sequence:
            5'-ATTCTAGAGCGCGCGCCGACATG-dT(30)BN-3' (where B = A,
            C, or G and N = A, C, G, or T). Average insert size 1.2
            kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
            by PCR. This library was enriched for full-length clones
            and was constructed by Clontech Laboratories (Palo Alto,
            CA)."

ORIGIN

```

Query Match 47.3%; Score 14.2; DB 2; Length 49;
 Best Local Similarity 70.4%; Pred. No. 2.6e+05;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 GGACTCAGTCCTTGGTCATCTCACCTT 28
 ||||| ||||| ||||| ||||| |||||
 Db 30 GGATTCGTCTCTGGTACACTCACTT 4

RESULT 6
 BX531144/c 49 bp DNA linear GSS 04-APR-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-472D08-019879,
 Genomic survey sequence.
 DEFINITION
 BX531144
 VERSION BX531144.1 GI:31408274
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
 Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana
 Bioinformatics 19 (11), 1441-1442 (2003)
 JOURNAL
 MEDLINE 22755829
 PUBMED 12874060

REFERENCE 2
 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
 Weisshaar, B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 flanking sequence tag-based reverse Genetics
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 JOURNAL
 MEDLINE 23117147
 PUBMED 14756321

REFERENCE 3
 Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
 Weisshaar, B.
 High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 BioTechniques 35 (6), 1164-1168 (2003)
 JOURNAL
 PUBMED 14582050

REFERENCE 4
 (bases 1 to 49)
 Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
 Direct Submission
 Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion close to or within gene At3g60040.
 Details on the protocols used for generation of the sequence are
 described in References 1-3. The sequences are generated at the MPI
 for Plant Breeding Research in the context of the GABI-Kat project.
 GABI-Kat is part of the German Plant Genomics program designated
 'GABI'. Information on line availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
 Location/Qualifiers
 1..49
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-472D08-019879"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector pAC161 (GenBank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.

ORIGIN
 Query Match 47.3%; Score 14.2; DB 9; Length 49;
 Best Local Similarity 84.2%; Pred. No. 2.6e+05;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 CTTGGTCATCTCACCTTCT 30
 ||||| ||||| ||||| ||||| |||||
 Db 24 CTTGGTCATCTCACCTTCT 6

RESULT 7
 AUI05600/c 50 bp mRNA linear EST 28-JAN-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence.
 DEFINITION
 AUI05600
 VERSION AUI05600.1 GI:13555121
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 JOURNAL
 MEDLINE 21270072
 PUBMED 11375929

COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES
 Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="ADSH01468"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
 Query Match 47.3%; Score 14.2; DB 1; Length 50;
 Best Local Similarity 70.4%; Pred. No. 2.6e+05;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 GGACTCAGTCCTTGGTCATCTCACCTT 28
 ||||| ||||| ||||| ||||| |||||
 Db 44 GGTTCGTCTCTCTGGTACACTCACTT 18

RESULT 8
 AJ622668 42 bp DNA linear GSS 28-JAN-2004
 LOCUS Drosophila melanogaster flanking sequence of RS P element insertion
 DEFINITION P[RS]CB-6697-3, clone library P[RS3], genomic survey sequence.
 VERSION AJ622668
 KEYWORDS GSS; genome survey sequence.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

ORIGIN						ORIGIN					
	Query Match	45.3%;	Score 13.6;	DB 1;	Length 34;		Query Match	45.3%;	Score 13.6;	DB 8;	Length 41;
	Best Local Similarity	67.9%;	Pred. No. 4.4e+05;				Best Local Similarity	80.0%;	Pred. No. 4.5e+05;		
	Matches 19;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;		Matches 16;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	2	GGACTCAGTCCTTGGTCATCTCACCTTC	29			Qy	8	AGTCCTTGTCATCTCACT	27		
Dd	33	GGACTCAGTCATGTTGCACACAGCCATC	6			Dd	21	AGTCCTGGTCAGCACCCCT	40		

Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES
source
ORIGIN
Query Match
Best Local Similarity
Matches
QY
Db
RESULT 16
AUI07622
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES
source
ORIGIN
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Best Local Similarity
Matches
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Db
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES
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ORIGIN
Query Match
Best Local Similarity
Matches
QY
Db
RESULT 18
BG260157
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

50 bp mRNA linear EST 28-JAN-2004
Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
mRNA sequence.
GI:13557144
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COLP4230"
/clone_lib="Sugano Homo sapiens cDNA library"
44.7%; Score 13.4; DB 1; Length 50;
73.9%; Pred. No. 5.5e+05;
0; Mismatches 6; Indels 0; Gaps 0;
3 GACTCAGTCCTTGGTCATCTCAC 25
|||||
14 GCCTGACTGCTTGGTCGTCAC 36
50 bp mRNA linear EST 28-JAN-2004
Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
mRNA sequence.
GI:13557143
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC12232"
/clone_lib="Sugano Homo sapiens cDNA library"
44.7%; Score 13.4; DB 1; Length 50;
73.9%; Pred. No. 5.5e+05;
0; Mismatches 6; Indels 0; Gaps 0;
3 GACTCAGTCCTTGGTCATCTCAC 25
|||||
17 GCCTGACTGCTTGGTCGTCAC 39
37 bp mRNA linear EST 13-FEB-2001
Homo sapiens cDNA clone IMAGE:4479254 5',
mRNA sequence.
GI:12769973
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10311 row: a column: 15
High quality sequence stop: 37.

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FEATURES
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        /db_xref="taxon:9606"
        /clone="IMAGE:4479254"
        /tissue_type="transitional cell papilloma, cell line"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH MGC 93"
        /note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: Not I; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
ORIGIN
  Query Match      44.0%; Score 13.2; DB 4; Length 37;
  Best Local Similarity 83.3%; Pred. No. 6.5e+05;
  Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCTTGCTC 18
    ||| ||| ||| ||| |||
Db 30 TGGTCACAGTCTTGCTC 13

RESULT 19
AUI02328
LOCUS
DEFINITION
  AUI02328 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
  KAT06002, mRNA sequence.
ACCESSION
  AUI02328
VERSION
  AUI02328.1 GI:13551848
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 50)
  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
  Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
  Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  Diverse transcriptional initiation revealed by fine, large-scale
  mapping of mRNA start sites
  EMBO Rep. 2 (5), 388-393 (2001)
  21270072
  11375929
  Contact: Yutaka Suzuki
  Department of Virology
  Institute of Medical Science, University of Tokyo
  4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
  Email: ysuzuki@ims.u-tokyo.ac.jp
  Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
  Sugano,S. Construction and characterization of a full
  length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
  143-156 (1997).
FEATURES
  source
    Location/Qualifiers
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="KAT06002"
        /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
  Query Match      44.0%; Score 13.2; DB 1; Length 50;
  Best Local Similarity 69.2%; Pred. No. 6.7e+05;
  Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 5 CTCAGTCTTGCTCATCTCCTTCT 30
    ||| ||| ||| ||| |||
Db 5 CTCGGTCCCGGCCCATCTCAGCGGCT 30

```

```

RESULT 20
H26079/c
LOCUS
DEFINITION
  H26079 Soares breast 3NbHst Homo sapiens cDNA clone
  IMAGE:162259 5' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION
  (HUMAN);, mRNA sequence.
ACCESSION
  H26079
VERSION
  H26079.1 GI:895202
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 28)
  Hillier,L., Clark,N., Dubuque,T., Eliston,K., Hawkins,M.,
  Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
  Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
  Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
  Wilson,R.
  The WashU-Merck EST Project
  Unpublished (1995)
  Contact: Wilson RK
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  Insert Size: 663
  High quality sequence starts: 1
  High quality sequence stops: 1
  Source: IMAGE Consortium, LLNL
  This clone is available royalty-free through LLNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Trace considered overall poor quality
  Insert Length: 663 Std Error: 0.00
  Seq primer: M13Rev
  High quality sequence stop: 1.
FEATURES
  source
    Location/Qualifiers
      1..28
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="GDB:576499"
        /db_xref="taxon:9606"
        /clone="IMAGE:162259"
        /sex="Female"
        /dev_stage="adult"
        /lab_host="DH10B (ampicillin resistant)"
        /clone_lib="Soares breast 3NbHst"
        /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
        modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
        strand cDNA was primed with a Not I - oligo(dT) primer [5',
        TGTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'],
        double-stranded cDNA was ligated to Eco RI adaptors
        (Pharmacia), digested with Not I and cloned into the Not I
        and Eco RI sites of a modified pT7T3 vector (Pharmacia).
        Library went through one round of normalization to a Cot =
        20. Library constructed by Bento Soares and M.Fatima
        Bonaldo."
ORIGIN
  Query Match      43.3%; Score 13; DB 7; Length 28;
  Best Local Similarity 76.2%; Pred. No. 7.6e+05;
  Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GACTCAGTCTTGTCATCTC 23
    ||| ||| ||| ||| |||
Db 21 GACCTGGTCTTGTCATCTC 1

RESULT 21
CC795628
LOCUS
DEFINITION
  CC795628 SALK_087613.35.10.x Arabidopsis thaliana TDNA insertion lines
  28 bp DNA linear GSS 01-JUL-2003

```

Arabidopsis thaliana genomic clone SALK_087613.35.10.x, genomic survey sequence.
 CC795628
 CC795628.1 GI:32390851
 GSS.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 28)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,U. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1. .28
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_087613.35.10.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
 Query Match 43.3%; Score 13; DB 9; Length 28;
 Best Local Similarity 76.2%; Pred. No. 7.6e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 10 TCCTTGGTCATCTCACCTTCT 30
 | | | | | | | | | | | | | | | | | | | |
 Db 2 TACTTGGTCATCTTAGATTCT 22

RESULT 22
 AZ309567/c
 LOCUS
 DEFINITION
 clone UUGC1M0016F07 F, genomic survey sequence.
 ACCESSION
 AZ309567
 VERSION
 AZ309567.1 GI:10350865
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 47)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source
 1. .47
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0016F07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource.
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match 43.3%; Score 13; DB 8; Length 47;
 Best Local Similarity 76.2%; Pred. No. 8.1e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 6 TCAGTCCTTGGTCATCTCACCC 26
 | | | | | | | | | | | | | | | | | | | |
 Db 21 TCAGTCCTTGGTCATCTCCAGC 1

RESULT 23
 A1746816
 LOCUS
 DEFINITION
 ul07g07.y1 Sugano mouse kidney mKia Mus musculus cDNA clone IMAGE:2065404 5' similar to WP:ZK721.1 CE05105 ; mRNA sequence.
 ACCESSION
 A1746816
 VERSION
 A1746816.1 GI:5125080
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 49)
 Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0016 row: F column: 07
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 47.
 Location/Qualifiers
 1. .47

FEATURES

source

Insert Length: 10000 Std Error: 0.00
 Plate: 0542 row: G column: 06
 Seq primer: CTTGTAAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers

FEATURES

source

1. .24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0542G06"
 /sex="Male"
 /lab_host="F. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PW42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.7%; Score 12.8; DB 8; Length 24;
 Best Local Similarity 70.8%; Pred. No. 9e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 7 CAGTCCTGTGTCATCTCACCTTCT 30
 ||||| ||||| ||||| |||||
 Db 24 CAGTCAGTGGCCATCATGTGTAT 1

RESULT 26

AI582089/c
 LOCUS AI582089 31 bp mRNA linear EST 06-APR-1999
 DEFINITION ar-96c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173456 3' similar to TR:O21792 O21792 CYTOCHROME B ;contains element MSR1 repetitive element ;, mRNA sequence.

ACCESSION AI582089
 VERSION AI582089.1 GI:4567986
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

AUTHORS Hallier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
 WASHU-NCI human EST Project
 Unpublished (1997)

JOURNAL

COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@atson.wustl.edu
 This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1. .31
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2173456"
 /sex="male"
 /dev_stage="adult, age 25"
 /lab_host="DH10B (phage resistant)"
 /clone_lib="Barstead colon HPLRB7"
 /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACGAATCTGAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [5' AATTCAGTAAAT 3' and 5' ATTACTAGT 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."

ORIGIN

Query Match 42.7%; Score 12.8; DB 1; Length 31;
 Best Local Similarity 87.5%; Pred. No. 9.3e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCTCTGG 16
 ||||| ||||| ||||| |||||
 Db 27 TGGGCTCACTCCTTGG 12

RESULT 27

DME545069
 LOCUS DME545069 34 bp DNA linear GSS 24-FEB-2003
 DEFINITION Drosophila melanogaster flanking sequence of RS P element insertion P{RS5}5-HA-1190, clone library P{RS5}, genomic survey sequence.

ACCESSION AJ545069.1 GI:28552745
 VERSION AJ545069
 KEYWORDS GSS; genome survey sequence.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster

REFERENCE

AUTHORS Ryder, E.J., Ashburner, M., Bagunya, J., Blows, F., Bucheton, A., Coulson, D., Dickson, B., Drummond, J., Glover, D., Gunton, N., Hafen, E., Hall, S., Heisenberg, M., Lepesant, J.A., Maroy, P., Mechler, B., O'Kane, C., Pflugfelder, G., Rasnussen-Lestander, A., Reuter, G., Roote, J., Szidonya, J., Wang, S., Webster, J. and Russell, S.
 Mapping of RS P element insertions in Drosophila melanogaster for the DrosDel second generation deficiency kit
 Unpublished
 2 (bases 1 to 34)
 Ryder, E.J.
 Direct Submission

JOURNAL

AUTHORS Ryder, E.J., Department of Genetics, University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM
 TITLE Submitted (17-FEB-2003)
 JOURNAL The insertion point of the P element is before base 1 of the sequence. Further information about this P element insertion line can be found at http://www.flyseq.org.uk and http://www.drosdel.org.uk.
 COMMENT Location/Qualifiers

FEATURES

source

1. .34
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /chromosome="2R"
 /clone="P{RS5}5-HA-1190"

```

misc_feature
1..34
/clone.lib="P{RSS}"
/note="read-5' end"
/note="P element insertion in the 5' to 3' orientation"

ORIGIN
Query Match 42.7%; Score 12.8; DB 9; Length 34;
Best Local Similarity 70.8%; Pred. No. 9.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 7 CAGTCCTTGGTCATCTCACCTTCT 30
Db 8 CATTTCATCAGTCATCTGACTCTCT 31

RESULT 28
H13124/c
LOCUS
DEFINITION
H13124 37 bp mRNA linear EST 27-JUN-1995
IMAGE:147959.5 similar to gb:U03496_cds1 GAP JUNCTION ALPHA-5
PROTEIN (HUMAN);, mRNA sequence.
H13124
H13124.1 GI:877944
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
Hillier, L., Clark, N., Dubucque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lemon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1178
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 1178 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.

```

```

FEATURES
source
1..37
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:559671"
/db_xref="taxon:9606"
/clone="IMAGE:147959"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta Mb2HP"
/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AACTGGAGAAATTCGCGCGCAGGAATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo. "

ORIGIN

```

```

Query Match 42.7%; Score 12.8; DB 7; Length 37;
Best Local Similarity 87.5%; Pred. No. 9.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 13 TTGGTCATCTCACCTT 28
Db 28 TAGGTCATCTGACCTT 13

```

```

RESULT 29
BH759504/c
LOCUS
DEFINITION
BH759504 37 bp DNA linear GSS 12-MAR-2002
KG04665-Sprime Drosophila melanogaster P(SUPor-P) P element
insertion lines Drosophila melanogaster genomic sequence recovered
from 5' end of P element, genomic survey sequence.
BH759504
BH759504.1 GI:19352743
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 37)
Levis, R., Hoskins, R., Liao, G., Mozdén, N., Teang, G., He, Y.,
Karpen, G., Bellen, H., Rubin, G. and Spradling, A.
The Berkeley Drosophila Genome Project Gene Disruption Project
Unpublished (2001)
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element
The P element insertion position is base 30 in the 37 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon-tagged.
Location/Qualifiers
1..37
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster P(SUPor-P) P element
insertion lines"
/note="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P(SUPor-P) P-element transposon insertion. The resultant
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
http://www.fruitfly.org/about/methods/inverse.pcr.html."

```

```

ORIGIN
Query Match 42.7%; Score 12.8; DB 8; Length 37;
Best Local Similarity 70.8%; Pred. No. 9.5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 7 CAGTCCTTGGTCATCTCACCTTCT 30
Db 30 CATTTCATCAGTCATCTGACTCTCT 7

```

```

RESULT 30
CN762433/c
LOCUS
DEFINITION
CN762433 43 bp mRNA linear EST 20-MAY-2004
ID04AAA4E04RM1 ApMS Acyrthosiphon pisum cDNA clone ID04AAA4E04 5',
mRNA sequence.
CN762433
ACCESSION
CN762433

```

VERSION CN762433.1 GI:47536356
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE 1 (bases 1 to 43)
AUTHORS Hunter W., Martinez-Torres D., Rahbe Y., Sabater-Munoz B., Stern D., Tagu D. and Wincker P.
TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 4 row: E column: 4.
Location/Qualifiers
1. 43
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="development stage"
/db_xref="taxon:7029"
/clone="ID0AA4AE04"
/tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="Xli-Blue"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: ID0AAA; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University; Soil conditions: Soil; Sowing date: 01/06/1999; Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 C)"
ORIGIN
Query Match 42.7%; Score 12.8; DB 7; Length 43;
Best Local Similarity 70.8%; Pred. No. 9.7e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TGGACTCAGTCCTGGTCATCTCA 24
Db 28 TTGACATAATCATTAGTCACTCA 5
RESULT 31
AZ479665 44 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0300D01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0300D01 R, genomic survey sequence.
ACCESSION AZ479665
VERSION AZ479665.1 GI:10639494
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 44)
AUTHORS Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamill C., Islam H., Longacre S., Mahmood M., Meenen E., Pedersen T., Reilly M., Rose M., Rose R., Stokes R., Tingey A., von

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0300 row: D column: 01
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 44.
Location/Qualifiers
1. 44
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0300D01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN
Query Match 42.7%; Score 12.8; DB 8; Length 44;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GGACTCAGTCCTTGGT 17
Db 5 GGACCCAGGCTTGGT 20
RESULT 32
CL675662/c 44 bp DNA linear GSS 09-JUL-2004
LOCUS PRI0115C B08_2 - PRI0115C-BR (44) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic survey sequence.
DEFINITION CL675662
VERSION CL675662.1 GI:50180358
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 44)
AUTHORS Srinivasan J., Otto G.W., Kahlow U., Geisler R. and Sommer R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism

Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498

Email: raif.sommer@cuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

1. .44
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match 42.7%; Score 12.8; DB 9; Length 44;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACTCAGTCTTGTCATCA 19

DB 18 ACTCAGTCTCGATCA 3

RESULT 33

AZ328994

LOCUS AZ328994 45 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0053105F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0053105 F, genomic survey sequence.

ACCESSION AZ328994.1 GI:10389268

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 45)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, W., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0053 row: I column: 05

Seq primer: CGTTGTAAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 45.

Location/Qualifiers

1. .45

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="CS7BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0053105"

FEATURES

source

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 42.7%; Score 12.8; DB 8; Length 45;
Best Local Similarity 70.8%; Pred. No. 9.7e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 TCAGTCTTGTCATCTCACCTTC 29

DB 1 TCATTACTTGCTCTCTCTTTTC 24

RESULT 34

BH791670/c

LOCUS BH791670 48 bp DNA linear GSS 02-APR-2002

DEFINITION SALK_060817.42.80.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_060817.42.80.x, genomic
survey sequence.

ACCESSION BH791670.1 GI:19885779

VERSION GSS.

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 48)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmermann, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At4g33590.

Class: TDNA tagged.

Location/Qualifiers

1. .48

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_060817.42.80.x"

/note="PCR was performed on Arabidopsis thaliana lines"

FEATURES

source

each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 42.7%; Score 12.8; DB 8; Length 48;
Best Local Similarity 70.8%; Pred. No. 9.8e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 TTAGCTCTGGTCATCTACCTTC 29
DB 36 TCTCTCCCTTGACATTCACCTTC 13

RESULT 35
AV833344
LOCUS
DEFINITION AV833344 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare cDNA clone bags612, mRNA sequence.
49 bp mRNA linear EST 22-JUN-2001

ACCESSION AV833344
VERSION AV833344.1 GI:14525433
KEYWORDS
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 49)
Sato, K. EST sequencing project in NIG and Okayama Univ
Barley EST (2001)
Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp
URL: <http://www.rib.okayama-u.ac.jp/barley/>
Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission;
database: <http://www.shigen.nig.ac.jp/barley/Barley.html>.

FEATURES source
1..49
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Haruna Nijo"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="bags612"
/tissue_type="shoots"
/dev_stage="germination"
/clone_lib="K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare shoots germination"

ORIGIN

Query Match 42.7%; Score 12.8; DB 1; Length 49;
Best Local Similarity 68.0%; Pred. No. 9.8e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCTTGGTCATCTACCTTC 28
DB 23 ACTTCGCCGCTGGNCATTACACCAT 47

RESULT 36
AG198679/c
LOCUS
DEFINITION AG198679 Pan troglodytes DNA, clone: RP43-079K02.T7, genomic survey sequence.
24 bp DNA linear GSS 06-MAR-2004

ACCESSION AG198679
VERSION AG198679.1 GI:45230855

GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43
2 (bases 1 to 24)
Unpublished
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail: redstone@mail.kribb.re.kr, URL: <http://phs.grc.kribb.re.kr/>, Tel: 82-42-866-7181, Fax: 82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI.
R.Site 2 : EcoRI.
1..24
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-079K02.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 42.0%; Score 12.6; DB 9; Length 24;
Best Local Similarity 78.9%; Pred. No. 1.1e+06;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 CTTGTGTCATCTACCTTCT 30
DB 24 CATGTTTCATGTCCTCTCT 6

RESULT 37
AZ309679
LOCUS
DEFINITION AZ309679 28 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0016B17 F, genomic survey sequence.
ACCESSION AZ309679
VERSION AZ309679.1 GI:10350733
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Bescorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: B column: 17

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 28.

FEATURES

Location/Qualifiers
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0016B17"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus CS7BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.0%; Score 12.6; DB 8; Length 28;
Best Local Similarity 78.9%; Pred. No. 1.1e+06;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 11 CCTTGTCATCTCCACCTTC 29

Db 8 CCTTGTCATCTCCACCTC 26

RESULT 38

CC798624

LOCUS

DEFINITION SALK_146625.31.65.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_146625.31.65.x, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabisopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 29)

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

FEATURES

Location/Qualifiers
1. .29
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_146625.31.65.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 42.0%; Score 12.6; DB 9; Length 29;

Best Local Similarity 78.9%; Pred. No. 1.1e+06;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CTCAGTCCTTGTCATCTC 23

Db 10 CTCGTCTTCTCATCTC 28

RESULT 39

AG189685/c

LOCUS

DEFINITION Pan troglodytes DNA, clone: RP43-064G18.T7, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Pan troglodytes (chimpanzee)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1

REFERENCE

AUTHORS

Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,

Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.

BAC end sequences of Library RP-43

Unpublished

2 (bases 1 to 32)

REFERENCE

AUTHORS

Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,

Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.

Direct Submission

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of

Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);

52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea

(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,

Tel:82-42-866-7181, Fax:82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC

end was generated during the R&D process and may have higher chance

of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : ECORI

R.Site 2 : ECORI.

Location/Qualifiers

1. .32

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-064G18.T7"

/sex="male"

ORIGIN

QY 3 GACTCAGTCCTTGGTCATCTCACCTTC 29
||| | | | | | | | | |
Dp 29 GACTAGGCATATAGTCAACTCACATTC 3

ACCESSION BH011404
VERSION BH011404.1
KEYWORDS GSS.

REFERENCE
1 (bases 1 to 36)
AUTHORS
Levis, R., Hoskins, R., Liao, G., Mozden, N., Tsang, G., He, Y.,
Karnen, G., Bellen, H., Rubin, G. and Spradling, A.

TITLE The Berkeley Drosophila Genome Project Gene Disruption Project
JOURNAL Unpublished (2001)

Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.

Sequence recovery method was inverse FCR. Sequence orientation is forward strand relative to 5' end of p element.

The P element insertion position is base 29 in the 36 bases. This insertion position refers to the first base of the 8 base target recognition sequence.

FEATURES
Location/Qualifiers
Class: transposon-tagged.
recognition sequence.

```

1. .36
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster P{GT1} P element
insertion lines"

```

```
insertion lines"
/notes="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P{G11} P-element transposon insertion. The resultant
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
bttrn.//www.fruitfly.org/about/methods/inverse.pcr.html."
```

ORIGIN

Query Match	42.0%	Score 12.6;	DB 8;	Length 36;
Best Local Similarity	78.9%;	Pred. No. 1.1e+06;		
Matches	15.	Conservative	0;	Indels 0;
			Matches 4;	Gaps 0;

Qy 12 CTGGTCATCTCACCTTCT 30
|||||
Db 36 CTGGTTTATCACCTCT 18

Search completed: November 23, 2004, 22:23:03
Job time : 1472.31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 594.247 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631B-5
Perfect score: 33
Sequence: 1 gccacatgagtggaaggcgtctggtgataccg 33

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl.*

1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	66.7	34	6	BD181366
2	22	66.7	34	6	AX523946
3	22	66.7	34	6	AX523944
4	16.4	49.7	43	6	AX524844
5	15.6	47.3	40	6	AX403706
6	15.6	47.3	40	6	CQ753200
7	15.4	46.7	30	6	AX930614
8	15.4	46.7	30	6	BD263504
9	15.4	46.7	33	6	AR124548
10	15.4	46.7	33	6	AR163199
11	15.4	46.7	33	6	AR493800
12	15.4	46.7	33	6	AX491667
13	15.4	46.7	33	6	AX498638
14	15.4	46.7	33	6	BD131354
15	15.4	46.7	34	6	AR048018
16	15.4	46.7	34	6	AR048020
17	15.4	46.7	34	6	AR059770
18	15.4	46.7	34	6	AR059772
19	15.4	46.7	34	6	AR068646

20	15.4	46.7	34	6	AR068648	AR068648	Sequence
21	15.4	46.7	34	6	AR094254	AR094254	Sequence
22	15.4	46.7	34	6	AR094256	AR094256	Sequence
23	15.4	46.7	38	6	AR048019	AR048019	Sequence
24	15.4	46.7	38	6	AR048021	AR048021	Sequence
25	15.4	46.7	38	6	AR059773	AR059773	Sequence
26	15.4	46.7	38	6	AR068647	AR068647	Sequence
27	15.4	46.7	38	6	AR068649	AR068649	Sequence
28	15.4	46.7	38	6	AR094255	AR094255	Sequence
29	15.4	46.7	38	6	AR094257	AR094257	Sequence
30	15.4	46.7	40	6	AR225168	AR225168	Sequence
31	15	45.5	38	6	AX665041	AX665041	Sequence
32	15	45.5	38	6	AX961520	AX961520	Sequence
33	15	45.5	46	6	AX665040	AX665040	Sequence
34	15	45.5	46	6	AX961519	AX961519	Sequence
35	15	45.5	50	6	CQ006075	CQ006075	Sequence
36	14.8	44.8	21	6	AX539350	AX539350	Sequence
37	14.8	44.8	21	6	AX539351	AX539351	Sequence
38	14.6	44.2	30	6	BD091354	BD091354	Methods a
39	14.6	44.2	40	6	A99000	A99000	Sequence 8
40	14.6	44.2	40	6	AR195317	AR195317	Sequence
41	14.6	44.2	48	6	AR119460	AR119460	Sequence
42	14.6	44.2	48	6	AR231748	AR231748	Sequence
43	14.4	43.6	20	6	BD085692	BD085692	Novel hum
44	14.4	43.6	21	6	AX539352	AX539352	Sequence
45	14.4	43.6	21	6	AX539353	AX539353	Sequence
46	14.4	43.6	21	6	AX706574	AX706574	Sequence
47	14.4	43.6	21	6	AX706575	AX706575	Sequence
48	14.4	43.6	21	6	AX707504	AX707504	Sequence
49	14.4	43.6	21	6	AX707505	AX707505	Sequence
50	14.4	43.6	40	6	BD016886	BD016886	DNA fragm
51	14.4	43.6	44	8	ATH552308	ATH552308	Arabidops
52	14.4	43.6	47	6	AR291259	AR291259	Sequence
53	14.2	43.0	50	6	CQ009166	CQ009166	Sequence
54	14	42.4	37	6	I33378	I33378	Sequence 1
55	14	42.4	40	6	CQ812935	CQ812935	Sequence
56	14	42.4	40	6	E15204	E15204	PCR primer
57	14	42.4	42	9	HSANW4B	HSANW4B	X72100 H.sapiens
58	14	42.4	45	6	AX662209	AX662209	Sequence
59	13.8	41.8	23	6	AR083022	AR083022	Sequence
60	13.8	41.8	23	6	AR153544	AR153544	Sequence
61	13.8	41.8	23	6	AR157559	AR157559	Sequence
62	13.8	41.8	23	6	BD232812	BD232812	Diagnosti
63	13.8	41.8	23	6	AX224933	AX224933	Sequence
64	13.8	41.8	23	6	AX039711	AX039711	Sequence
65	13.8	41.8	23	6	BD006031	BD006031	An optina
66	13.8	41.8	23	6	BD070491	BD070491	Methods f
67	13.8	41.8	36	6	A30931	A30931	oligonucleo
68	13.8	41.8	36	6	AR362484	AR362484	Sequence
69	13.8	41.8	38	6	AX219893	AX219893	Sequence
70	13.8	41.8	39	6	BD190225	BD190225	Humanized
71	13.8	41.8	39	6	BD190226	BD190226	Humanized
72	13.8	41.8	41	6	AR036473	AR036473	Sequence
73	13.8	41.8	41	6	AR069432	AR069432	Sequence
74	13.8	41.8	41	6	I73454	I73454	Sequence 6
75	13.8	41.8	45	6	AR164104	AR164104	Sequence
76	13.8	41.8	46	9	HSAGC110	HSAGC110	Human aggre
77	13.8	41.8	47	6	AX160228	AX160228	Sequence
78	13.8	41.8	50	6	AX093078	AX093078	Sequence
79	13.6	41.2	20	6	AR170760	AR170760	Sequence
80	13.6	41.2	20	6	AR176139	AR176139	Sequence
81	13.6	41.2	22	6	AX003312	AX003312	Sequence
82	13.6	41.2	33	6	AR143453	AR143453	Sequence
83	13.6	41.2	33	6	AX598104	AX598104	Sequence
84	13.6	41.2	40	6	AR224179	AR224179	Sequence
85	13.6	41.2	42	6	AR021425	AR021425	Sequence
86	13.6	41.2	42	6	AR042987	AR042987	Sequence
87	13.6	41.2	42	6	AR161321	AR161321	Sequence
88	13.6	41.2	42	6	AR164106	AR164106	Sequence
89	13.6	41.2	42	6	I43966	I43966	Sequence 57
90	13.6	41.2	42	6	I62978	I62978	Sequence 10
91	13.6	41.2	42	6	I88731	I88731	Sequence 10
92	13.6	41.2	42	6	AR369914	AR369914	Sequence

93	13.6	41.2	42	6	BD096551	BD096551 Transgeni	166	13.2	40.0	39	6	AX763682	AX763682 Sequence
c 94	13.6	41.2	44	6	AR076166	AR076166 Sequence	c 167	13.2	40.0	40	6	AX703378	AX703378 Sequence
c 95	13.6	41.2	44	6	AR076857	AR076857 Sequence	c 168	13.2	40.0	41	6	AX515036	AX515036 Sequence
c 96	13.6	41.2	44	6	AR149824	AR149824 Sequence	c 169	13.2	40.0	41	6	AX516762	AX516762 Sequence
c 97	13.6	41.2	45	6	AR164108	AR164108 Sequence	c 170	13.2	40.0	41	6	AX518925	AX518925 Sequence
c 98	13.6	41.2	45	6	AX611799	AX611799 Sequence	c 171	13.2	40.0	41	6	AX520859	AX520859 Sequence
c 99	13.6	41.2	50	6	CQ003466	CQ003466 Sequence	c 172	13.2	40.0	42	6	AR079470	AR079470 Sequence
c 100	13.6	41.2	50	6	CQ004857	CQ004857 Sequence	c 173	13.2	40.0	43	6	AX394937	AX394937 Sequence
c 101	13.6	41.2	50	6	AX107690	AX107690 Sequence	c 174	13.2	40.0	44	6	AX0437	AX0437 Sequence
c 102	13.6	41.2	20	6	AX128604	AX128604 Sequence	c 175	13.2	40.0	44	6	I04544	I04544 Sequence
c 103	13.4	40.6	21	6	BD268689	BD268689 Isolation	c 176	13.2	40.0	44	6	AR217968	AR217968 Sequence
c 104	13.4	40.6	21	6	I87914	I87914 Sequence	c 177	13.2	40.0	44	6	AR217968	AR217968 Sequence
c 105	13.4	40.6	24	6	AX289974	AX289974 Sequence	c 178	13.2	40.0	44	6	BD134913	BD134913 High-affi
c 106	13.4	40.6	27	6	AR012082	AR012082 Sequence	c 179	13.2	40.0	44	6	BD134919	BD134919 High-affi
c 107	13.4	40.6	27	6	AR012083	AR012083 Sequence	c 180	13.2	40.0	45	6	AR088048	AR088048 Sequence
c 108	13.4	40.6	30	6	CQ0802941	CQ0802941 Sequence	c 181	13.2	40.0	45	6	BD233864	BD233864 Novel met
c 109	13.4	40.6	35	6	BD170140	BD170140 Method of	c 182	13.2	40.0	45	6	AX025282	AX025282 Sequence
c 110	13.4	40.6	38	6	I41102	I41102 Sequence	c 183	13.2	40.0	47	6	AR284920	AR284920 Sequence
c 111	13.4	40.6	41	6	AX514019	AX514019 Sequence	c 184	13.2	40.0	47	6	AR289723	AR289723 Sequence
c 112	13.4	40.6	41	6	AX516285	AX516285 Sequence	c 185	13.2	40.0	48	6	CQ0809436	CQ0809436 Sequence
c 113	13.4	40.6	41	6	AX518485	AX518485 Sequence	c 186	13.2	40.0	49	9	AB010655	AB010655 Homo sapi
c 114	13.4	40.6	41	6	AX518485	AX518485 Sequence	c 187	13.2	39.4	16	6	AR211597	AR211597 Sequence
c 115	13.4	40.6	41	6	AX518619	AX518619 Sequence	c 188	13.2	39.4	17	6	AR211617	AR211617 Sequence
c 116	13.4	40.6	41	6	AX520844	AX520844 Sequence	c 189	13.2	39.4	17	6	AX802008	AX802008 Sequence
c 117	13.4	40.6	42	6	I32723	I32723 Sequence	c 190	13.2	39.4	18	6	BD244768	BD244768 Isolation
c 118	13.4	40.6	50	6	AR075351	AR075351 Sequence	c 191	13.2	39.4	18	6	AR255274	AR255274 Sequence
c 119	13.4	40.6	50	6	AX159930	AX159930 Sequence	c 192	13.2	39.4	25	6	BD245830	BD245830 Developme
c 120	13.2	40.0	20	6	BD012252	BD012252 A novel g	c 193	13.2	39.4	25	6	I81294	I81294 Sequence
c 121	13.2	40.0	21	6	AX539354	AX539354 Sequence	c 194	13.2	39.4	25	6	AX784857	AX784857 Sequence
c 122	13.2	40.0	21	6	AX539355	AX539355 Sequence	c 195	13.2	39.4	25	6	AX784858	AX784858 Sequence
c 123	13.2	40.0	21	6	AX706572	AX706572 Sequence	c 196	13.2	39.4	25	6	AX784859	AX784859 Sequence
c 124	13.2	40.0	21	6	AX707502	AX707502 Sequence	c 197	13.2	39.4	25	6	AX784860	AX784860 Sequence
c 125	13.2	40.0	21	6	AX707503	AX707503 Sequence	c 198	13.2	39.4	27	6	BD206663	BD206663 Enzymatic
c 126	13.2	40.0	25	6	AX782528	AX782528 Sequence	c 199	13.2	39.4	27	6	BD206912	BD206912 Enzymatic
c 127	13.2	40.0	25	6	AX782529	AX782529 Sequence	c 200	13.2	39.4	27	6	BD211734	BD211734 Drug as c
c 128	13.2	40.0	25	6	AX782530	AX782530 Sequence	c 201	13.2	39.4	29	6	AX153594	AX153594 Sequence
c 129	13.2	40.0	25	6	AX782531	AX782531 Sequence	c 202	13.2	39.4	30	6	CQ816714	CQ816714 Sequence
c 130	13.2	40.0	25	6	AX782532	AX782532 Sequence	c 203	13.2	39.4	30	6	CQ816715	CQ816715 Sequence
c 131	13.2	40.0	25	6	AX782533	AX782533 Sequence	c 204	13.2	39.4	30	6	CQ816717	CQ816717 Sequence
c 132	13.2	40.0	25	6	AX782534	AX782534 Sequence	c 205	13.2	39.4	33	6	BD246982	BD246982 Improved
c 133	13.2	40.0	25	6	AX782535	AX782535 Sequence	c 206	13.2	39.4	34	6	BD010736	BD010736 Helicobac
c 134	13.2	40.0	30	6	A38307	A38307 Sequence	c 207	13.2	39.4	37	9	AF505544	AF505544 Homo sapi
c 135	13.2	40.0	30	6	BD244422	BD244422 Mutants o	c 208	13.2	39.4	38	6	AR091388	AR091388 Sequence
c 136	13.2	40.0	30	6	BD244423	BD244423 Mutants o	c 209	13.2	39.4	38	6	AR392579	AR392579 Sequence
c 137	13.2	40.0	30	6	AX027139	AX027139 Sequence	c 210	13.2	39.4	38	6	BD165911	BD165911 Human sta
c 138	13.2	40.0	30	6	AX027140	AX027140 Sequence	c 211	13.2	39.4	39	1	AFU430249	AFU430249 Archaeogl
c 139	13.2	40.0	30	6	AX244134	AX244134 Sequence	c 212	13.2	39.4	39	6	AX3184	AX3184 Sequence
c 140	13.2	40.0	30	6	AX244135	AX244135 Sequence	c 213	13.2	39.4	39	6	AR182916	AR182916 Sequence
c 141	13.2	40.0	33	6	AR012128	AR012128 Sequence	c 214	13.2	39.4	39	6	BD096889	BD096889 Chemical
c 142	13.2	40.0	33	6	AR012130	AR012130 Sequence	c 215	13.2	39.4	40	6	CQ816732	CQ816732 Sequence
c 143	13.2	40.0	33	6	AR012132	AR012132 Sequence	c 216	13.2	39.4	41	6	CQ816733	CQ816733 Sequence
c 144	13.2	40.0	33	6	AR108210	AR108210 Sequence	c 217	13.2	39.4	41	6	I81295	I81295 Sequence
c 145	13.2	40.0	33	6	AR108212	AR108212 Sequence	c 218	13.2	39.4	41	6	I81299	I81299 Sequence
c 146	13.2	40.0	33	6	AR108214	AR108214 Sequence	c 219	13.2	39.4	41	6	AX515201	AX515201 Sequence
c 147	13.2	40.0	33	6	AR374477	AR374477 Sequence	c 220	13.2	39.4	41	6	AX517669	AX517669 Sequence
c 148	13.2	40.0	33	6	AR374479	AR374479 Sequence	c 221	13.2	39.4	41	6	AX694485	AX694485 Sequence
c 149	13.2	40.0	33	6	AR374481	AR374481 Sequence	c 222	13.2	39.4	42	6	AR055004	AR055004 Sequence
c 150	13.2	40.0	36	6	BD079949	BD079949 Genetic m	c 223	13.2	39.4	42	6	AR156253	AR156253 Sequence
c 151	13.2	40.0	38	6	CQ816290	CQ816290 Sequence	c 224	13.2	39.4	42	6	E33305	E33305 DsBA/Dabb/D
c 152	13.2	40.0	38	6	CQ816322	CQ816322 Sequence	c 225	13.2	39.4	42	6	AR448527	AR448527 Sequence
c 153	13.2	40.0	38	6	CQ818885	CQ818885 Sequence	c 226	13.2	39.4	42	6	AX343177	AX343177 Sequence
c 154	13.2	40.0	38	6	CQ818917	CQ818917 Sequence	c 227	13.2	39.4	45	6	E11413	E11413 Primer. 9/1
c 155	13.2	40.0	38	6	AR333190	AR333190 Sequence	c 228	13.2	39.4	46	6	AR101846	AR101846 Sequence
c 156	13.2	40.0	38	6	AX022994	AX022994 Sequence	c 229	13.2	39.4	46	6	BD135890	BD135890 Methods f
c 157	13.2	40.0	38	6	AX220494	AX220494 Sequence	c 230	13.2	39.4	50	6	CQ003415	CQ003415 Sequence
c 158	13.2	40.0	38	6	AX228254	AX228254 Sequence	c 231	13.2	39.4	50	6	CQ005618	CQ005618 Sequence
c 159	13.2	40.0	38	6	AX273923	AX273923 Sequence	c 232	13.2	39.4	50	6	CQ005619	CQ005619 Sequence
c 160	13.2	40.0	38	6	AX424577	AX424577 Sequence	c 233	13.2	39.4	50	6	AX923393	AX923393 Sequence
c 161	13.2	40.0	38	6	AX424610	AX424610 Sequence	c 234	12.8	38.8	20	6	AX295467	AX295467 Sequence
c 162	13.2	40.0	38	6	AX701035	AX701035 Sequence	c 235	12.8	38.8	21	6	AX095832	AX095832 Sequence
c 163	13.2	40.0	39	6	A59579	A59579 Sequence	c 236	12.8	38.8	22	6	AX117850	AX117850 Sequence
c 164	13.2	40.0	39	6	AX223819	AX223819 Sequence	c 237	12.8	38.8	24	6	AX059420	AX059420 Sequence
c 165	13.2	40.0	39	6	AX763674	AX763674 Sequence	c 238	12.8	38.8	24	6	AX290834	AX290834 Sequence

c 239	12.8	38.8	25	6	AR217972 Sequence	312	12.6	38.2	36	6	AX637082	AX637082 Sequence
c 240	12.8	38.8	25	6	BD134917	313	12.6	38.2	36	6	AX637592	AX637592 Sequence
c 241	12.8	38.8	27	6	BD207842	314	12.6	38.2	36	6	AX638187	AX638187 Sequence
c 242	12.8	38.8	28	6	AG9149	315	12.6	38.2	38	6	AX638187	AX638187 Sequence
c 243	12.8	38.8	29	6	BD253320	316	12.6	38.2	38	6	AX1274	AX1274 Sequence
c 244	12.8	38.8	29	6	I73291	317	12.6	38.2	38	6	AX1274	AX1274 Sequence
c 245	12.8	38.8	29	6	AX546608	318	12.6	38.2	38	6	AX1274	AX1274 Sequence
c 246	12.8	38.8	30	6	AR074455	319	12.6	38.2	38	6	AX1274	AX1274 Sequence
c 247	12.8	38.8	30	6	AR081135	320	12.6	38.2	38	6	AX1274	AX1274 Sequence
c 248	12.8	38.8	30	6	AR085332	321	12.6	38.2	38	6	AX1274	AX1274 Sequence
c 249	12.8	38.8	30	6	AR088080	322	12.6	38.2	38	6	AX1274	AX1274 Sequence
c 250	12.8	38.8	30	6	AR104239	323	12.6	38.2	39	6	AR059295	AR059295 Sequence
c 251	12.8	38.8	30	6	AR143503	324	12.6	38.2	39	6	BD248568	BD248568 Identific
c 252	12.8	38.8	30	6	AR171407	325	12.6	38.2	39	6	AR305263	AR305263 Sequence
c 253	12.8	38.8	30	6	AR171578	326	12.6	38.2	39	6	AR305263	AR305263 Sequence
c 254	12.8	38.8	30	6	BD243168	327	12.6	38.2	39	6	AX025656	AX025656 Sequence
c 255	12.8	38.8	31	6	AX192433	328	12.6	38.2	39	6	BD106174	BD106174 Novel IDL
c 256	12.8	38.8	33	10	S76560	329	12.6	38.2	40	6	AX12864	AX12864 Sequence
c 257	12.8	38.8	34	6	AR148507	330	12.6	38.2	41	6	AX514279	AX514279 Sequence
c 258	12.8	38.8	34	6	AR179180	331	12.6	38.2	41	6	AX514522	AX514522 Sequence
c 259	12.8	38.8	36	6	AR056642	332	12.6	38.2	41	6	AX514885	AX514885 Sequence
c 260	12.8	38.8	36	6	AR114400	333	12.6	38.2	41	6	AX517236	AX517236 Sequence
c 261	12.8	38.8	36	6	AX633701	334	12.6	38.2	41	6	AX520060	AX520060 Sequence
c 262	12.8	38.8	38	6	I05821	335	12.6	38.2	41	6	AX520461	AX520461 Sequence
c 263	12.8	38.8	38	6	I06863	336	12.6	38.2	42	6	AR231384	AR231384 Sequence
c 264	12.8	38.8	38	6	I07314	337	12.6	38.2	42	6	AR231385	AR231385 Sequence
c 265	12.8	38.8	38	6	AR332005	338	12.6	38.2	42	6	BD003035	BD003035 Design, c
c 266	12.8	38.8	38	6	AR334176	339	12.6	38.2	42	6	BD003036	BD003036 Design, c
c 267	12.8	38.8	38	6	AR335227	340	12.6	38.2	45	6	AR168070	AR168070 Sequence
c 268	12.8	38.8	38	6	AX228271	341	12.6	38.2	45	6	AR204841	AR204841 Sequence
c 269	12.8	38.8	38	6	AX424923	342	12.6	38.2	45	6	YSCMTCBL2	Y01473 Saccharomyc
c 270	12.8	38.8	39	6	BD249050	343	12.6	38.2	47	6	AR289765	AR289765 Sequence
c 271	12.8	38.8	41	6	AX280210	344	12.6	38.2	47	6	AR290078	AR290078 Sequence
c 272	12.8	38.8	42	6	E31999	345	12.6	38.2	48	6	AR021432	AR021432 Sequence
c 273	12.8	38.8	48	6	AX277271	346	12.6	38.2	48	6	AR042994	AR042994 Sequence
c 274	12.8	38.8	48	9	SC2614	347	12.6	38.2	48	6	AR161328	AR161328 Sequence
c 275	12.8	38.8	50	6	CQ004080	348	12.6	38.2	48	6	I43973	I43973 Sequence
c 276	12.8	38.8	50	6	CQ008430	349	12.6	38.2	48	6	I62985	I62985 Sequence
c 277	12.8	38.8	50	6	AR356249	350	12.6	38.2	48	6	I88738	I88738 Sequence
c 278	12.6	38.2	24	6	AX46857	351	12.6	38.2	48	6	AR369921	AR369921 Sequence
c 279	12.6	38.2	24	6	AX289976	352	12.6	38.2	48	6	BD096558	BD096558 Transgeni
c 280	12.6	38.2	24	6	AX444343	353	12.6	38.2	50	6	AR032882	AR032882 Sequence
c 281	12.6	38.2	25	6	AX448308	354	12.6	38.2	50	6	CQ003473	CQ003473 Sequence
c 282	12.6	38.2	25	6	AX689218	355	12.6	38.2	50	6	CQ005412	CQ005412 Sequence
c 283	12.6	38.2	25	6	AX689219	356	12.6	38.2	50	6	I29622	I29622 Sequence
c 284	12.6	38.2	25	6	AX689220	357	12.6	38.2	50	6	I91296	I91296 Sequence
c 285	12.6	38.2	25	6	AX689221	358	12.6	38.2	50	6	AR209546	AR209546 Sequence
c 286	12.6	38.2	25	6	AX689222	359	12.6	38.2	50	6	AX752746	AX752746 Sequence
c 287	12.6	38.2	25	6	AX689223	360	12.6	38.2	50	6	AX752751	AX752751 Sequence
c 288	12.6	38.2	25	6	AX689224	361	12.6	38.2	50	9	HSTCRDV06	HSTCRDV06 Sequence
c 289	12.6	38.2	25	6	AX838488	362	12.4	37.6	18	6	AR116124	AR116124 Sequence
c 290	12.6	38.2	27	6	BD207547	363	12.4	37.6	18	6	AR322341	AR322341 Sequence
c 291	12.6	38.2	27	6	AX117396	364	12.4	37.6	18	6	BD062479	BD062479 Phosphodi
c 292	12.6	38.2	29	6	BD253456	365	12.4	37.6	21	6	AR381404	AR381404 Sequence
c 293	12.6	38.2	29	6	E27930	366	12.4	37.6	22	6	AR489251	AR489251 Sequence
c 294	12.6	38.2	30	6	AX125673	367	12.4	37.6	22	6	AX233444	AX233444 Sequence
c 295	12.6	38.2	30	6	I47085	368	12.4	37.6	23	6	I11908	I11908 Sequence
c 296	12.6	38.2	30	6	AX236558	369	12.4	37.6	23	6	AX298783	AX298783 Sequence
c 297	12.6	38.2	31	6	AX1283	370	12.4	37.6	24	6	AX106712	AX106712 Sequence
c 298	12.6	38.2	31	6	AX5065	371	12.4	37.6	25	6	CO772384	CO772384 Sequence
c 299	12.6	38.2	31	6	AR222437	372	12.4	37.6	25	6	AR258986	AR258986 Sequence
c 300	12.6	38.2	33	6	AX961199	373	12.4	37.6	25	6	AX382470	AX382470 Sequence
c 301	12.6	38.2	33	6	BD096592	374	12.4	37.6	25	6	AX769448	AX769448 Sequence
c 302	12.6	38.2	35	6	AR369958	375	12.4	37.6	26	6	AR026887	AR026887 Sequence
c 303	12.6	38.2	35	6	BD096592	376	12.4	37.6	26	6	AR049313	AR049313 Sequence
c 304	12.6	38.2	35	6	AR018069	377	12.4	37.6	26	6	AR065571	AR065571 Sequence
c 305	12.6	38.2	36	6	AR018069	378	12.4	37.6	26	6	AR089945	AR089945 Sequence
c 306	12.6	38.2	36	6	AR041624	379	12.4	37.6	26	6	AR196980	AR196980 Sequence
c 307	12.6	38.2	36	6	AR042134	380	12.4	37.6	26	6	AR259134	AR259134 Sequence
c 308	12.6	38.2	36	6	I39223	381	12.4	37.6	29	6	AR018053	AR018053 Sequence
c 309	12.6	38.2	36	6	I77468	382	12.4	37.6	29	6	AR071943	AR071943 Sequence
c 310	12.6	38.2	36	6	AX407217	383	12.4	37.6	29	6	AR157879	AR157879 Sequence
c 311	12.6	38.2	36	6	AX635500	384	12.4	37.6	29	6	BD197241	BD197241 Method an

385	12.4	37.6	29	6	BD198157 Method an	458	12.2	37.0	22	6	BD103840	BD103840 A method
386	12.4	37.6	29	6	BD253413 Regulatio	459	12.2	37.0	23	6	CQ816286	CQ816286 Sequence
387	12.4	37.6	29	6	AX657915 Sequence	460	12.2	37.0	23	6	CQ818881	CQ818881 Sequence
388	12.4	37.6	30	6	BD118750 Sequence	461	12.2	37.0	23	6	E06292	E06292 Primer, 9/1
389	12.4	37.6	30	6	BD175011 Cis-regul	C 462	12.2	37.0	23	6	E06488	E06488 Primer, 9/1
390	12.4	37.6	30	6	BD187501 Sequence	C 463	12.2	37.0	24	6	AX446309	AX446309 Sequence
391	12.4	37.6	30	6	Q0818732 Sequence	C 464	12.2	37.0	24	6	AX548409	AX548409 Sequence
392	12.4	37.6	30	6	I06383 Sequence 3	465	12.2	37.0	25	6	C0620106	C0620106 Sequence
393	12.4	37.6	32	6	AX589670 Sequence	C 466	12.2	37.0	25	6	C0630374	C0630374 Sequence
394	12.4	37.6	32	6	AR213645 Sequence	467	12.2	37.0	25	6	CQ818223	CQ818223 Sequence
395	12.4	37.6	32	6	AX740019 Sequence	468	12.2	37.0	25	6	AR342872	AR342872 Sequence
396	12.4	37.6	32	6	BD057703 Sequence	469	12.2	37.0	25	6	AR461169	AR461169 Sequence
397	12.4	37.6	32	6	BD081533 Fusion pr	C 470	12.2	37.0	25	6	AR471437	AR471437 Sequence
398	12.4	37.6	33	6	BD081533 Soluble s	C 471	12.2	37.0	25	6	AX692124	AX692124 Sequence
399	12.4	37.6	33	6	AR194221 Sequence	C 472	12.2	37.0	25	6	AX692125	AX692125 Sequence
400	12.4	37.6	33	6	AR194233 Sequence	473	12.2	37.0	25	6	AX782527	AX782527 Sequence
401	12.4	37.6	33	6	AR207101 Sequence	474	12.2	37.0	25	6	AX782536	AX782536 Sequence
402	12.4	37.6	33	6	AR221356 Sequence	475	12.2	37.0	25	6	BD087313	BD087313 Mammalian
403	12.4	37.6	33	6	AR232490 Sequence	476	12.2	37.0	26	6	A31982	A31982 Synthetic H
404	12.4	37.6	33	6	AR281838 Sequence	C 477	12.2	37.0	26	6	A31983	A31983 Synthetic H
405	12.4	37.6	33	6	AX391296 Sequence	C 478	12.2	37.0	26	6	AR090410	AR090410 Sequence
406	12.4	37.6	34	6	BD075807 TIE recep	C 479	12.2	37.0	26	6	AR131401	AR131401 Sequence
407	12.4	37.6	34	6	A50694 Sequence 33	C 480	12.2	37.0	26	6	AR131402	AR131402 Sequence
408	12.4	37.6	36	6	AR083325 Sequence	C 481	12.2	37.0	26	6	AR197445	AR197445 Sequence
409	12.4	37.6	36	6	Q0832126 Sequence	C 482	12.2	37.0	26	6	AR259599	AR259599 Sequence
410	12.4	37.6	37	6	BD170141 Method of	C 483	12.2	37.0	26	6	BD001806	BD001806 Immunogen
411	12.4	37.6	37	6	E37999 Process for	C 484	12.2	37.0	26	6	BD001808	BD001808 Immunogen
412	12.4	37.6	37	6	AX183802 Sequence	C 485	12.2	37.0	27	6	AR019387	AR019387 Sequence
413	12.4	37.6	38	6	AX361213 Sequence	486	12.2	37.0	27	6	AR028940	AR028940 Sequence
414	12.4	37.6	38	6	AX801864 Sequence	487	12.2	37.0	27	6	AR049630	AR049630 Sequence
415	12.4	37.6	39	6	I09581 Sequence 16	488	12.2	37.0	27	6	AR145287	AR145287 Sequence
416	12.4	37.6	39	6	AX373137 Sequence	489	12.2	37.0	27	6	AR183482	AR183482 Sequence
417	12.4	37.6	39	6	AX059020 Sequence	490	12.2	37.0	27	6	AR264737	AR264737 Sequence
418	12.4	37.6	39	12	AX098366 Sequence	491	12.2	37.0	27	6	BD080955	BD080955 Agonist, a
419	12.4	37.6	41	6	S76973 Mus sp. tra	492	12.2	37.0	28	6	BD260569	BD260569 Novel pla
420	12.4	37.6	41	6	E37997 Process for	493	12.2	37.0	28	6	AR287212	AR287212 Sequence
421	12.4	37.6	41	6	AX516515 Sequence	C 494	12.2	37.0	29	6	BD198030	BD198030 Method an
422	12.4	37.6	42	6	AX159942 Sequence	495	12.2	37.0	29	6	BD198406	BD198406 Method an
423	12.4	37.6	42	6	AR123483 Sequence	496	12.2	37.0	29	6	BD253205	BD253205 Regulatio
424	12.4	37.6	42	6	E37995 Process for	497	12.2	37.0	29	6	BD253275	BD253275 Regulatio
425	12.4	37.6	43	6	Q0775450 Sequence	C 498	12.2	37.0	29	6	BD255630	BD255630 Regulatio
426	12.4	37.6	43	6	AR489285 Sequence	C 499	12.2	37.0	29	6	BD256078	BD256078 Regulatio
427	12.4	37.6	44	6	AX484569 Sequence	C 500	12.2	37.0	29	6	BD257186	BD257186 Regulatio
428	12.4	37.6	45	6	AX523102 Sequence	C 501	12.2	37.0	29	6	AR342616	AR342616 Sequence
429	12.4	37.6	45	6	AR083218 Sequence	C 502	12.2	37.0	29	6	AX174858	AX174858 Sequence
430	12.4	37.6	45	6	AR164103 Sequence	C 503	12.2	37.0	29	6	AX298215	AX298215 Sequence
431	12.4	37.6	45	11	BD251077 Protectiv	C 504	12.2	37.0	30	6	AS1855	AS1855 Sequence 19
432	12.4	37.6	46	6	AX664039 Arabidops	C 505	12.2	37.0	30	6	AS1859	AS1859 Sequence 23
433	12.4	37.6	49	6	AX683441 Sequence	C 506	12.2	37.0	30	6	AR085828	AR085828 Sequence
434	12.4	37.6	49	6	Q0775464 Sequence	507	12.2	37.0	30	6	E54041	E54041 Gene diagno
435	12.4	37.6	50	6	Q008140 Sequence	C 508	12.2	37.0	30	6	AR214162	AR214162 Sequence
436	12.4	37.6	50	6	Q008824 Sequence	C 509	12.2	37.0	31	6	AX192433	AX192433 Sequence
437	12.4	37.6	50	6	AX128400 Sequence	510	12.2	37.0	31	6	AX249689	AX249689 Sequence
438	12.4	37.6	50	6	AX165814 Sequence	511	12.2	37.0	32	6	AR123472	AR123472 Sequence
439	12.4	37.6	50	6	BD013721 Method of	C 512	12.2	37.0	32	6	AR219996	AR219996 Sequence
440	12.4	37.6	50	10	BD013721 Method of	C 513	12.2	37.0	32	6	AR220713	AR220713 Sequence
441	12.2	37.0	17	6	U71391 Mus muscul	514	12.2	37.0	32	6	AR287475	AR287475 Sequence
442	12.2	37.0	17	6	AX781784 Sequence	C 515	12.2	37.0	32	6	AX805712	AX805712 Sequence
443	12.2	37.0	18	6	AR106973 Sequence	C 516	12.2	37.0	32	6	BD063041	BD063041 Protease-
444	12.2	37.0	18	6	AR116131 Sequence	517	12.2	37.0	33	6	AR032309	AR032309 Sequence
445	12.2	37.0	18	6	AR322348 Sequence	518	12.2	37.0	33	6	AR084265	AR084265 Sequence
446	12.2	37.0	18	6	BD062486 Phosphodi	519	12.2	37.0	33	6	BD243521	BD243521 Nuclleotid
447	12.2	37.0	19	6	E37137 Method for	520	12.2	37.0	33	6	AX034944	AX034944 Sequence
448	12.2	37.0	20	6	AR165355 Sequence	C 521	12.2	37.0	33	6	BD170411	BD170411 Method of
449	12.2	37.0	20	6	E31749 Blast resis	C 522	12.2	37.0	34	6	AX659015	AX659015 Sequence
450	12.2	37.0	20	6	E37107 Method for	C 523	12.2	37.0	35	6	I28730	I28730 Sequence 34
451	12.2	37.0	20	6	I81470 Sequence 7	C 524	12.2	37.0	35	6	I89384	I89384 Sequence 34
452	12.2	37.0	20	6	AX676286 Sequence	C 525	12.2	37.0	36	6	AR041619	AR041619 Sequence
453	12.2	37.0	20	6	AX707124 Sequence	C 526	12.2	37.0	36	6	AR133028	AR133028 Sequence
454	12.2	37.0	20	6	BD160833 Method fo	C 527	12.2	37.0	36	6	AR133466	AR133466 Sequence
455	12.2	37.0	20	6	BD169536 Method of	C 528	12.2	37.0	36	6	AR133467	AR133467 Sequence
456	12.2	37.0	21	6	AX154181 Sequence	C 529	12.2	37.0	36	6	AR133468	AR133468 Sequence
457	12.2	37.0	22	6	AR112932 Sequence	C 530	12.2	37.0	36	6	I62099	I62099 Sequence 65

C 531	12.2	37.0	36	6	I89302	I89302 Sequence 16	604	12	36.4	15	6	I38943	I38943 Sequence 53
C 532	12.2	37.0	36	6	AX636505	AX636505 Sequence	605	12	36.4	15	6	I87974	I87974 Sequence 53
C 533	12.2	37.0	36	6	AX637077	AX637077 Sequence	606	12	36.4	17	6	AX687721	AX687721 Sequence
C 534	12.2	37.0	37	6	AR411038	AR411038 Sequence	607	12	36.4	17	6	AX687722	AX687722 Sequence
C 535	12.2	37.0	38	6	AR046649	AR046649 Sequence	608	12	36.4	17	6	AX687723	AX687723 Sequence
C 536	12.2	37.0	38	6	I37753	I37753 Sequence 76	609	12	36.4	17	6	AX687724	AX687724 Sequence
C 537	12.2	37.0	38	6	I35501	I35501 Sequence 12	610	12	36.4	17	6	AX687725	AX687725 Sequence
C 538	12.2	37.0	38	6	I94603	I94603 Sequence 76	611	12	36.4	17	6	AX687726	AX687726 Sequence
C 539	12.2	37.0	38	6	AR286953	AR286953 Sequence	612	12	36.4	20	6	AR2562	AR2562 Sequence 36
C 540	12.2	37.0	38	6	AR331791	AR331791 Sequence	613	12	36.4	20	6	AR101050	AR101050 Sequence
C 541	12.2	37.0	38	6	AR332630	AR332630 Sequence	614	12	36.4	20	6	E29054	E29054 Mutant S182
C 542	12.2	37.0	38	6	AR333408	AR333408 Sequence	615	12	36.4	20	6	E29056	E29056 Mutant S182
C 543	12.2	37.0	38	6	AR334450	AR334450 Sequence	616	12	36.4	20	6	E29064	E29064 Mutant S182
C 544	12.2	37.0	38	6	AR334597	AR334597 Sequence	617	12	36.4	21	6	I30540	I30540 Sequence 3
C 545	12.2	37.0	38	6	AR398943	AR398943 Sequence	618	12	36.4	21	6	I81272	I81272 Sequence 23
C 546	12.2	37.0	38	6	AX218533	AX218533 Sequence	619	12	36.4	22	6	AX250146	AX250146 Sequence
C 547	12.2	37.0	38	6	AX219417	AX219417 Sequence	620	12	36.4	22	6	AX015794	AX015794 Sequence
C 548	12.2	37.0	38	6	AX423947	AX423947 Sequence	621	12	36.4	23	6	AX167366	AX167366 Sequence
C 549	12.2	37.0	38	6	AX423968	AX423968 Sequence	622	12	36.4	24	6	AR074528	AR074528 Sequence
C 550	12.2	37.0	38	6	AX424461	AX424461 Sequence	623	12	36.4	24	6	AR369692	AR369692 Sequence
C 551	12.2	37.0	38	6	AX424514	AX424514 Sequence	624	12	36.4	24	6	AR289209	AR289209 Sequence
C 552	12.2	37.0	38	6	AX424609	AX424609 Sequence	625	12	36.4	25	6	AR238927	AR238927 Sequence
C 553	12.2	37.0	38	6	AX424800	AX424800 Sequence	626	12	36.4	25	6	AX278729	AX278729 Sequence
C 554	12.2	37.0	38	6	AX425435	AX425435 Sequence	627	12	36.4	25	6	AX689225	AX689225 Sequence
C 555	12.2	37.0	38	6	AX580370	AX580370 Sequence	628	12	36.4	25	6	AX689226	AX689226 Sequence
C 556	12.2	37.0	38	6	AX581121	AX581121 Sequence	629	12	36.4	25	6	AX689227	AX689227 Sequence
C 557	12.2	37.0	38	6	AX665049	AX665049 Sequence	630	12	36.4	25	6	AX689228	AX689228 Sequence
C 558	12.2	37.0	38	6	AX961528	AX961528 Sequence	631	12	36.4	25	6	AX689229	AX689229 Sequence
C 559	12.2	37.0	39	6	AX384023	AX384023 Sequence	632	12	36.4	25	6	AX689230	AX689230 Sequence
C 560	12.2	37.0	40	6	AR053674	AR053674 Sequence	633	12	36.4	25	6	AX689231	AX689231 Sequence
C 561	12.2	37.0	40	6	AR059120	AR059120 Sequence	634	12	36.4	25	6	AX784856	AX784856 Sequence
C 562	12.2	37.0	40	6	AR168200	AR168200 Sequence	635	12	36.4	25	6	AX784862	AX784862 Sequence
C 563	12.2	37.0	40	6	AR258609	AR258609 Sequence	636	12	36.4	27	6	AR143859	AR143859 Sequence
C 564	12.2	37.0	40	6	AX456329	AX456329 Sequence	637	12	36.4	27	6	BD206536	BD206536 Enzymatic
C 565	12.2	37.0	40	6	AX528105	AX528105 Sequence	638	12	36.4	27	6	BD209483	BD209483 Enzymatic
C 566	12.2	37.0	41	6	AR148815	AR148815 Sequence	639	12	36.4	27	6	E17050	E17050 Primer. 7/1
C 567	12.2	37.0	41	6	AR200861	AR200861 Sequence	640	12	36.4	28	6	AR473410	AR473410 Sequence
C 568	12.2	37.0	41	6	AX513844	AX513844 Sequence	641	12	36.4	28	6	AX092224	AX092224 Sequence
C 569	12.2	37.0	41	6	AX513940	AX513940 Sequence	642	12	36.4	28	6	BD138046	BD138046 Expression
C 570	12.2	37.0	41	6	AX515722	AX515722 Sequence	643	12	36.4	29	6	A87519	A87519 Sequence 5
C 571	12.2	37.0	41	6	AX516011	AX516011 Sequence	644	12	36.4	29	6	BD199676	BD199676 Method an
C 572	12.2	37.0	41	6	AX517049	AX517049 Sequence	645	12	36.4	29	6	BD252451	BD252451 Regulatio
C 573	12.2	37.0	41	6	AX517721	AX517721 Sequence	646	12	36.4	29	6	BD253328	BD253328 Regulatio
C 574	12.2	37.0	41	6	AX518317	AX518317 Sequence	647	12	36.4	29	6	BD257246	BD257246 Regulatio
C 575	12.2	37.0	41	6	AX519279	AX519279 Sequence	648	12	36.4	29	6	BD257253	BD257253 Regulatio
C 576	12.2	37.0	41	6	AX519572	AX519572 Sequence	649	12	36.4	29	6	AR254072	AR254072 Sequence
C 577	12.2	37.0	41	6	AX786812	AX786812 Sequence	650	12	36.4	29	6	AX100907	AX100907 Sequence
C 578	12.2	37.0	44	6	AX642221	AX642221 Sequence	651	12	36.4	29	6	AX100909	AX100909 Sequence
C 579	12.2	37.0	45	6	AR041121	AR041121 Sequence	652	12	36.4	29	6	BD135102	BD135102 Polyzinc
C 580	12.2	37.0	45	6	AR066015	AR066015 Sequence	653	12	36.4	30	6	CQ816716	CQ816716 Sequence
C 581	12.2	37.0	45	6	AR072757	AR072757 Sequence	654	12	36.4	30	6	AX166327	AX166327 Sequence
C 582	12.2	37.0	46	6	AR082267	AR082267 Sequence	655	12	36.4	30	6	AX320318	AX320318 Sequence
C 583	12.2	37.0	46	6	AR120809	AR120809 Sequence	656	12	36.4	31	6	AR117112	AR117112 Sequence
C 584	12.2	37.0	46	6	I78313	I78313 Sequence 11	657	12	36.4	31	6	AR338155	AR338155 Sequence
C 585	12.2	37.0	46	6	AX665048	AX665048 Sequence	658	12	36.4	31	6	AX249589	AX249589 Sequence
C 586	12.2	37.0	46	6	AX961527	AX961527 Sequence	659	12	36.4	31	6	AX429230	AX429230 Sequence
C 587	12.2	37.0	47	6	E37138	E37138 Method for	660	12	36.4	33	6	BD246984	BD246984 Improved
C 588	12.2	37.0	47	6	I04682	I04682 Sequence 6	661	12	36.4	33	6	BD270569	BD270569 Family of
C 589	12.2	37.0	47	6	AR289765	AR289765 Sequence	662	12	36.4	33	6	AR208966	AR208966 Sequence
C 590	12.2	37.0	47	6	AR290290	AR290290 Sequence	663	12	36.4	33	6	AR228359	AR228359 Sequence
C 591	12.2	37.0	47	6	AR290514	AR290514 Sequence	664	12	36.4	33	6	AX046964	AX046964 Sequence
C 592	12.2	37.0	47	6	BD016412	BD016412 Method of	665	12	36.4	33	6	AX428366	AX428366 Sequence
C 593	12.2	37.0	48	6	CQ816302	CQ816302 Sequence	666	12	36.4	33	6	BD082729	BD082729 Family of
C 594	12.2	37.0	48	6	CQ818897	CQ818897 Sequence	667	12	36.4	34	6	BD235856	BD235856 Gene-modi
C 595	12.2	37.0	48	9	S82270	S82270 Homo sapien	668	12	36.4	34	6	I28719	I28719 Sequence 22
C 596	12.2	37.0	49	6	A06246	A06246 Synthetic H	669	12	36.4	34	6	I89373	I89373 Sequence 22
C 597	12.2	37.0	49	6	AX769772	AX769772 Sequence	670	12	36.4	36	6	I01740	I01740 Sequence 7
C 598	12.2	37.0	50	6	CQ003143	CQ003143 Sequence	671	12	36.4	36	6	I79582	I79582 Sequence 5
C 599	12.2	37.0	50	6	CQ008834	CQ008834 Sequence	672	12	36.4	36	6	AX092228	AX092228 Sequence
C 600	12.2	37.0	50	6	CQ008835	CQ008835 Sequence	673	12	36.4	37	6	A03922	A03922 Nucleotide
C 601	12.2	37.0	50	6	CQ008836	CQ008836 Sequence	674	12	36.4	37	6	A03931	A03931 Nucleotide
C 602	12.2	37.0	50	6	AR282139	AR282139 Sequence	675	12	36.4	37	6	CQ759376	CQ759376 Sequence
C 603	12.2	37.0	50	6	AX225280	AX225280 Sequence	676	12	36.4	37	6	AR473388	AR473388 Sequence

677	12	36.4	37	6	BD138024	BD138024 Expressio	750	12	36.4	49	6	C0812187	C0812187 Sequence
678	12	36.4	38	6	AR045482	Sequence	751	12	36.4	49	6	C0816633	Sequence
679	12	36.4	38	6	AR045482	Sequence	752	12	36.4	49	6	AX451996	Sequence
680	12	36.4	38	6	AR046424	Sequence	753	12	36.4	49	6	AX452003	Sequence
681	12	36.4	38	6	AR047527	Sequence	754	12	36.4	49	6	AX538088	Sequence
682	12	36.4	38	6	I52534	Sequence 80	755	12	36.4	49	6	AX538088	Sequence
683	12	36.4	38	6	I52534	Sequence 27	756	12	36.4	49	6	AX538775	Sequence
684	12	36.4	38	6	I53476	Sequence 12	757	12	36.4	49	6	AX538786	Sequence
685	12	36.4	38	6	I54579	Sequence 23	758	12	36.4	50	6	AR032866	Sequence
686	12	36.4	38	6	I54579	Sequence 80	759	12	36.4	50	6	AR032866	Sequence
687	12	36.4	38	6	AR182142	Sequence	760	12	36.4	50	6	C0008995	Sequence
688	12	36.4	38	6	AR286888	Sequence	761	12	36.4	50	6	C0818808	Sequence
689	12	36.4	38	6	AR287080	Sequence	762	12	36.4	50	6	I29606	Sequence 47
690	12	36.4	38	6	AR330026	Sequence	763	12	36.4	50	6	I29606	Sequence 47
691	12	36.4	38	6	AR330279	Sequence	764	12	36.4	50	6	AR209530	Sequence
692	12	36.4	38	6	AR330833	Sequence	765	12	36.4	50	6	AR486916	Sequence
693	12	36.4	38	6	AR331579	Sequence	766	12	36.4	50	6	AR486928	Sequence
694	12	36.4	38	6	AR332280	Sequence	767	12	36.4	50	6	AX418536	Sequence
695	12	36.4	38	6	AR332374	Sequence	768	12	36.4	50	6	AX418548	Sequence
696	12	36.4	38	6	AR332774	Sequence	769	12	36.4	50	6	AX538790	Sequence
697	12	36.4	38	6	AR333379	Sequence	770	12	36.4	50	6	AX538790	Sequence
698	12	36.4	38	6	AR333552	Sequence	771	11.8	35.8	17	6	AX952287	Sequence
699	12	36.4	38	6	AR334446	Sequence	772	11.8	35.8	17	6	AX960361	Sequence
700	12	36.4	38	6	AR334634	Sequence	773	11.8	35.8	17	6	AX457016	Sequence
701	12	36.4	38	6	AR334881	Sequence	774	11.8	35.8	18	6	AX781782	Sequence
702	12	36.4	38	6	AR335180	Sequence	775	11.8	35.8	18	6	BD244767	Isolation
703	12	36.4	38	6	AR336234	Sequence	776	11.8	35.8	19	6	AR255273	Sequence 13
704	12	36.4	38	6	AR339878	Sequence	777	11.8	35.8	19	6	I33289	Sequence
705	12	36.4	38	6	AR399070	Sequence	778	11.8	35.8	20	6	AX286618	Sequence
706	12	36.4	38	6	AX166338	Sequence	779	11.8	35.8	20	6	AR009308	Sequence
707	12	36.4	38	6	AX169683	Sequence	780	11.8	35.8	20	6	AR009367	Sequence
708	12	36.4	38	6	AX219766	Sequence	781	11.8	35.8	20	6	AR220993	Sequence
709	12	36.4	38	6	AX219836	Sequence	782	11.8	35.8	20	6	AR475590	Sequence
710	12	36.4	38	6	AX222319	Sequence	783	11.8	35.8	20	6	AX119392	Sequence
711	12	36.4	38	6	AX222379	Sequence	784	11.8	35.8	20	6	AX293633	Sequence
712	12	36.4	38	6	AX227957	Sequence	785	11.8	35.8	20	6	AX293842	Sequence
713	12	36.4	38	6	AX273746	Sequence	786	11.8	35.8	21	6	AX488338	Sequence
714	12	36.4	38	6	AX273985	Sequence	787	11.8	35.8	21	6	AB1440	Sequence 3
715	12	36.4	38	6	AX424347	Sequence	788	11.8	35.8	21	6	AB1609	Sequence 3
716	12	36.4	38	6	AX424440	Sequence	789	11.8	35.8	21	6	AX096455	Sequence
717	12	36.4	38	6	AX424902	Sequence	790	11.8	35.8	21	6	AX282116	Sequence
718	12	36.4	38	6	AX425394	Sequence	791	11.8	35.8	21	6	BD005339	Enhanced
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ALIGNMENTS

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LOCUS A method for determination of a nucleic acid using a control.
DEFINITION
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VERSION BD181366.1 GI:30792284
KEYWORDS JP 2002335981-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1 (bases 1 to 34)
          Jaeger,S.
AUTHORS A method for determination of a nucleic acid using a control
TITLE Patent: JP 2002335981-A 5 26-NOV-2002;
JOURNAL F. HOFFMANN LA ROCHE AG
COMMENT OS Artificial Sequence
PN JP 2002335981-A/5
PD 26-NOV-2002 JP 2002057515
PF 04-MAR-2002 EP 01105172.9
PR 02-MAR-2001 EP 01105172.9
PI STEPHAN JAEGER
PC C12N15/09,C12Q1/68,G01N33/50,G01N33/53,G01N33/566,G01N33/58,
PC C12N15/00
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Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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LOCUS Sequence 5 from Patent EP1236804.
DEFINITION
ACCESSION AX523946
VERSION AX523946.1 GI:25168877
KEYWORDS synthetic construct
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ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
          Jaeger,S.
AUTHORS A method for determination of a nucleic acid using a control
TITLE Patent: EP 1236804-A 5 04-SEP-2002;
JOURNAL Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
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RESULT 3
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LOCUS Sequence 5 from Patent EP1236805.
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ACCESSION AX524844
VERSION AX524844.1 GI:25169938
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ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
          Jaeger,S.
AUTHORS A method for the determination of a nucleic acid using a control
TITLE Patent: EP 1236805-A 5 04-SEP-2002;
JOURNAL Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
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DEFINITION Sequence 61 from Patent WO0077037.
ACCESSION AX403706
VERSION AX403706.1 GI:21437151
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ashkenazi,A., Baker,K., Botstein,D., Desnoyers,I., Eaton,D.L.,
Ferrara,N., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P., Gurney,A., Kljavin,I.J., Mather,J.,
Napier,M., Pan,J., Paoni,N., Roy,M., Tamas,D., Watanabe,C.,
Williams,P.M., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: WO 0077037-A 61 21-DEC-2000;
Genentech Inc. (US)
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Db 43 GCCACATGAGTGGC-AAGGCGTCTGGT 18

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DEFINITION Sequence 27 from Patent WO2004001032.
ACCESSION CQ753200
VERSION CQ753200.1 GI:44844676
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Vogels,R., Havenga,M.J. and Zuidgeest,D.A.
TITLE Stable adenoviral vectors and methods for propagation thereof
JOURNAL Patent: WO 2004001032-A 27 31-DEC-2003;
Crucell Holland B.V. (NL)
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source Location/Qualifiers
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DEFINITION Sequence 7 from Patent WO03087371.
ACCESSION AX930614
VERSION AX930614.1 GI:40312362
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS de Haan,P.T.
TITLE Antiviral therapy on the basis of rna interference
JOURNAL Patent: WO 03087371-A 7 23-OCT-2003;
Viruvation B.V. (NL)
FEATURES
source Location/Qualifiers
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ORIGIN
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Best Local Similarity 81.8%; Pred. No. 4.5e+04;
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Qy 1 GCCACATGAGTGGCAAGGCGTC 22
Db 12 GCCGATGGTGGCAAGTGGTC 33

RESULT 7
LOCUS BD263504 30 bp DNA linear PAT 17-JUL-2003
DEFINITION Humanized antibody specific to human 4-1BB and medicinal
compositions containing the same.
ACCESSION BD263504
VERSION BD263504.1 GI:33073272
KEYWORDS JP 2002531383-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Hong,H.J., Park,S.S., Kang,Y.J., Kang,C.Y. and Yo,S.K.
TITLE Humanized antibody specific to human 4-1BB and medicinal
compositions containing the same
JOURNAL Patent: JP 2002531383-A 4 24-SEP-2002;
LG CHEMICAL LTD
COMMENT OS Artificial Sequence
PN JP 2002531383-A/4
PD 24-SEP-2002
PF 17-NOV-1999 JP 2000582430
PR 17-NOV-1998 KR 1998/49177,11-MAY-1999 KR 1999/16750 PI
HYO JEONG HONG, SUNG SUP PARK, YOUNG JUN KANG, CHANG YUL KANG, PI
SUNG KWAN YOON
PC A61K39/395, A61K38/00, A61P19/02, A61P29/00, A61P37/06, C07K16/28,
C07K16/46,
PC
C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/09, G01N33/15, G01N33/PC
50,
PC C12N15/00, C12N5/00, A61K37/02
CC primer KX
FH Key Location/Qualifiers
FT source 1..30
/organism="Artificial Sequence".
FEATURES
Location/Qualifiers


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FEATURES             Location/Qualifiers
  source              1..33
                    /organism="unidentified"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32644"
ORIGIN
Query Match          46.7%; Score 15.4; DB 6; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
    ||||| ||||| ||||| ||||| |||||
Db 32 ATGAGTGGCAGGCGCGGGCGGTAATA 8

RESULT 13
LOCUS AX498638 33 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 28 from Patent EP1229113.
ACCESSION AX498638
VERSION AX498638.1 GI:23343435
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 28 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES             Location/Qualifiers
  source              1..33
                    /organism="unidentified"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32644"
ORIGIN
Query Match          46.7%; Score 15.4; DB 6; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
    ||||| ||||| ||||| ||||| |||||
Db 32 ATGAGTGGCAGGCGCGGGCGGTAATA 8

RESULT 14
LOCUS BD131354/c 33 bp DNA linear PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination
ACCESSION BD131354
VERSION BD131354.1 GI:23226299
KEYWORDS JP 2002500861-A/28.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 33)
AUTHORS Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 28 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Artificial Sequence
PN JP 2002500861-A/28
PD 15-JAN-2002
PP 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
C12N15/09, C12Q1/68, C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
FT source 1..33

FEATURES             Location/Qualifiers
  source              1..33
                    /organism="unassigned DNA"
                    /db_xref="taxon:32644"
ORIGIN
Query Match          46.7%; Score 15.4; DB 6; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
    ||||| ||||| ||||| ||||| |||||
Db 32 ATGAGTGGCAGGCGCGGGCGGTAATA 8

RESULT 15
LOCUS AR048018 34 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 22 from patent US 5820871.
ACCESSION AR048018
VERSION AR048018.1 GI:5970361
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Palese, P. and Garcia-Sastre, A.
TITLE Recombinant negative strand RNA virus expression systems and
vaccines
JOURNAL Patent: US 5820871-A 22 13-OCT-1998;
INVITROGEN CORPORATION (US)
FEATURES             Location/Qualifiers
  source              1..34
                    /organism="unknown"
                    /mol_type="unassigned DNA"
ORIGIN
Query Match          46.7%; Score 15.4; DB 6; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
    ||||| ||||| ||||| ||||| |||||
Db 7 ATGAGTGGCAGGCGCGGGCGGTAATA 31

RESULT 16
LOCUS AR048020 34 bp DNA linear PAT 29-SEP-1999.
DEFINITION Sequence 24 from patent US 5820871.
ACCESSION AR048020
VERSION AR048020.1 GI:5970363
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Palese, P. and Garcia-Sastre, A.
TITLE Recombinant negative strand RNA virus expression systems and
vaccines
JOURNAL Patent: US 5820871-A 24 13-OCT-1998;
INVITROGEN CORPORATION (US)
FEATURES             Location/Qualifiers
  source              1..34
                    /organism="unknown"
                    /mol_type="unassigned DNA"
ORIGIN
Query Match          46.7%; Score 15.4; DB 6; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
    ||||| ||||| ||||| ||||| |||||
Db 7 ATGAGTGGCAGGCGCGGGCGGTAATA 31
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Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 7 ATGAGTGGCAGGCGGGCGGCGTAATA 31

RESULT 22
AR094256 LOCUS 34 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 24 from patent US 6001634.
ACCESSION AR094256
VERSION AR094256.1 GI:10021011
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Palese, P. and Garcia-Sastre, A.
TITLE Recombinant negative strand RNA viruses
JOURNAL Patent: US 6001634-A 24 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..34
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 46.7%; Score 15.4; DB 6; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 7 ATGAGTGGCAGGCGGGCGGCGTAATA 31

RESULT 23
AR048019/c LOCUS 38 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 23 from patent US 5820871.
ACCESSION AR048019
VERSION AR048019.1 GI:5970362
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Palese, P. and Garcia-Sastre, A.
TITLE Recombinant negative strand RNA virus expression systems and vaccines
JOURNAL Patent: US 5820871-A 23 13-OCT-1998;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 46.7%; Score 15.4; DB 6; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGGCGGCGTAATA 8

RESULT 24
AR048021/c LOCUS 38 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 25 from patent US 5820871.
ACCESSION AR048021
VERSION AR048021.1 GI:5970364
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 38)
AUTHORS Palese, P. and Garcia-Sastre, A.
TITLE Recombinant negative strand RNA virus expression systems and vaccines
JOURNAL Patent: US 5820871-A 25 13-OCT-1998;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 46.7%; Score 15.4; DB 6; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGGCGGCGTAATA 8

RESULT 25
AR059773/c LOCUS 38 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 23 from patent US 5840520.
ACCESSION AR059773
VERSION AR059773.1 GI:5986223
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Clarke, D. Kirkwood, and Palese, P. M.
TITLE Recombinant negative strand RNA virus expression systems
JOURNAL Patent: US 5840520-A 23 24-NOV-1998;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 46.7%; Score 15.4; DB 6; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGGCGGCGTAATA 8

RESULT 26
AR068647/c LOCUS 38 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 23 from patent US 5854037.
ACCESSION AR068647
VERSION AR068647.1 GI:6000854
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Palese, P. and Garcia-Sastre, A.
TITLE Recombinant negative strand RNA virus expression systems and vaccines
JOURNAL Patent: US 5854037-A 23 29-DEC-1998;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 46.7%; Score 15.4; DB 6; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8
|||||

RESULT 27
AR068649/c
LOCUS AR068649 38 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 25 from patent US 5854037.
ACCESSION AR068649
VERSION AR068649.1 GI:6000856
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 38)
AUTHORS Palese, P. and Garcia-Sastre, A.
TITLE Recombinant negative strand RNA virus expression systems and vaccines
JOURNAL Patent: US 5854037-A 25 29-DEC-1998;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 46.7%; Score 15.4; DB 6; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8
|||||

RESULT 28
AR094255/c
LOCUS AR094255 38 bp DNA PAT 08-SEP-2000
DEFINITION Sequence 23 from patent US 6001634.
ACCESSION AR094255
VERSION AR094255.1 GI:10021010
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 38)
AUTHORS Palese, P. and Garcia-Sastre, A.
TITLE Recombinant negative strand RNA viruses
JOURNAL Patent: US 6001634-A 23 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 46.7%; Score 15.4; DB 6; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8
|||||

RESULT 29
AR094257/c
LOCUS AR094257 38 bp DNA PAT 08-SEP-2000
DEFINITION Sequence 25 from patent US 6001634.
ACCESSION AR094257
VERSION AR094257.1 GI:10021013
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Palese, P. and Garcia-Sastre, A.
TITLE Recombinant negative strand RNA viruses
JOURNAL Patent: US 6001634-A 25 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 46.7%; Score 15.4; DB 6; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8
|||||

RESULT 30
AR225168/c
LOCUS AR225168 40 bp RNA PAT 26-SEP-2002
DEFINITION Sequence 1 from patent US 6441158.
ACCESSION AR225168
VERSION AR225168.1 GI:23334332
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 40)
AUTHORS Dynan, W.S. and Yoo, S.
TITLE Oligomers that bind to ku protein
JOURNAL Patent: US 6441158-A 1 27-AUG-2002;
FEATURES Location/Qualifiers
source 1..40
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 46.7%; Score 15.4; DB 6; Length 40;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CCACATGAGTGGCAAGCGCTCTGGT 26
|||||
Db 37 CAAGACCAAGTGGGAGGCGGTATGTT 13
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RESULT 31
AX665041/c
LOCUS AX665041 38 bp DNA PAT 26-MAR-2003
DEFINITION Sequence 87 from Patent EP1275728.
ACCESSION AX665041
VERSION AX665041.1 GI:29290196
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS Nomoto, T., Yano, T., Kozaki, S. and Honma, T.
TITLE Polyhydroxyalkanoate-containing structure and manufacturing method thereof
JOURNAL Patent: EP 1275728-A 87 15-JAN-2003;
FEATURES Location/Qualifiers
source 1..38
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer for PCR multiplication"

ORIGIN

Query Match 45.5%; Score 15; DB 6; Length 38;
Best Local Similarity 67.7%;
Matches 21; Conservative 0; Mismatches 10; Indels
Pred. No. 8.6e+04;

Qy 2 CCACATGAGTGGCAAGGCGTCTGGTGATACC 32
Db 38 CAACGTGACCACGACCGCGTTTATTGATACC 8

RESULT 32
AX961520/c

LOCUS	AX961520	38 bp	DNA	linear	PAT 14-JAN-2004
DEFINITION	Sequence 66 from Patent EP1371983.				
ACCESSION	AX961520				
VERSION	AX961520.1	GI:40880979			

KEYWORDS
SOURCE ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
1
HONMA, T.; YANO, T.; NOMOTO, T. and KOZAKI, S.

TITLE Immunoassay, reagent for immunoassay, and production method of the same
JOURNAL Patent: EP 1371983-A 66 17-DEC-2003;

FEATURES	Location/Qualifiers
source	1. .38

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1. 38
source
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="complementary to 65"

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ORIGIN

Query Match 45.5%; Score 15; DB 6; Length 38;
Best Local Similarity 67.7%;
Pred. NO. 8.6e+04;
Matches 21; Conservative 0; Mismatches 10; Indels

Qy 2 CCACATGAGTGGCAAGCGCTCTGTGATACC 32
| | | | | | | | | | | | | | | |
Db 38 CAACGTGACCAAGCACC CGCGTTTATTGATACC 8

RESULT 33
AX665040

AX665040	LOCUS	AX665040	Sequence 86 from Patent EP1275728.	46 bp	DNA	linear	PAT 26-MAR-2003
	DEFINITION						
	ACCESSION	AX665040					
	VERSION	AX665040.1	GI:29290195				

KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences

artificial sequences.

AUTHORS NOMOTO, I., IANO, I., KOZAKI, S. and HONMA, I.
TITLE Polyhydroxyalkanoate-containing structure and manufacturing method thereof
JOURNAL Patent: EP 1275728-A 86 15-JAN-2003;

FEATURES	Location/Qualifiers
source	1. .46

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1. 40
source
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer for PCR multiplex

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ORIGIN

Query Match 45.5%; Score 15; DB 6; Length 46;
Best Local Similarity 67.7%; Pred. No. 8.6e+04;
Matches 21; Conservative 0; Mismatches 10; Indels

2 CCACATGAGTGGCAAGGCGTCTGGTGATACC 32

Db
5 CAACGTGACCAGCACCGCGTTATTGATACC 35

AX961519
LOCUS AX961519
DEFINITION Sequence 65 from Patent
ACCESSION AX961519
VERSION AX961519.1 GI:40880978

NEW WORDS
SOURCE
ORGANISM

ORGANISM

REFERENCE

1 Honma, T., Yano, T., Nomoto, T. and Kozaki, S. Immunoadsorbent reagent for immunoassay and production method of the synthetic antigenic sequences.

JOURNAL same
Patent: EP 1371983-A 65 17-DEC-2003;
Canon Kabushiki Kaisha (JP)
FEATURES Location/Qualifiers

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FEATURES
source
1. .46
LOCATION/Qualifiers
/organism="synthetic construct"

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="binding peptide"

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ORIGIN

Query Match 45.5%; Score 15; DB 6; Length 46;
Best Local Similarity 67.7%; Pred. No. 8.6e+04;
Matches 21; Conservative 0; Mismatches 10; Indels

Qy 2 CCACATGACTGGCAAGCGTCTGGTGATACC 32
 | | | | | | | | | | | | | | | |
Db 5 CAACGTGACAGCACC CGCGTTTATTGATACC 35

RESULT 35
C0006075/c

CQ006075/c	CQ006075	50 bp	DNA	linear	PAT 16-JAN-2004
LOCUS					
DEFINITION	Sequence 4715 from Patent WO0147944.				
ACCESSION	CQ006075				
VERSION	CQ006075.1	GI:41012707			

KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

REFERENCE

Shimkute P. A. and Leach M

ARTHROPS

TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

JOURNAL Patent: WO 0147944-A 4715 05-JUL-2001; Curagen Corporation (US)

Curagen Corporation (US)	Location/Qualifiers
1	50

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1. .50
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature
25. .26
/note="Nucleotide deleted between bases 25 and 26"
Accession number C943256.169

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ORIGIN

Query Match 45.5%; Score 15; DB 6; Length 50;
Best Local Similarity 67.7%; Pred.No. 8.6e+04;
Matches 21; Conservative 0; Mismatches 10; Indels

Qy 2 CCACATGAGTGGCAAGGCGTCTGGTGATAACC 32
||| | ||| | ||| | ||| | ||| | |||
Db 49 CCAGCTAAGGGGCCCTGGCCACTGTGTGCACC 19

RESULT 36
AX539350/c
LOCUS AX539350 21 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 137 from Patent WO02059142.
ACCESSION AX539350
VERSION AX539350.1 GI:25272666
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE Polymorphisms in the human gene for the multidrug
resistance-associated protein 1 (mrp-1) and their use in diagnostic
and therapeutic applications
JOURNAL Patent: WO 02059142-A 137 01-AUG-2002;
Epidaurus Biotechnologie AG (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 44.8%; Score 14.8; DB 6; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCCACATGAGTGGCAAGG 18
|||||
Db 18 GCCACAGAGTGGAAAGG 1
RESULT 37
AX539351
LOCUS AX539351 21 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 138 from Patent WO02059142.
ACCESSION AX539351
VERSION AX539351.1 GI:25272668
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE Polymorphisms in the human gene for the multidrug
resistance-associated protein 1 (mrp-1) and their use in diagnostic
and therapeutic applications
JOURNAL Patent: WO 02059142-A 138 01-AUG-2002;
Epidaurus Biotechnologie AG (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 44.8%; Score 14.8; DB 6; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCCACATGAGTGGCAAGG 18
|||||
Db 4 GCCACAGAGTGGAAAGG 21
RESULT 38
BD091354/c
LOCUS BD091354 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods and compositions for detection of specific nucleotide
sequences.
ACCESSION BD091354
VERSION BD091354.1 GI:22636965

KEYWORDS JP 2001522588-A/8.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ramberg,E.R.
TITLE Methods and compositions for detection of specific nucleotide
JOURNAL Patent: JP 2001522588-A 8 20-NOV-2001;
CYGENE INC
COMMENT OS Artificial Sequence
PN JP 2001522588-A/8
PD 20-NOV-2001
PF 12-NOV-1998 JP 2000519613 60/075812 PR
PR 12-NOV-1997 US 60/065378,24-FEB-1998 US
05-MAR-1998 US 60/076872
PI ELLIOT R RAMBERG
PC C12Q1/68,C12N15/09,C12N15/00
CC Description of Artificial Sequence: primary probe FH Key
Location/Qualifiers
FT source 1..30
FT Location/Qualifiers
1..30
/organism="Artificial Sequence".
FEATURES
source
Location/Qualifiers
1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 44.2%; Score 14.6; DB 6; Length 30;
Best Local Similarity 69.0%; Pred. No. 1.3e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 5 CATGAGTGGCAAGCGCTCTGGTGATACCG 33
|||||
Db 30 CCTGAGTAGCAAGCTATCTAGTGGTACTG 2
RESULT 39
A99000/c
LOCUS A99000 40 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 8 from Patent WO9909055.
ACCESSION A99000
VERSION A99000.1 GI:6781957
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 40)
AUTHORS Sablon,E. and Buysee,M.
TITLE INTERFERON-GAMMA-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
JOURNAL Patent: WO 9909055-A 8 25-FEB-1999;
INNOGENETICS NV (BE); SABLON ERWIN (BE)
FEATURES
source
1..40
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 44.2%; Score 14.6; DB 6; Length 40;
Best Local Similarity 69.0%; Pred. No. 1.3e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 4 ACATGAGTGGCAAGCGCTCTGGTGATACC 32
|||||
Db 37 AGATCAGCTGCAAAAGCGCGGTATACC 9
RESULT 40
AR195317/c
LOCUS AR195317 40 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 8 from patent US 6350860.

ORIGIN

Search completed: November 23, 2004, 18:47:14
Job time : 598.247 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:49:29 ; Search time 177.112 Seconds
(without alignments)
978.085 Million cell updates/sec

Title: US-10-087-631B-5
Perfect score: 33
Sequence: 1 gccacatgagtgcaaggctctggtgataccg 33

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3992700

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq_23Sep04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	49.7	23	10	Adf52991 Hepatitis
2	16.4	49.7	23	10	Adf52934 Hepatitis
C 3	16.4	49.7	43	4	Aac87004 Probe use
C 4	16.4	49.7	43	8	Aca04963 Novel hum
C 5	16.4	49.7	43	8	Aca60493 Human sec
C 6	16.4	49.7	43	8	Aca04483 Human sec
C 7	16.4	49.7	43	9	Aca65624 Human sec
C 8	16.4	49.7	43	9	Ada47233 Human sec
C 9	16.4	49.7	43	9	Adc30240 Human sec
C 10	16.4	49.7	43	10	Adg63742 Human sec
C 11	16.4	49.7	43	10	Adc42354 Novel hum
C 12	16.4	49.7	43	12	Adc41156 Human sec
C 13	16.4	49.7	43	12	Adg63591 Human sec
C 14	15.6	47.3	25	9	Adf52992 Human mic
C 15	15.6	47.3	21	10	Adf52946 Hepatitis
C 16	15.4	46.7	21	10	Adf52946 Hepatitis
C 17	15.4	46.7	21	10	Adf53003 Hepatitis
C 18	15.4	46.7	25	9	Adf52909 Human mic
C 19	15.4	46.7	30	3	Adc00911 PCR Prime
C 20	15.4	46.7	33	2	Aat48229 Chloramph
C 21	15.4	46.7	33	2	Aax78962 Oligonucl

95	14.4	43.6	25	9	ACK13456	ACK13456 Human mic	168	13.6	41.2	20	12	ADN96726	Adn96726 Human NOV
96	14.4	43.6	40	5	AA171225	Aa171225 Plasmid p	c 169	13.6	41.2	22	2	AXX85553	Aax85553 PCR prime
97	14.4	43.6	43	12	ADJ95951	Adj95951 Immunogl	170	13.6	41.2	25	9	ACI14695	Act14695 Human mic
98	14.2	43.0	19	12	ADQ62425	Adq62425 Anti-Hist	c 171	13.6	41.2	37	6	AXX91887	Aax91887 Porphoryn
99	14.2	43.0	22	12	ADJ14714	Adj14714 Debrisoqu	172	13.6	41.2	38	6	ACN30324	Acn30324 WNV minus
100	14.2	43.0	22	12	ADJ14518	Adj14518 Debrisoqu	173	13.6	41.2	38	6	ACN29982	Acn29982 WNV minus
101	14.2	43.0	22	12	ADO60620	Ado60620 Human deb	174	13.6	41.2	38	11	ADL52327	Adl52327 Human NOG
102	14.2	43.0	22	12	ADO60817	Ado60817 Human deb	175	13.6	41.2	38	11	ADL56467	Adl56467 Human PRR
103	14.2	43.0	22	12	ADO60917	Ado60917 Human deb	176	13.6	41.2	40	6	AAT95262	Aat95262 Primer fo
104	14.2	43.0	22	12	ADG34433	Adg34433 Humanised	c 177	13.6	41.2	41	6	ABZ48340	Abz48340 Human org
105	14.2	43.0	41	12	ADJ14717	Adj14717 Debrisoqu	c 178	13.6	41.2	41	6	ABZ46176	Abz46176 Human oxg
106	14.2	43.0	41	12	ADJ14521	Adj14521 Debrisoqu	c 179	13.6	41.2	41	6	ABR01168	Abra01168 Human pho
107	14.2	43.0	41	12	ADO60623	Ado60623 Human deb	180	13.6	41.2	42	2	AAQ22420	Aaq22420 Human VH
108	14.2	43.0	41	12	ADO60920	Ado60920 Human deb	181	13.6	41.2	42	2	AAQ44190	Aaq44190 Probe Oli
109	14.2	43.0	41	12	ADO60820	Ado60820 Human deb	182	13.6	41.2	42	2	AAQ37278	Aaq37278 Rearrange
110	14.2	43.0	45	4	AAAC82265	Aaac82265 Human ret	183	13.6	41.2	42	2	AAV12573	Aav12573 Probe oli
111	14.2	43.0	50	4	AAAL34598	Aaal34598 Human SNP	184	13.6	41.2	42	2	AAV73476	Aav73476 Human hea
112	14.2	43.0	50	6	ABZ05608	Abz05608 Human leu	185	13.6	41.2	42	2	AAT70523	Aat70523 Human imm
113	14	42.4	25	9	AC165293	Ac165293 Human mic	186	13.6	41.2	42	2	AAV38165	Aav38165 Probe oli
114	14	42.4	29	12	ADM88540	Adm88540 Gene expr	187	13.6	41.2	42	2	AAV06045	Aav06045 Human VH
115	14	42.4	37	6	ACN19377	Acn19377 WNV Zinz	c 188	13.6	41.2	42	2	AAZ28390	Aaz28390 DNA seque
116	14	42.4	40	2	AAV17256	Aav17256 Primer ML	189	13.6	41.2	42	2	AAZ21961	Aaz21961 Probe spe
117	14	42.4	40	12	ADO47155	Ado47155 PCR prime	190	13.6	41.2	42	10	ADF15433	Adf15433 Human alb
118	14	42.4	41	12	ADH06128	Adh06128 Gene poly	c 191	13.6	41.2	44	3	AAW1687	Aaw1687 Plasmid p
119	14	42.4	45	8	ABZ22715	Abz22715 Oligonucle	c 192	13.6	41.2	44	4	AAW09819	Aaw09819 Oligo #1
120	13.8	41.8	19	10	ADA132173	Ada132173 Human IL-	c 193	13.6	41.2	45	2	AAZ28392	Aaz28392 DNA seque
121	13.8	41.8	21	9	ADA13876	Ada13876 Short int	c 194	13.6	41.2	47	2	AAQ64632	Aaq64632 Probes fo
122	13.8	41.8	21	9	ADA13828	Ada13828 Short int	c 195	13.6	41.2	47	3	AAZ67111	Aaz67111 Human map
123	13.8	41.8	21	9	ADA13821	Ada13821 Short int	c 196	13.6	41.2	49	3	AAZ67111	Aaz67111 TGF-beta-
124	13.8	41.8	21	10	ADF52845	Adf52845 Hepatitis	c 197	13.6	41.2	50	2	AAQ64635	Aaq64635 Probes fo
125	13.8	41.8	21	10	ADF52852	Adf52852 Hepatitis	c 198	13.6	41.2	50	2	AAQ64633	Aaq64633 Probes fo
126	13.8	41.8	21	10	ADF52879	Adf52879 Hepatitis	c 199	13.6	41.2	50	4	AAAL30289	Aaal30289 Human SNP
127	13.8	41.8	22	9	ACC48049	Acc48049 Cauliflow	c 200	13.6	41.2	50	4	AAAL28898	Aaal28898 Human SNP
128	13.8	41.8	22	9	ACC48048	Acc48048 Cauliflow	c 201	13.6	41.2	50	4	AAH50314	Aah50314 Bacterial
129	13.8	41.8	23	2	AAV53058	Aav53058 Cytochrom	c 202	13.6	41.2	50	6	ABZ02253	Abz02253 Human leu
130	13.8	41.8	23	2	AAV37918	Aav37918 Antisense	c 203	13.4	40.6	20	4	AD04744	Ado4744 Sindbis v
131	13.8	41.8	23	3	AAZ57241	Aaz57241 Human mlt	c 204	13.4	40.6	21	2	AAV05133	Aav05133 Probe use
132	13.8	41.8	23	3	AAA29276	Aaa29276 Primer 2C	c 205	13.4	40.6	21	3	AAA63562	Aaa63562 Oligonucle
133	13.8	41.8	23	3	AAZ67603	Aaz67603 Alzheimer	c 206	13.4	40.6	22	3	AAZ37863	Aaz37863 PCR prime
134	13.8	41.8	23	4	AAO06352	Aao06352 Murine cy	c 207	13.4	40.6	22	12	ADQ80760	Adq80760 Porcine 3
135	13.8	41.8	23	4	AAO08723	Aao08723 Murine cy	c 208	13.4	40.6	24	6	AB185869	Abi85869 Capture o
136	13.8	41.8	25	9	AC157908	Ac157908 Human mic	c 209	13.4	40.6	24	6	AB185868	Abi85868 Capture o
137	13.8	41.8	25	9	AC123709	Ac123709 Human mic	c 210	13.4	40.6	25	9	ACI71428	Act71428 Human mic
138	13.8	41.8	25	9	AC197719	Ac197719 Human mic	c 211	13.4	40.6	25	10	ADL07659	Adl07659 Bacterial
139	13.8	41.8	29	4	AAZ57338	Aaz57338 3' primer	c 212	13.4	40.6	25	12	AD014104	Ado14104 Corynebact
140	13.8	41.8	29	10	ADB79349	Adb79349 E-tag med	c 213	13.4	40.6	27	6	ABS61064	Abs61064 Human aut
141	13.8	41.8	30	2	AAV25364	Aav25364 PCR prime	c 214	13.4	40.6	27	12	ADO06564	Ado06564 Methylo
142	13.8	41.8	31	2	AAZ06122	Aaz06122 Human bia	c 215	13.4	40.6	30	12	ADN11910	Adn11910 M tritici
143	13.8	41.8	36	2	AAQ10260	Aaq10260 Probe R83	c 216	13.4	40.6	31	8	ACD43580	Act43580 Human gen
144	13.8	41.8	36	6	ABX02714	Abx02714 HCV hamme	c 217	13.4	40.6	33	2	AAQ67027	Aaq67027 3' end of
145	13.8	41.8	38	4	ABK05335	Abk05335 Human NOG	c 218	13.4	40.6	33	6	ABZ25712	Abz25712 Human NAD
146	13.8	41.8	38	6	ACN17610	Acn17610 WNV Inozy	c 219	13.4	40.6	33	8	ABZ57491	Abz57491 Pogo tran
147	13.8	41.8	38	6	ACN28284	Acn28284 WNV minus	c 220	13.4	40.6	33	12	ADH39833	Adh39833 Subtilisi
148	13.8	41.8	39	8	ABZ99487	Abz99487 FGF-8 rel	c 221	13.4	40.6	34	8	ABZ24404	Abz24404 HIV envel
149	13.8	41.8	39	8	ABZ99488	Abz99488 FGF-8 rel	c 222	13.4	40.6	34	10	ACF79710	Act79710 HIV-1 env
150	13.8	41.8	39	10	ADE36524	Ad36524 Anti-FGF-	c 223	13.4	40.6	35	6	ABR85547	Ab85547 35S promo
151	13.8	41.8	39	10	ABZ36525	Abz36525 Anti-FGF-	c 224	13.4	40.6	37	6	ACN31006	Acn31006 WNV minus
152	13.8	41.8	41	6	ABZ45699	Abz45699 Human ATP	c 225	13.4	40.6	37	6	ACN18972	Acn18972 WNV Zinz
153	13.8	41.8	41	6	ABZ47899	Abz47899 Human ATP	c 226	13.4	40.6	38	2	AAO88041	Aao88041 Oligo U6A
154	13.8	41.8	41	6	ABZ48034	Abz48034 Human ATP	c 227	13.4	40.6	38	2	AAO36439	Aao36439 U6 specif
155	13.8	41.8	41	10	ABZ57521	Abz57521 IGF bindi	c 228	13.4	40.6	38	8	ABZ24403	Abz24403 HIV envel
156	13.8	41.8	41	10	ABZ57522	Abz57522 IGF bindi	c 229	13.4	40.6	38	10	ACF79709	Act79709 HIV-1 env
157	13.8	41.8	43	8	AAZ55658	Aaz55658 5' forwar	c 230	13.4	40.6	41	6	ABA93677	Ab93677 Human kin
158	13.8	41.8	44	10	ADB38873	Adb38873 PCR prime	c 231	13.4	40.6	41	6	ABA93677	Ab93677 Human kin
159	13.8	41.8	47	4	AAI76615	Aai76615 Human sal	c 232	13.4	40.6	41	6	ABZ50260	Abz50260 Human tra
160	13.8	41.8	48	2	AAZ99204	Aaz99204 M. avium	c 233	13.4	40.6	41	6	ABZ43433	Abz43433 Human tra
161	13.8	41.8	50	4	AAO03080	Aao03080 1466-92 P	c 234	13.4	40.6	41	6	ABZ44615	Abz44615 Human ATP
162	13.8	41.8	50	6	ADZ05885	Adz05885 Human leu	c 235	13.4	40.6	41	6	ABZ47083	Abz47083 Human ATP
163	13.8	41.8	50	12	ADP93338	Adp93338 Microorga	c 236	13.4	40.6	41	11	ADP75529	Adp75529 Human ADA
164	13.6	41.2	20	2	AAZ27015	Aaz27015 Kappa fat	c 237	13.4	40.6	42	2	AAQ54958	Aaq54958 cyd-lac2
165	13.6	41.2	20	2	AAZ95010	Aaz95010 Castor ka	c 238	13.4	40.6	49	10	ADC03175	Adc03175 Colon spe
166	13.6	41.2	20	9	ACD06830	Act06830 Forward R	c 239	13.4	40.6	50	2	AAV81433	Aav81433 Antisense
167	13.6	41.2	20	10	ADC98371	Act98371 ITGA08 po	c 240	13.4	40.6	50	2	AAZ26185	Aaz26185 Antisens

C 241	13.4	40.6	50	4	AAI76317	Aai76317 Human sil	314	13.2	40.0	40	12	ADP53987	Adp53987 Positive
242	13.4	40.6	50	6	ABZ05256	Abz05256 Human leu	315	13.2	40.0	40	12	ADP53965	Adp53965 Candida a
C 243	13.2	40.0	19	12	ADQ62427	Adq62427 Anti-HIST	316	13.2	40.0	41	6	ABS58364	Abs58364 Hmonorphi
C 244	13.2	40.0	20	4	AAH47274	Aah47274 Nucleotid	C 317	13.2	40.0	41	6	ABZ50275	Abz50275 Human cyt
245	13.2	40.0	20	10	ADF72267	Adf72267 Human CD4	C 318	13.2	40.0	41	6	ABZ44450	Abz44450 Human cyt
246	13.2	40.0	20	10	ABZ92207	Abz92207 Human oli	C 319	13.2	40.0	41	8	ABZ57493	Abz57493 Pogo tran
C 247	13.2	40.0	20	11	ABD28437	Abd28437 R78585-de	320	13.2	40.0	42	2	AAT93080	Aat93080 PCR prime
C 248	13.2	40.0	21	2	AXA226635	Axa226635 PCR prime	321	13.2	40.0	42	9	ADB39065	Adb39065 Human tra
C 249	13.2	40.0	21	4	AAF96245	Aaf96245 Human gen	C 322	13.2	40.0	43	6	AAI46486	Aai46486 M catarrh
C 250	13.2	40.0	21	6	ABS66806	Abs66806 Human MRP	323	13.2	40.0	44	2	AAV74273	Aav74273 HTLV-III
251	13.2	40.0	21	6	ABS66807	Abs66807 Human MRP	C 324	13.2	40.0	44	6	ABO78093	Abq78093 HuVKF tel
252	13.2	40.0	21	8	ACF62441	Acf62441 Cancer ba	C 325	13.2	40.0	44	6	ABQ78087	Abq78087 Humanised
C 253	13.2	40.0	21	8	ACF62440	Acf62440 Cancer ba	C 326	13.2	40.0	44	6	ABK15776	Abk15776 Mutation
254	13.2	40.0	21	8	ADB21112	Adb21112 MRP1 base	C 327	13.2	40.0	44	8	ACA171684	Act171684 Human ATP
C 255	13.2	40.0	21	8	ADB21111	Adb21111 MRP1 base	C 328	13.2	40.0	44	8	ACA171602	Act171602 Humanised
C 256	13.2	40.0	21	10	ADB88200	Adb88200 Human UGT	329	13.2	40.0	44	9	ACD27913	Acd27913 E' bacter
257	13.2	40.0	21	10	ADB88201	Adb88201 Human UGT	C 330	13.2	40.0	44	10	ACD13576	Acd13576 Humanised
C 258	13.2	40.0	21	10	ADB97183	Adb97183 Human MRP	C 331	13.2	40.0	44	12	ADH29128	Adh29128 Humanised
C 259	13.2	40.0	21	10	ADB97184	Adb97184 Human MRP	332	13.2	40.0	44	12	ADO26438	Ado26438 HTLV-III
260	13.2	40.0	21	10	ADB92375	Adb92375 Human MRP	333	13.2	40.0	44	12	AAQ95042	Aaq95042 Human hip
C 261	13.2	40.0	21	10	ADB92374	Adb92374 Human MRP	334	13.2	40.0	45	2	AAQ95042	Aaq95042 Human hip
262	13.2	40.0	21	12	ADO16379	Ado16379 4 synthet	335	13.2	40.0	45	3	AAA40154	Aaa40154 H. pylori
263	13.2	40.0	22	2	AAT08691	Aat08691 CRH relat	336	13.2	40.0	45	6	ABK88133	Abk88133 DNA encod
264	13.2	40.0	25	9	ACI41258	Act41258 Human mic	337	13.2	40.0	45	9	AAI60622	Aai60622 Mouse ant
265	13.2	40.0	25	9	ACI91817	Act91817 Human mic	338	13.2	40.0	45	12	ADJ87929	Adj87929 Mouse Hef
266	13.2	40.0	25	10	ADF62961	Adf62961 Human PCC	339	13.2	40.0	47	3	AAZ68644	Aaz68644 Human map
267	13.2	40.0	25	10	ADF62958	Adf62958 Human PCC	340	13.2	40.0	47	3	AAZ68644	Aaz68644 Human map
268	13.2	40.0	25	10	ADF62959	Adf62959 Human PCC	341	13	39.4	16	2	AAZ57818	Aaz57818 PCR prime
269	13.2	40.0	25	10	ADF62960	Adf62960 Human PCC	C 342	13	39.4	17	2	AAZ57838	Aaz57838 PCR prime
270	13.2	40.0	25	10	ADF62957	Adf62957 Human PCC	C 343	13	39.4	17	10	ADH79342	Adh79342 Human pro
271	13.2	40.0	25	10	ADF62955	Adf62955 Human PCC	344	13	39.4	20	2	AAZ79780	Aaz79780 PCR prime
272	13.2	40.0	25	10	ADF62962	Adf62962 Human PCC	345	13	39.4	20	10	ADF32512	Adf32512 Chlamydia
273	13.2	40.0	25	10	ADF62956	Adf62956 Human PCC	C 346	13	39.4	21	12	ADQ78336	Adq78336 Bovine po
274	13.2	40.0	25	12	ADP16940	Adp16940 Renal cel	C 347	13	39.4	22	2	AAQ68521	Aaq68521 Bacillus
C 275	13.2	40.0	28	10	ADD01566	Add01566 Human Fc	C 348	13	39.4	22	2	AAQ68521	Aaq68521 Bacillus
C 276	13.2	40.0	29	12	ADE52184	Ade52184 Rhesus mo	C 349	13	39.4	24	6	ABX97283	Abx97283 Human NOV
C 277	13.2	40.0	30	3	AAE64835	Aae64835 PCR prime	350	13	39.4	24	12	ADN62185	Adn62185 Human NOV
C 278	13.2	40.0	30	3	AAE64836	Aae64836 PCR prime	C 351	13	39.4	25	3	AAA68806	Aaa68806 Bacteriop
C 279	13.2	40.0	30	5	AAI16849	Aai16849 Mutagenic	C 352	13	39.4	25	9	ACH64741	Ach64741 DNA targe
280	13.2	40.0	30	5	ADL16848	Adl16848 Mutagenic	353	13	39.4	25	10	ADF65284	Adf65284 Human PCC
C 281	13.2	40.0	32	12	ADJ93354	Adj93354 Bptatase 3	354	13	39.4	25	10	ADF65287	Adf65287 Human PCC
C 282	13.2	40.0	33	2	AT42740	Aat42740 Human FGF	355	13	39.4	25	10	ADF65285	Adf65285 Human PCC
283	13.2	40.0	33	2	AAV23987	Aav23987 PCR prime	356	13	39.4	25	10	ADF65286	Adf65286 Human PCC
284	13.2	40.0	33	3	AAA75025	Aaa75025 PCR prime	357	13	39.4	25	10	ADF65288	Adf65288 Human PCC
285	13.2	40.0	33	3	AAA75027	Aaa75027 PCR prime	C 358	13	39.4	26	6	ABX78782	Abx78782 Human NOV
286	13.2	40.0	33	3	AAA75029	Aaa75029 PCR prime	C 359	13	39.4	26	10	ADD28531	Add28531 Escherich
287	13.2	40.0	33	5	AAZ91273	Aaz91273 Human FGF	C 360	13	39.4	26	10	ADD28530	Add28530 Escherich
288	13.2	40.0	33	5	AAZ91271	Aaz91271 Human FGF	361	13	39.4	27	3	AAZ62085	Aaz62085 Hammerhea
289	13.2	40.0	33	5	AAZ91269	Aaz91269 Human FGF	362	13	39.4	27	3	AAZ62334	Aaz62334 Hammerhea
290	13.2	40.0	35	2	AAZ32397	Aaz32397 PCR prime	363	13	39.4	29	2	AAZ23442	Aaz23442 Human p75
C 291	13.2	40.0	35	8	ABZ24402	Abz24402 HIV envel	364	13	39.4	30	2	AAZ24471	Aaz24471 Bovine my
C 292	13.2	40.0	35	10	ACF79708	Acf79708 HIV-1 env	365	13	39.4	33	3	AAA05658	Aaa05658 Oligonuc
C 293	13.2	40.0	38	4	AH96412	Ah96412 Human Chk	C 366	13	39.4	33	3	AAZ57745	Aaz57745 PCR prime
294	13.2	40.0	38	4	ABK05936	Abk05936 Human NOG	C 367	13	39.4	33	3	AAZ57745	Aaz57745 PCR prime
295	13.2	40.0	38	4	ABL47859	AbL47859 Human GRI	C 368	13	39.4	35	10	ADH71103	Adh71103 Infectiou
C 296	13.2	40.0	38	6	ABK20266	Abk20266 Human ERG	C 369	13	39.4	35	10	ADH62859	Adh62859 Infectiou
297	13.2	40.0	38	6	ABK20299	Abk20299 Human ERG	370	13	39.4	37	6	ACN19632	Acn19632 WNV Zinz
C 298	13.2	40.0	38	6	ACN15983	Act15983 WNV Hamme	C 371	13	39.4	38	3	AAZ39308	Aaz39308 Human sta
C 299	13.2	40.0	38	6	ACN29981	Act29981 WNV minus	372	13	39.4	38	6	ABS52995	Abs52995 Human sta
C 300	13.2	40.0	38	6	ACN15467	Act15467 WNV Hamme	373	13	39.4	38	10	ADI30572	Adi30572 Human sta
C 301	13.2	40.0	38	6	ACN30138	Act30138 WNV minus	374	13	39.4	38	10	ADI30572	Adi30572 Human sta
302	13.2	40.0	38	6	ACN26240	Act26240 WNV minus	C 375	13	39.4	39	2	AAV72036	Aav72036 Human CPG
C 303	13.2	40.0	38	6	ACD50802	Act50802 HBV hamme	C 376	13	39.4	41	2	AAV47778	Aav47778 Maize pol
304	13.2	40.0	38	10	ADB67710	Adb67710 HIV-1 nef	C 377	13	39.4	41	2	AAV47777	Aav47777 Maize pol
C 305	13.2	40.0	38	11	ADL55798	Adl55798 Human PKR	C 378	13	39.4	41	4	AAI71685	Aai71685 Human ATP
C 306	13.2	40.0	38	11	ADL55915	Adl55915 Human PKR	C 379	13	39.4	41	4	AAI71684	Aai71684 Human ATP
307	13.2	40.0	38	11	ADMS5144	Adm55144 Zinzyme t	C 380	13	39.4	41	6	ABZ46650	Abz46650 Human ATP
308	13.2	40.0	38	12	ADQ38174	Adq38174 HIV envel	381	13	39.4	41	6	ABZ49877	Abz49877 Human HNK
309	13.2	40.0	38	12	ADO38206	Ado38206 HIV envel	382	13	39.4	41	6	ABZ43693	Abz43693 Human HNK
310	13.2	40.0	38	12	ADO38095	Ado38095 HIV envel	383	13	39.4	41	9	ADA01593	Ada01593 Mouse car
311	13.2	40.0	38	12	ADO38063	Ado38063 HIV envel	384	13	39.4	41	10	ADB71332	Adb71332 Mouse car
312	13.2	40.0	39	2	AAT85562	Aat85562 HIV-1 LAI	C 385	13	39.4	42	2	AAT13811	Aat13811 Murine VR
C 313	13.2	40.0	40	8	ABV77144	Abv77144 Reverse p	386	13	39.4	42	2	AAT86880	Aat86880 Plasmid p

387	13	39.4	42	2	AAV64697	Aav64697 HIV anti-	c 460	12.8	38.8	38	8	ACA07304	Aca07304 Necrosis
388	13	39.4	42	3	AA12575	Aa12575 PCR prime	461	12.8	38.8	38	12	ADN97472	Adn97472 Artificia
389	13	39.4	42	4	AH24709	Aah24709 Nucleotid	c 462	12.8	38.8	39	2	AAQ74723	Aaq74723 KHCv NS3
c 390	13	39.4	42	6	AD30364	Aad30364 vpu (-) p	c 463	12.8	38.8	41	6	AD22961	Aad22961 Human Zal
391	13	39.4	42	8	AC74015	Aca74015 Hepatitis	c 464	12.8	38.8	41	9	ADA44847	Ada44847 Primer #2
c 392	13	39.4	45	2	AA35016	Aat35016 TIMP-1/fi	c 465	12.8	38.8	42	3	AA299138	Aaz299138 B. subtil
393	13	39.4	46	2	AA52176	Aax02176 E. coli d	c 466	12.8	38.8	42	4	AAH79307	Aah79307 Hepatitis
c 394	13	39.4	47	2	AA52568	Aax52568 Human gen	c 467	12.8	38.8	45	8	AAH51304	Aad51304 Primer #9
395	13	39.4	47	3	AA26746	Aaz67466 Human map	c 468	12.8	38.8	47	12	ADN11492	Adn11492 Ubiquitin
c 396	13	39.4	47	3	AA267153	Aaz67153 Human map	c 469	12.8	38.8	48	4	AAD20760	Aad20760 Human PHI
397	13	39.4	48	1	AAH71061	Aan71061 5'-3' pro	c 470	12.8	38.8	48	10	ABX79115	Abx79115 Mucin 1 b
398	13	39.4	48	2	AA59202	Aax9202 M. bovis	471	12.8	38.8	49	9	ACC58597	Acc58597 Anti-tiss
c 399	13	39.4	48	2	AA59202	Aax9202 M. tuberc	472	12.8	38.8	49	12	ADL35039	Adl35039 Mitegenic
400	13	39.4	48	2	AA59205	Aax9205 M. fortui	c 473	12.8	38.8	50	2	AAQ57535	Aaq57535 PCR prime
c 401	13	39.4	48	10	AA60636	Aad60636 L1B3E1 DN	c 474	12.8	38.8	50	2	AAV76678	Aav76678 Staphyloc
c 402	13	39.4	50	4	AA131050	Aal31050 Human SNP	c 475	12.8	38.8	50	4	AA129512	Aal29512 Human SNP
c 403	13	39.4	50	4	AA128847	Aal28847 Human SNP	c 476	12.8	38.8	50	4	AA133862	Aal33862 Human SNP
c 404	13	39.4	50	4	AA131051	Aal31051 Human SNP	c 477	12.8	38.8	50	6	ABZ00101	Abz00101 Human leu
c 405	13	39.4	50	6	ABZ00993	Abz00993 Human leu	c 478	12.8	38.8	50	6	ABZ04903	Abz04903 Human leu
c 406	13	39.4	50	10	ADD93341	Ad93341 Flt1 gene	c 479	12.8	38.8	50	6	ABZ07389	Abz07389 Human leu
c 407	12.8	38.8	18	9	AA57831	Aad57831 Reverse p	c 480	12.8	38.8	50	6	ABZ01452	Abz01452 Human leu
c 408	12.8	38.8	20	6	AB195509	Abi95509 Capture o	c 481	12.8	38.8	50	6	ABZ07221	Abz07221 Human leu
c 409	12.8	38.8	20	12	ADN89338	Adn89338 Human CD2	c 482	12.8	38.8	50	10	ADG33585	Adg33585 Human DNA
c 410	12.8	38.8	22	4	AAH40177	Aah40177 SNP speci	c 483	12.6	38.2	19	10	ADH16247	Adh16247 Human BAC
c 411	12.8	38.8	24	2	AAQ02607	Aax02607 PCR prime	c 484	12.6	38.2	19	10	ADH16572	Adh16572 Human BAC
c 412	12.8	38.8	24	3	AA22247	Aaf22247 Arabidops	c 485	12.6	38.2	20	12	ADL58756	Adl58756 Human ESM
c 413	12.8	38.8	24	6	AB187569	Abi87569 Capture o	c 486	12.6	38.2	20	12	ADL58704	Adl58704 Human ESM
c 414	12.8	38.8	24	6	AB187568	Abi87568 Capture o	c 487	12.6	38.2	22	3	AA09103	Aaa09103 PCR prime
c 415	12.8	38.8	25	6	ABQ78091	Abq78091 Humanised	c 488	12.6	38.2	22	3	AA09103	Aaa09103 PCR prime
c 416	12.8	38.8	25	6	ABQ78096	Abq78096 HuvKF rel	c 489	12.6	38.2	24	6	AA06026	Aat06026 Oligonuc
c 417	12.8	38.8	25	6	ABK15780	Abk15780 Mutation	c 490	12.6	38.2	24	6	ABQ11868	Abq11868 Oligonuc
c 418	12.8	38.8	25	8	ACF64246	Acf64246 Human var	c 491	12.6	38.2	24	6	ABQ05588	Abq05588 Oligonuc
c 419	12.8	38.8	25	8	ABX10690	Abx10690 Humanisn	c 492	12.6	38.2	24	6	ABQ00791	Abq00791 Oligonuc
c 420	12.8	38.8	25	8	ACA71606	Aca71606 Humanised	c 493	12.6	38.2	24	6	ABQ01834	Abq01834 Oligonuc
c 421	12.8	38.8	25	9	AC144547	Aci44547 Human mic	c 494	12.6	38.2	24	6	AB185872	Abi85872 Capture o
c 422	12.8	38.8	25	9	AC146250	Aci46250 Human mic	c 495	12.6	38.2	24	6	AB185873	Abi85873 Capture o
c 423	12.8	38.8	25	9	ACK13457	Ack13457 Human mic	c 496	12.6	38.2	25	6	ABQ13404	Abq13404 Oligonuc
c 424	12.8	38.8	25	9	AC171479	Aci71479 Human mic	c 497	12.6	38.2	25	6	ABQ13370	Abq13370 Oligonuc
c 425	12.8	38.8	25	9	AC157407	Aci57407 Human mic	c 498	12.6	38.2	25	8	ADB00968	Adb00968 Human MDZ
c 426	12.8	38.8	25	9	ACK23103	Ack23103 Human mic	c 499	12.6	38.2	25	8	ADB00966	Adb00966 Human MDZ
c 427	12.8	38.8	25	9	AC194597	Aci94597 Human mic	c 500	12.6	38.2	25	8	ADB00965	Adb00965 Human MDZ
c 428	12.8	38.8	25	9	AC147508	Aci47508 Human mic	c 501	12.6	38.2	25	8	ADB00964	Adb00964 Human MDZ
c 429	12.8	38.8	25	9	ACH51076	Ach51076 DNA targe	c 502	12.6	38.2	25	8	ADB00970	Adb00970 Human MDZ
c 430	12.8	38.8	25	9	ACH54325	Ach54325 DNA targe	c 503	12.6	38.2	25	8	ADB00967	Adb00967 Human MDZ
c 431	12.8	38.8	25	10	ADC13580	Adc13580 Humanised	c 504	12.6	38.2	25	9	ADB00969	Adb00969 Human MDZ
c 432	12.8	38.8	25	12	ADH29132	Adh29132 Humanised	c 505	12.6	38.2	25	9	ACI99154	Aci99154 Human mic
c 433	12.8	38.8	27	3	AA263264	Aaz63264 Hammerhea	c 506	12.6	38.2	25	9	ACI16186	Aci16186 Human mic
c 434	12.8	38.8	28	2	AAV10595	Aav10595 Primer us	c 507	12.6	38.2	25	9	ACI99780	Aci99780 Human mic
c 435	12.8	38.8	29	2	AAQ53254	Aaq53254 HIV-1 RNA	c 508	12.6	38.2	25	10	ADE50922	Ad50922 Escherich
c 436	12.8	38.8	29	2	AAV91563	Aav91563 Human C-r	c 509	12.6	38.2	27	3	AAZ62969	Aaz62969 Hammerhea
c 437	12.8	38.8	29	3	AAAF01122	Aaf01122 Hammerhea	c 510	12.6	38.2	27	4	AAH39723	Aah39723 SNP speci
c 438	12.8	38.8	29	6	ABSG63199	Absg63199 Identific	c 511	12.6	38.2	28	6	AAZ30365	Aaz30365 nef (+) p
c 439	12.8	38.8	30	3	AAAL6556	Aaal6556 Human MN	c 512	12.6	38.2	29	2	AAZ10217	Aaz10217 PCR prime
c 440	12.8	38.8	30	3	AAAS2475	Aaas2475 Human MN	c 513	12.6	38.2	29	3	AAAF01258	Aaf01258 Hammerhea
c 441	12.8	38.8	30	5	AAAF30540	Aaf30540 Anchor pr	c 514	12.6	38.2	29	12	ADP90908	Adp90908 Human RAS
c 442	12.8	38.8	30	6	ABA92068	Abas2068 Anchor pr	c 515	12.6	38.2	30	2	AAQ63039	Aaq63039 Random re
c 443	12.8	38.8	30	9	ADA19475	Ada19475 Primer Se	c 516	12.6	38.2	30	2	AAQ98318	Aaq98318 bFGF fami
c 444	12.8	38.8	30	10	AAAD64971	Aad64971 Anchor pr	c 517	12.6	38.2	30	2	AAQX98318	Aaqx98318 bFGF fami
c 445	12.8	38.8	30	10	ADI66851	Adi66851 Anchor pr	c 518	12.6	38.2	30	4	AAAF70553	Aaf70553 SELEX exp
c 446	12.8	38.8	31	4	ADQ09871	Adq09871 Human CIP	c 519	12.6	38.2	30	5	AAAS43991	Aas43991 Neisseria
c 447	12.8	38.8	33	6	ABL49836	Ab149836 Human neu	c 520	12.6	38.2	31	2	AAQ79634	Aaq79634 Primer 60
c 448	12.8	38.8	33	6	ABV77374	Abv77374 Zinc fing	c 521	12.6	38.2	31	2	AAH60992	Aah60992 Tomato TD
c 449	12.8	38.8	34	2	AAAT17207	Aat17207 SRE-ZBP D'	c 522	12.6	38.2	33	4	AAH78917	Aah78917 Human spe
c 450	12.8	38.8	34	2	AAAT39162	Aat39162 Primer fo	c 523	12.6	38.2	33	6	ABK10406	Abk10406 Human ATP
c 451	12.8	38.8	35	2	AAV72328	Aav72328 Human ste	c 524	12.6	38.2	33	6	AAH77183	Aah77183 B. burgdo
c 452	12.8	38.8	35	12	ADL65322	Adl65322 Leishmani	c 525	12.6	38.2	33	12	ADH96961	Adh96961 P. aerugi
c 453	12.8	38.8	36	2	AAAT52640	Aat52640 Human ICA	c 526	12.6	38.2	35	2	AAV5964	Aav5964 3' PCR pr
c 454	12.8	38.8	36	6	ABX01886	Abx01886 HCV hamme	c 527	12.6	38.2	35	4	AAV65969	Aav65969 Forward p
c 455	12.8	38.8	37	10	ADP70287	Adp70287 Human pro	c 528	12.6	38.2	36	2	AAQ91229	Aaq91229 Human Wnt
c 456	12.8	38.8	38	3	AAAS4001	Aaas4001 PCR prime	c 529	12.6	38.2	36	2	AAQ56021	Aaq56021 Human TNF
c 457	12.8	38.8	38	4	AAH96429	Aah96429 Human Chk	c 530	12.6	38.2	36	2	AAAT56531	Aat56531 Mouse TNF
c 458	12.8	38.8	38	6	ABK20612	Abk20612 Human ERG	c 531	12.6	38.2	36	2	AAAT57126	Aat57126 RSV IC ha
c 459	12.8	38.8	38	6	ACN16358	Acn16358 Huv Hamme	c 532	12.6	38.2	36	2	AAAT54439	Aat54439 Human IL-

533	12.6	38.2	36	6	ABX02368	Abx02368 HCV hamme	606	12.6	38.2	50	2	AA17494	Aax17494 Test sequ
534	12.6	38.2	36	6	ABX02002	Abx02002 HCV hamme	607	12.6	38.2	50	4	AA130844	Aa130844 Human SNP
535	12.6	38.2	36	6	AD35819	Ad35819 Human MIS	608	12.6	38.2	50	4	AA128905	Aa128905 Human SNP
C 536	12.6	38.2	37	10	ADC59339	Adc59339 Cell deat	C 609	12.6	38.2	50	6	AA20297	Aa20297 Human Ig
C 537	12.6	38.2	37	8	AA151603	Aa151603 Human jun	C 610	12.6	38.2	50	6	AA202320	Aa202320 Human svn
538	12.6	38.2	38	2	AA64192	Aax64192 Rabbit et	611	12.6	38.2	50	6	ABK82985	Abk82985 DNA bindi
539	12.6	38.2	38	4	AAH96852	Aah96852 Human Chk	C 612	12.6	38.2	50	6	AB208063	Ab208063 Human leu
540	12.6	38.2	38	4	ABK04957	Abk04957 Human NOG	C 613	12.6	38.2	50	6	AB202278	Ab202278 Human leu
541	12.6	38.2	38	6	ABK19581	Abk19581 Human ERG	C 614	12.6	38.2	50	6	AB204108	Ab204108 Human leu
542	12.6	38.2	38	6	ABK20506	Abk20506 Human ERG	C 615	12.6	38.2	50	6	AB204909	Ab204909 Human leu
543	12.6	38.2	38	6	ACN17241	Acn17241 WNV Inozy	616	12.6	38.2	50	6	AB203177	Ab203177 Human leu
544	12.6	38.2	38	6	ACN18571	Acn18571 WNV Inozy	C 617	12.6	38.2	50	8	AC71883	Acc71883 Synthetic
545	12.6	38.2	38	6	ACN29921	Acn29921 WNV minus	618	12.6	38.2	50	8	AC71888	Acc71888 Synthetic
546	12.6	38.2	38	6	ACN26039	Acn26039 WNV minus	619	12.6	38.2	50	12	ADE80524	Ade80524 Duplex oi
547	12.6	38.2	38	6	ACN26195	Acn26195 WNV minus	620	12.6	38.2	18	2	AA336717	Aax336717 PCR prime
548	12.6	38.2	38	6	ACN18465	Acn18465 WNV Inozy	621	12.6	38.2	18	4	AA666690	Aac66690 Human PDB
549	12.6	38.2	38	6	ACN17114	Acn17114 WNV Inozy	622	12.6	38.2	18	10	AA59995	Aad59995 Human PDB
550	12.6	38.2	38	8	ACN07006	Acn07006 Necrosis	623	12.6	38.2	18	12	ADM34026	Adm34026 Human PDB
551	12.6	38.2	38	8	ACN07495	Acn07495 Necrosis	C 624	12.6	38.2	18	12	ADP75385	Adp75385 Human NRG
552	12.6	38.2	38	8	ACD50819	Adc50819 HBV hamme	625	12.6	38.2	20	11	AAA73211	Aaa73211 Cyclooxxyg
553	12.6	38.2	38	8	ACD52232	Adc52232 HBV inozy	C 626	12.6	38.2	21	3	AA43612	Aas43612 Corneodes
554	12.6	38.2	38	11	ADL75361	Adl75361 Human PTG	C 627	12.6	38.2	22	5	ABQ74976	Abq74976 Chloromph
555	12.6	38.2	38	11	ADL75364	Adl75364 Human PTG	C 628	12.6	38.2	23	2	AAQ42227	Aaq42227 PCR prime
556	12.6	38.2	38	11	ADL5581	Adl5581 Human PKR	629	12.6	38.2	23	2	ADG78004	Adg78004 Canine di
557	12.6	38.2	38	12	ADM61336	Adm61336 Hepatitis	630	12.6	38.2	23	6	AA597807	Aas97807 Murine SA
558	12.6	38.2	38	12	ADM60642	Adm60642 Hepatitis	631	12.6	38.2	23	12	ADM16147	Adm16147 Murine SA
559	12.6	38.2	39	2	AAQ99901	Aaq99901 Humanized	C 632	12.6	38.2	24	3	AAZ98411	Aaz98411 Rat GAPDH
560	12.6	38.2	39	2	AA74767	Aat74767 Alpha-4 i	633	12.6	38.2	24	4	AD03677	Aad03677 2C21763 P
561	12.6	38.2	39	2	AAV85722	Aav85722 LRP5 exon	C 634	12.6	38.2	24	6	ABK40750	Abk40750 Rat GAPDH
C 562	12.6	38.2	39	3	AA61063	Aa61063 SEN virus	C 635	12.6	38.2	24	6	ABK05030	Abk05030 Human foc
563	12.6	38.2	39	4	AAFP8605	Aaf8605 PCR prime	C 636	12.6	38.2	25	2	AAAT39525	Aat39525 Flea calr
564	12.6	38.2	40	2	AAQ74085	Aaq74085 Human BMP	C 637	12.6	38.2	25	6	ABK40746	Abk40746 Rat GAPDH
565	12.6	38.2	40	3	AAZ95749	Aaz95749 Human bon	C 638	12.6	38.2	25	9	ACK13358	Ack13358 Human mic
C 566	12.6	38.2	40	10	AA60412	Aad60412 R-8D' rev	C 639	12.6	38.2	25	9	ACI54111	Act54111 Human mic
C 567	12.6	38.2	40	12	ADI34581	Adi34581 Human ESM	640	12.6	38.2	25	9	ACI20712	Act20712 Human mic
C 568	12.6	38.2	41	4	AA168175	Adi168175 Human mol	641	12.6	38.2	25	9	ACI48136	Act48136 Human mic
C 569	12.6	38.2	41	6	AAK47591	Abk47591 Human tro	642	12.6	38.2	25	9	ACI88530	Act88530 Human mic
C 570	12.6	38.2	41	6	AB04790	Ab04790 Ribosomal	643	12.6	38.2	25	9	ACI20713	Act20713 Human mic
C 571	12.6	38.2	41	6	AB248987	Ab248987 Human ALD	C 644	12.6	38.2	25	9	ACI22507	Act22507 Human mic
C 572	12.6	38.2	41	6	AB245136	Ab245136 Human ATP	C 645	12.6	38.2	25	9	ACI46878	Act46878 Human mic
C 573	12.6	38.2	41	6	AB246463	Ab246463 Human ALD	C 646	12.6	38.2	25	9	ACI50692	Act50692 Human mic
C 574	12.6	38.2	41	6	AB247731	Ab247731 Human ATP	647	12.6	38.2	25	9	ACK01458	Act01458 Human mic
C 575	12.6	38.2	41	11	ADP75599	Adp75599 Human ADA	C 648	12.6	38.2	25	9	ACH60776	Act60776 DNA targe
C 576	12.6	38.2	41	12	ADK17891	Adk17891 Cytochrom	C 649	12.6	38.2	25	9	ACH51077	Act51077 DNA targe
C 577	12.6	38.2	42	2	ABX17659	Abx17659 Modified	C 650	12.6	38.2	25	10	ADG74293	Adg74293 Human fri
C 578	12.6	38.2	42	2	ABX17658	Abx17658 Modified	651	12.6	38.2	25	12	ADJ58462	Adj58462 Primer #2
C 579	12.6	38.2	42	12	ADQ76049	Adq76049 TBEL in f	652	12.6	38.2	26	2	AAQ56221	Aaq56221 pX amplif
C 580	12.6	38.2	44	2	AA786307	Aat86307 Primer ol	653	12.6	38.2	26	2	AAAT08932	Aat08932 Forward p
C 581	12.6	38.2	45	2	AAQ04944	Aaq04944 Oligonocl	654	12.6	38.2	26	2	AAV66288	Aav66288 5' PCR pr
C 582	12.6	38.2	45	2	AAV27926	Aav27926 rGALR3 pr	655	12.6	38.2	26	2	AAV56251	Aav56251 HCV forwa
C 583	12.6	38.2	45	6	AAAD35869	Aad35869 Rat galan	656	12.6	38.2	26	2	AA16479	Aax16479 PCR prime
C 584	12.6	38.2	45	9	ACD28979	Adc28979 Human gal	657	12.6	38.2	26	2	AA02526	Aax02526 US5856134
C 585	12.6	38.2	45	10	AA61145	Aad61145 Rat galan	658	12.6	38.2	26	2	AAV82222	Aav82222 Spodopter
C 586	12.6	38.2	47	2	AA52568	Aax52568 Human gen	659	12.6	38.2	26	6	ABK65977	Abk65977 Human gen
C 587	12.6	38.2	47	3	AA67153	Aaf67153 Human map	C 660	12.6	38.2	26	12	ADP11332	Adp11332 Taqman pr
C 588	12.6	38.2	47	4	AA61215	Aaf61215 Coxackie	C 661	12.6	38.2	27	12	ADG31438	Adg31438 PCR prime
C 589	12.6	38.2	47	4	AA255336	Aaf255336 Multiplex	C 662	12.6	38.2	27	12	ADK41849	Adk41849 Human MN
C 590	12.6	38.2	47	4	AA255336	Aaf255336 Multiplex	663	12.6	38.2	29	2	AAV00585	Aav00585 PCR prime
C 591	12.6	38.2	48	2	AAQ22423	Aaq22423 Human V k	664	12.6	38.2	29	2	AAAT84969	Aat84969 PCR prime
C 592	12.6	38.2	48	2	AAQ50327	Aaq50327 Human kap	665	12.6	38.2	29	2	AAV17632	Aav17632 Homo sapi
C 593	12.6	38.2	48	2	AAQ44193	Aaq44193 Probe Oli	666	12.6	38.2	29	2	AAV77314	Aax77314 Arginase
C 594	12.6	38.2	48	2	AAAT37184	Aat37184 Human var	667	12.6	38.2	29	2	AAAL7041	Aaal7041 Aryl hydr
C 595	12.6	38.2	48	2	AAAT37281	Aat37281 Human art	668	12.6	38.2	29	2	AAAL7041	Aaal7041 Aryl hydr
C 596	12.6	38.2	48	2	AAV12576	Aav12576 Probe oli	669	12.6	38.2	29	2	AAZ07630	Aaz07630 HCV NS3-N
C 597	12.6	38.2	48	2	AAV73479	Aat73479 Human kap	670	12.6	38.2	29	2	AAV92303	Aav92303 Human A-R
C 598	12.6	38.2	48	2	AAV70526	Aat70526 Human imm	671	12.6	38.2	29	3	AAA03891	Aaa03891 Polymorph
C 599	12.6	38.2	48	2	AAV38172	Aat38172 Probe oli	672	12.6	38.2	29	3	AAA08068	Aaa08068 Human arg
C 600	12.6	38.2	48	2	AAAX06048	Aax06048 Human kap	673	12.6	38.2	29	3	AAAF01215	Aaf01215 Hammerhea
C 601	12.6	38.2	48	2	AAZ21964	Aaz21964 Probe spe	C 674	12.6	38.2	29	4	AAH44062	Aah44062 Human SMN
C 602	12.6	38.2	48	2	AAZ21973	Aaz21973 Probe spe	675	12.6	38.2	29	6	ABA00439	Ab00439 Human arg
C 603	12.6	38.2	50	2	AAQ69744	Aaq69744 Herpes si	676	12.6	38.2	29	6	AAI72345	Aai72345 Human arg
C 604	12.6	38.2	50	2	AA64206	Aat64206 Herpes si	C 677	12.6	38.2	29	8	ADA47346	Ada47346 Mutagenic
C 605	12.6	38.2	50	2	AA231138	Aaz31138 RNA ligan	C 678	12.6	38.2	29	9	ACA62507	ACA62507 Human SMN

679	12.4	37.6	29	12	ADN35130	Adn35130 Primer of	752	12.4	37.6	50	5	ABL01018	Ab101018 Human SNP
680	12.4	37.6	29	12	ADP88461	Adp88461 Antibody	c 753	12.4	37.6	50	6	ABZ02384	Abz02384 Human leu
681	12.4	37.6	30	6	ABS55396	Abs55396 Arabidops	754	12.4	37.6	50	6	ABZ01228	Abz01228 Human leu
682	12.4	37.6	30	10	AAD36857	Aad36857 Chloramph	755	12.2	37.0	17	8	ACD55737	AcD55737 HBV amber
683	12.4	37.6	30	12	ADQ04218	Ado04218 Primer P1	756	12.2	37.0	17	10	ADP62211	Adp62211 Human PCC
684	12.4	37.6	31	8	ABX08328	Abx08328 Forward R	757	12.2	37.0	17	10	ADF62212	Adf62212 Human PCC
685	12.4	37.6	31	11	ADM79775	Adm79775 Thermus t	758	12.2	37.0	17	12	ADM60271	Adm60271 Hepatitis
686	12.4	37.6	32	2	AAV54297	Aav54297 Primer JW	759	12.2	37.0	18	2	AAX36724	Aax36724 PCR prime
687	12.4	37.6	32	2	AAX55379	Aax55379 Soluble s	760	12.2	37.0	18	2	AAX36724	Aax36724 PCR prime
688	12.4	37.6	32	9	ADA73934	Ada73934 Carcinoma	761	12.2	37.0	18	4	AAA92634	Aaa92634 Antisense
689	12.4	37.6	32	9	ADA02408	Ada02408 Mouse car	762	12.2	37.0	18	4	AAC66697	Aac66697 Human PDB
690	12.4	37.6	32	10	ADB72147	Adb72147 Mouse car	763	12.2	37.0	18	10	AA600002	AA600002 Human PDB
691	12.4	37.6	32	10	ADK12384	Adk12384 Cytochrom	764	12.2	37.0	19	12	ADM34033	Adm34033 Human PDB
692	12.4	37.6	33	2	AAX33976	Aax33976 Probe for	765	12.2	37.0	20	3	AA705687	AA705687 HB15 3' I
693	12.4	37.6	33	3	AAA60543	Aaa60543 Human TIE	766	12.2	37.0	20	3	AAZ46684	Aaz46684 Blast dis
694	12.4	37.6	33	4	AA502926	Aaa02926 PCR prime	767	12.2	37.0	20	3	AAA72027	Aaa72027 HIV-1 pro
695	12.4	37.6	33	4	AA168121	Aai68121 Human gro	768	12.2	37.0	20	6	ABK90234	Abk90234 Dog multi
696	12.4	37.6	33	4	AAC97393	Aac97393 Human PRO	769	12.2	37.0	20	6	AA138136	AA138136 HIV-1 RNA
697	12.4	37.6	33	4	AAC90584	Aac90584 Human PRO	770	12.2	37.0	20	9	ACC058259	Acc058259 Primer cl
698	12.4	37.6	33	6	ABL58581	Ab158581 Oligonuc1	771	12.2	37.0	20	9	ACD06833	AcD06833 Forward R
699	12.4	37.6	33	6	ABQ79779	Abq79779 Human TIE	772	12.2	37.0	20	10	ABZ91513	Abz91513 Human oli
700	12.4	37.6	33	6	ADQ32089	Adq32089 Human TIE	773	12.2	37.0	20	10	ABZ98911	Abz98911 Human PDE
701	12.4	37.6	33	9	ACA62660	ACA62660 TIE ligan	774	12.2	37.0	20	11	ABD27743	Abd27743 AA102454-
702	12.4	37.6	33	10	AD133461	Ad133461 DNA oligo	775	12.2	37.0	20	11	ABD31942	Abd31942 Human PDE
703	12.4	37.6	33	10	ABX13830	Abx13830 Human TIE	776	12.2	37.0	20	11	ABD31942	Abd31942 Human PDE
704	12.4	37.6	33	10	ABZ83477	Abz83477 Toxicolog	777	12.2	37.0	20	12	ADH44489	Adh44489 Extracell
705	12.4	37.6	33	12	ADP84074	Adp84074 Small nuc	778	12.2	37.0	20	12	ADJ32665	Adj32665 Human ERK
706	12.4	37.6	34	2	AA700568	Aat00568 Hemagglut	779	12.2	37.0	20	12	ADJ32632	Adj32632 Human ERK
707	12.4	37.6	34	12	ADP67064	Adp67064 TGR5 CDNA	780	12.2	37.0	20	12	ADJ60794	Adj60794 Oligonuc1
708	12.4	37.6	36	3	AA35700	Aaa35700 Fermentin	781	12.2	37.0	20	12	ADO46283	Ado46283 Human oli
709	12.4	37.6	36	6	ABK85548	Abk85548 35S promo	782	12.2	37.0	20	12	ADO53280	Ado53280 Farnesoid
710	12.4	37.6	36	12	AD136970	Ad136970 Human HLR	783	12.2	37.0	20	12	ADO54162	Ado54162 Farnesoid
711	12.4	37.6	36	12	ADQ25971	Adq25971 Method of	784	12.2	37.0	20	12	ADO53113	Ado53113 Farnesoid
712	12.4	37.6	36	12	ADQ25966	Adq25966 Method of	785	12.2	37.0	20	12	ADO54244	Ado54244 Farnesoid
713	12.4	37.6	36	12	ADQ25983	Adq25983 Method of	786	12.2	37.0	20	12	ADN31407	Adn31407 Human for
714	12.4	37.6	37	3	ACA66121	Aac66121 PCR prime	787	12.2	37.0	20	12	ADP85767	Adp85767 Mitochond
715	12.4	37.6	37	4	AAH91231	Aah91231 Human inf	788	12.2	37.0	20	12	ADP85843	Adp85843 Mitochond
716	12.4	37.6	37	6	ACN31163	Acn31163 WNV minus	789	12.2	37.0	21	4	AAF96868	Aaf96868 Human gen
717	12.4	37.6	37	6	ACN19340	Acn19340 WNV Zinzv	790	12.2	37.0	22	4	AAV72810	Aav72810 Tryptophan
718	12.4	37.6	37	6	ACN19683	Acn19683 WNV Zinzv	791	12.2	37.0	22	6	ACA65353	Aca65353 Human TPO
719	12.4	37.6	38	6	ACN145275	Aac145275 Human pap	792	12.2	37.0	22	6	ABL31906	Ab131906 Human CYP
720	12.4	37.6	38	10	ADH79198	Adh79198 Mallard d	793	12.2	37.0	22	10	ABZ99041	Abz99041 Human PDE
721	12.4	37.6	39	2	AAQ22111	Aaq22111 S2 chimera	794	12.2	37.0	22	11	ABD32072	Abd32072 Human PDE
722	12.4	37.6	39	4	AA500942	Aas00942 Beetle lu	795	12.2	37.0	22	12	ADK95817	Adk95817 Primer of
723	12.4	37.6	39	5	AAF28341	Aaf28341 eryAI gen	796	12.2	37.0	22	12	ADJ61300	Adj61300 Oligonuc1
724	12.4	37.6	39	10	ADG79066	Adg79066 Schizophr	797	12.2	37.0	22	12	ADJ60924	Adj60924 Oligonuc1
725	12.4	37.6	39	12	ADL60999	Adl60999 Human org	798	12.2	37.0	22	12	ADO46413	Ado46413 Human oli
726	12.4	37.6	40	3	AAA38886	Aaa38886 PCR prime	799	12.2	37.0	22	12	ADO46690	Ado46690 Human oli
727	12.4	37.6	40	6	ADE31881	Ade31881 Surfactin	800	12.2	37.0	23	2	AAQ32567	Aaq32567 HCV NS4-N
728	12.4	37.6	40	6	ADE31843	Ade31843 Surfactin	801	12.2	37.0	23	2	AAQ35679	Aaq35679 PCR prime
729	12.4	37.6	41	3	ACA66119	Aac66119 PCR prime	802	12.2	37.0	23	10	ADB67778	Adb67778 HIV-1 nef
730	12.4	37.6	41	6	ABA95874	Ab95874 Human dih	803	12.2	37.0	23	12	ADO38170	Ado38170 HIV envel
731	12.4	37.6	41	10	ACC71672	Acc71672 Human mac	804	12.2	37.0	23	12	ADO38059	Ado38059 HIV envel
732	12.4	37.6	41	12	ADK17689	Adk17689 Cytochrom	805	12.2	37.0	24	6	AEQ02757	Abq02757 Oligonuc1
733	12.4	37.6	41	12	ADK17790	Adk17790 Cytochrom	806	12.2	37.0	24	6	AEQ09453	Abq09453 Oligonuc1
734	12.4	37.6	42	3	AAAC66117	Aac66117 PCR prime	807	12.2	37.0	24	6	AEQ09412	Abq09412 Oligonuc1
735	12.4	37.6	42	4	AAF31523	Aaf31523 Oligonuc1	808	12.2	37.0	24	6	ABT03812	Abt03812 Human TRA
736	12.4	37.6	43	6	ABQ74991	Abq74991 Chloramph	809	12.2	37.0	25	2	AAAX77708	Aax77708 Murine Zc
737	12.4	37.6	43	6	ABZ27922	Abz27922 Candida e	810	12.2	37.0	25	6	ABN04854	Abn04854 Human GDM
738	12.4	37.6	43	12	ADJ93304	Adj93304 Ghrelin-b	811	12.2	37.0	25	6	ABN15122	Abn15122 Human GDM
739	12.4	37.6	44	8	ABZ09612	Abz09612 Human oli	812	12.2	37.0	25	8	ADB25828	Adb25828 Human CYP
740	12.4	37.6	44	10	ABZ79065	Abz79065 Tumour su	813	12.2	37.0	25	8	ADB03871	Adb03871 Human MD2
741	12.4	37.6	45	2	AAQ94195	Aaq94195 Transmembr	814	12.2	37.0	25	8	ADB03870	Adb03870 Human MD2
742	12.4	37.6	45	3	AAAS2168	Aaa52168 Haemophil	815	12.2	37.0	25	9	ACK19992	Ack19992 Human mic
743	12.4	37.6	46	8	ACF19116	Acf19116 Tumour ce	816	12.2	37.0	25	9	ACI29518	Act29518 Human mic
744	12.4	37.6	46	8	ABV76178	Abv76178 Chloramph	817	12.2	37.0	25	9	ACI12010	Act12010 Human mic
745	12.4	37.6	46	10	ADC84939	Adc84939 MCP-7 bre	818	12.2	37.0	25	9	ACI97718	Act97718 Human mic
746	12.4	37.6	49	12	ADJ93018	Adj93018 Ghrelin-b	819	12.2	37.0	25	9	ACI35963	Act35963 Human mic
747	12.4	37.6	50	2	AAT40902	Aat40902 HIV neutr	820	12.2	37.0	25	9	ACK00981	Ack00981 Human mic
748	12.4	37.6	50	4	AA134256	Aal34256 Human SNP	821	12.2	37.0	25	9	ACI31493	Act31493 Human mic
749	12.4	37.6	50	4	AA133572	Aal33572 Human SNP	822	12.2	37.0	25	9	ACK08351	Ack08351 Human mic
750	12.4	37.6	50	4	AA060699	Aad06099 Drosophil	823	12.2	37.0	25	9	ACI49017	Act49017 Human mic
751	12.4	37.6	50	4	AAH25964	Aah25964 Rice geno	824	12.2	37.0	25	9	ACI99434	Act99434 Human mic

971	12.2	37.0	47	12	ADN11538	Adn11538
972	12.2	37.0	48	12	ADH17790	Adh17790
973	12.2	37.0	48	12	ADO32116	Ado32116
974	12.2	37.0	48	12	ADO32121	Ado32121
975	12.2	37.0	48	12	ADO38186	Ado38186
976	12.2	37.0	48	12	ADO38075	Ado38075
977	12.2	37.0	49	2	AAZ22836	Aaz22836
978	12.2	37.0	49	10	ADC60966	Adc60966
979	12.2	37.0	50	2	AAW52110	Aaw52110
980	12.2	37.0	50	4	AAU34267	Aau34267
981	12.2	37.0	50	4	AAU34266	Aau34266
982	12.2	37.0	50	4	AAU34268	Aau34268
983	12.2	37.0	50	4	AAU28575	Aau28575
984	12.2	37.0	50	4	AAU17298	Aau17298
985	12.2	37.0	50	6	ABZ02969	Abz02969
986	12.2	37.0	50	6	ABZ04364	Abz04364
987	12.2	37.0	50	12	ADQ303995	Adq303995
988	12.2	37.0	50	12	ADQ303997	Adq303997
989	12	36.4	17	8	ADA99466	Ada99466
990	12	36.4	17	8	ADA99467	Ada99467
991	12	36.4	17	8	ADA99464	Ada99464
992	12	36.4	17	8	ADA99468	Ada99468
993	12	36.4	17	8	ADA99465	Ada99465
994	12	36.4	17	8	ADA99469	Ada99469
995	12	36.4	20	2	AAU73404	Aat73404
996	12	36.4	20	2	AAU93655	Aat93655
997	12	36.4	20	2	AAV00284	Avv00284
998	12	36.4	20	2	AAV83883	Avv83883
999	12	36.4	20	3	AAZ49936	Aaz49936
1000	12	36.4	20	3	AAZ40602	Aaz40602

ALIGNMENTS

RESULT 1	
ADFS52991	
ID	ADFS52991 standard; RNA; 23 BP.
XX	
XX	
AC	ADFS52991;
XX	
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Hepatitis C virus modified siNA sense strand SeqID1582.
XX	
KW	short interfering nucleic acid; siNA; virus replication inhibition;
KW	hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW	hepatocellular cancer; cytotostatic; RNA interference; HCV infection; liver failure;
KW	hepatocellular cancer; cirrhosis; ss.

WPI; 2003-689778/65.

New double-stranded short interfering nucleic acid comprises sugar-
modified pyrimidine bases useful for treating infection with hepatitis C
virus.

Example 3; SEQ ID NO 1582; 183pp; English.

This invention relates to novel double-stranded short interfering nucleic
acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
one strand is an antisense strand (ASS) that is complementary to (part
of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
ASS, and where most of the pyrimidine nucleotides comprise a sugar
modification. The invention may allow development of compounds with
virucide, antiinflammatory, hepatotropic or cytostatic activities by
modulation (inhibition) of expression or activity of HCV RNA, by RNA
interference. The siNA's of the invention may be used to inhibit
replication of HCV, in cells, tissue explants or organisms, for treating
HCV infection and its consequences (liver failure; hepatocellular cancer
and cirrhosis), and also for drug screening, diagnosis, target
identification and validation, genetic engineering, pharmacogenomics,
studying gene function and gene mapping (for example of single-nucleotide
polymorphisms). The chemical modification improves stability, activity,
cellular uptake and/or binding affinity. The siNA can be directed to
conserved regions of HCV genes, so are active against many different
strains. NOTE: This sequence may contain one or more of several
modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
(T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
base 5-nitroindole (X); universal base 3-nitropyrolole (Z). These
modifications are specified in table 3 of the specification (pages 150-
158).

Adnl1538	Mouse	USP
Adh17790	Primer EM	
Ado32116	Mouse ant	
Ado32121	Mouse ant	
Ado32186	HIV envel	
Ado38075	HIV envel	
Aa222836	Extreme t	
Ado60966	NASBA pri	
Axa521110	Synthetic	
Axa134267	Human SNP	
Aa134266	Human SNP	
Aa134268	Human SNP	
Aa128575	Human SNP	
Adb17298	Human rib	
Ab720295	Human leu	
Ab204364	Human leu	
Adq30397	GFP expre	
Adq30399	GFP expre	
AdA99466	Human MDZ	
AdA99467	Human MDZ	
AdA99464	Human MDZ	
AdA99468	Human MDZ	
AdA99465	Human MDZ	
AdA99469	Human MDZ	
Aat73404	S182 gene	
Aat93655	Presenili	
Aav02044	ES-1 gene	
Avu08383	Reverse p	
Aa240962	Human tum	
Aa409602	Human coa	

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PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX PA
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
XX Example 3; SEQ ID NO 1525; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 159).
XX
XX Sequence 23 BP; 3 A; 4 C; 8 G; 2 T; 4 U; 2 Other;
SQ
Query Match 49.7%; Score 16.4; DB 10; Length 23;
Best Local Similarity 77.8%; Pred. No. 2.3e+03;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 12 GCCAAGGCGTCTGGTGAT 29
DB 4 GCCAAGGCGCUGUGAT 21
RESULT 3
AAC87004/c
ID AAC87004 standard; DNA; 43 BP.
AC
AC AAC87004;
XX
XX 20-APR-2001 (first entry)
XX
XX Probe used to isolate cDNA encoding human polypeptide PRO4999.
XX
XX Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW PRO246; PRO265; PRO941; PRO1096; PRO6003; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
KW probe; ss.
XX
XX Homo sapiens.
OS
XX WO200077037-A2.
PN
XX

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PD 21-DEC-2000.
XX 22-MAY-2000; 2000WO-US014042.
XX
XX 15-JUN-1999; 99US-0139695P.
PR 26-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnovers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Klijavin IO, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
XX WPI; 2001-050091/06.
XX
XX Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides.
XX
XX Example 17; Page 112; 244pp; English.
XX
XX The present probe was used to isolate cDNA encoding a human secreted and
XX transmembrane polypeptide. The specification describes human
XX polypeptides, designated PRO196, PRO444, PRO183, PRO185, PRO210, PRO215,
XX PRO217, PRO242, PRO288, PRO365, PRO1361, PRO1308, PRO1183, PRO1272,
XX PRO1419, PRO4999, PRO7170, PRO248, PRO353, PRO1318, PRO1600, PRO9940,
XX PRO533, PRO301, PRO187, PRO337, PRO411, PRO4356, PRO246, PRO265, PRO941,
XX PRO1096, PRO6003, PRO6004, PRO350, PRO2630 and PRO6309. The biological
XX activity of cells can be modulated with agents that bind to these
XX polypeptides, resulting in the death of the cells. The polynucleotides
XX encoding these polypeptides are useful in the recombinant production of
XX the polypeptides, as a hybridisation probe to screen libraries to isolate
XX homologous sequences, or to map the gene. They may also be used for
XX analysing genetic disorders, and to produce transgenic animals which are
XX useful for the development and screening of therapeutically useful
XX reagents. The polynucleotides can also be used in gene therapy e.g. to
XX replace a defective gene
XX
XX Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;
SQ
Query Match 49.7%; Score 16.4; DB 4; Length 43;
Best Local Similarity 76.9%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GCCACATGATGTCGACGCGTCTGCT 26
DB 43 GCCACATGTCGCAAGATGTGCT 18
RESULT 4
ACA04963/c

```

ID ACA04963 standard; DNA; 43 BP.
 AC ACA04963;
 DT 28-MAY-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein related probe #9.
 XX
 KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
 KW PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
 KW PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
 KW fibroblast growth factor receptor; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
 KW obesity; diabetes; insulinemia; vascular permeability;
 KW cardiac insufficiency disorder; immune response; hearing loss;
 KW auditory hair cell regeneration; bone disorder; cartilage disorder;
 KW sports injury; arthritis; probe; ss.
 XX
 OS Homo sapiens.
 XX
 XX US2003032063-A1.
 PN
 XX 13-FEB-2003.
 PD
 XX
 PF 01-FEB-2002; 2002US-00066494.
 XX
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-006364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 10-AUG-1998; 98US-0095998P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 14-SEP-1998; 98WO-US019093.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US0214855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 99WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.

PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL; for
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goodard A;
 PI Gadowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PN;
 PI Wood WI, Zhang Z;
 XX
 DR WPI; 2003-341964/32.

XX Thirty seven nucleic acids encoding novel secreted and transmembrane PRO
 PT polypeptides, useful for modulating biological activity of cell
 PT expressing the polypeptide, and in chromosome and gene mapping.

Example 17; Page 60; 255pp; English.

CC The invention describes an isolated, secreted and transmembrane
 CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
 CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
 CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
 CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
 CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 CC cell expressing the polypeptides. The bioactive molecule causes cell
 CC death. (II) Is useful as hybridisation probes, in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, in the preparation of
 CC PRO polypeptide, for generating transgenic animals or knockout animals
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, and for chromosome
 CC identification. (I) Or Ab is useful for the preparation of medicament for
 CC treating conditions which are responsive to the PRO polypeptide or anti-
 CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
 CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
 CC inhibiting tumour growth, enhances vascular permeability and immune
 CC response, for inducing regeneration of auditory hair cells and for
 CC treating hearing loss in mammals, and for treating bone and/or cartilage
 CC disorders such as sports injuries and arthritis. This sequence represents
 CC a probe used to detect DNA encoding a novel human secreted and
 CC transmembrane polypeptide

Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 8; Length 43;
 Best Local Similarity 76.9%; Pred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGATGGCGAAGGGCTGTGT 26
 DB 43 GCCACAGTTGTGGCAAGATGTGTGT 18

RESULT 5
 ID ACA60493/c
 AC ACA60493 standard; DNA; 43 BP.
 AC ACA60493;
 DT 11-JUN-2003 (first entry)
 DE Human secreted and transmembrane protein related probe #9.
 KW Human; secreted and transmembrane polypeptide; PRO;
 KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
 KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
 KW FGFR-2; PRO6004; PRO4350; PRO2630; PRO265; PRO951; bioactive molecule;
 KW toxin; radiolabel; antibody; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy;
 KW tissue typing; PCR; primer; ss.
 OS Homo sapiens.
 XX US2002177165-A1.
 PN 28-NOV-2002.
 XX 01-FEB-2002; 2002US-00066500.
 XX 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-00591115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062288P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0095998P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 10-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-NAR-1999; 99WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Gadowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW;
 XX Wood WI, Zhang Z;
 DR WPI; 2003-328482/31.
 XX
 PT Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, for identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.
 XX
 PS Example 17; Page 60; 254pp; English.
 CC The invention describes an isolated, secreted and transmembrane
 CC polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
 CC (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337, PRO1411,
 CC PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor receptor
 CC (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or
 CC PRO951 polypeptide, and for linking a bioactive molecule to a cell
 CC expressing the above polypeptides. The bioactive molecule, a toxin,
 CC radiolabel or an antibody, causes cell death. PRO is useful in assays to
 CC identify other proteins or molecules involved in binding interaction. The
 CC polynucleotide (II) encoding (I) is useful in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, for generating
 CC transgenic animals or knockout animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, to
 CC construct hybridisation probes for mapping the gene which encodes the PRO
 CC and for the genetic analysis of individuals with genetic disorders, in
 CC gene therapy, for chromosome identification and as a chromosome marker.
 CC (I) and (II) are useful for tissue typing. This sequence represents a
 CC novel human secreted and transmembrane PRO polypeptide associated primer
 XX
 SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 8; Length 43;
 Best Local Similarity 76.9%; Pred. No. 2.5e+03;

	Matches	20;	Conservative	0;	Mismatches	6;	Indels	0;	Gaps	0;
QY	1	GCACATGATGCGCAGGCGTCTGGT	26							
DB	43	GCACACATGTTGGCAAGATGTGTGGT	18							
RESULT 6										
ACA04483/C										
ID	ACA04483	standard; DNA; 43 BP.								
XX	ACA04483;									
AC	ACA04483;									
XX										
DT	28-MAY-2003	(first entry)								
XX										
DE	Human secreted and transmembrane protein related probe #9.									
XX										
KW	Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;									
KW	PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;									
KW	PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;									
KW	fibroblast growth factor receptor; cell death; chromosome mapping;									
KW	gene mapping; transgenic animal; knockout animal; gene therapy; tumour;									
KW	obesity; diabetes; insulinemia; vascular permeability;									
KW	cardiac insufficiency disorder; immune response; hearing loss;									
KW	auditory hair cell regeneration; bone disorder; cartilage disorder;									
KW	sports injury; arthritis; gene; ss.									
OS	Homo sapiens.									
XX										
PN	US2003032062-A1.									
XX										
PD	13-FEB-2003.									
XX										
XX	01-FEB-2002; 2002US-00066273.									
PR	26-AUG-1997; 97US-0056974P.									
PR	17-SEP-1997; 97US-0059115P.									
PR	18-SEP-1997; 97US-0059263P.									
PR	19-SEP-1997; 97US-0059588P.									
PR	17-OCT-1997; 97US-0062285P.									
PR	24-OCT-1997; 97US-0062816P.									
PR	24-OCT-1997; 97US-0063082P.									
PR	27-OCT-1997; 97US-0063329P.									
PR	29-OCT-1997; 97US-0063733P.									
PR	21-NOV-1997; 97US-0066364P.									
PR	25-NOV-1997; 97US-0066840P.									
PR	16-DEC-1997; 97US-0069694P.									
PR	09-FEB-1998; 98US-0074086P.									
PR	09-FEB-1998; 98US-0074092P.									
PR	25-MAR-1998; 98US-0079294P.									
PR	08-APR-1998; 98US-0081049P.									
PR	14-JUL-1998; 98WO-US014552.									
PR	10-AUG-1998; 98US-0095998P.									
PR	18-AUG-1998; 98US-0097000P.									
PR	09-SEP-1998; 98US-0099601P.									
PR	10-SEP-1998; 98US-0099803P.									
PR	10-SEP-1998; 98US-0099811P.									
PR	10-SEP-1998; 98US-0099812P.									
PR	10-SEP-1998; 98WO-US018824.									
PR	14-SEP-1998; 98WO-US019093.									
PR	16-SEP-1998; 98WO-US019130.									
PR	17-SEP-1998; 98US-0100058P.									
PR	17-SEP-1998; 98WO-US019437.									
PR	24-SEP-1998; 98US-0101922P.									
PR	28-OCT-1998; 98US-0106032P.									
PR	20-NOV-1998; 98US-0109304P.									
PR	20-NOV-1998; 98WO-US024855.									
PR	25-NOV-1998; 98WO-US025190.									
PR	01-DEC-1998; 98WO-US025108.									
PR	08-MAR-1999; 99WO-US005028.									
PR	23-MAR-1999; 99US-0125778P.									
PR	02-JUN-1999; 99WO-US012252.									
PR	15-JUN-1999; 99US-0139695P.									

20-JUL-1999; 99US-0145070P.
 26-JUL-1999; 99US-0145698P.
 17-AUG-1999; 99US-0149396P.
 01-SEP-1999; 99WO-US020111.
 08-SEP-1999; 99WO-US020594.
 15-SEP-1999; 99WO-US021090.
 15-SEP-1999; 99WO-US021547.
 30-NOV-1999; 99WO-US028313.
 01-DEC-1999; 99WO-US028301.
 02-DEC-1999; 99WO-US028565.
 07-DEC-1999; 99US-0169495P.
 20-DEC-1999; 99WO-US030999.
 05-JAN-2000; 2000WO-US000219.
 18-FEB-2000; 2000WO-US004341.
 18-FEB-2000; 2000WO-US004342.
 22-FEB-2000; 2000WO-US004414.
 01-MAR-2000; 2000WO-US005601.
 02-MAR-2000; 2000WO-US005841.
 09-MAR-2000; 2000WO-US006471.
 20-MAR-2000; 2000WO-US007377.
 30-MAR-2000; 2000WO-US008439.
 15-MAY-2000; 2000WO-US013358.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 11-AUG-2000; 2000WO-US022031.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 01-DEC-2000; 2000WO-US032678.
 28-FEB-2001; 2001WO-US006520.
 30-MAY-2001; 2001WO-US017443.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 15-NOV-2001; 2001US-00002796.

(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Rotstein DA, Desnoyers L, Eaton DL;
 Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Godowski PJ, Gurney AL, Klijavin IJ, Mather JP, Napier MA, Pan J;
 Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW;
 Wood WI, Zhang Z;
 WPI; 2003-341963/32.

New secreted and transmembrane polypeptide for modulating biological activity of a cell expressing the polypeptide, identifying agonists or antagonists of the polypeptide, and as molecular weight markers.

Example 17; Page 60; 254pp; English.

The invention describes an isolated, secreted and transmembrane polypeptide (I), termed PRO polypeptide. (I) is useful for detecting PRO533, PRO301, PRO187, PRO1411, PRO10096, PRO246, PRO6307, PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a cell expressing the polypeptides. The bioactive molecule causes cell death. (iii) Is useful as hybridisation probes, in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, and for the genetic analysis of individuals with genetic disorders, in gene therapy, and for chromosome identification. (i) Or Ab is useful for the preparation of medicament for treating conditions which are responsive to the PRO polypeptide or anti-PRO antibody e.g. a tumour. (i) is useful for treating obesity, diabetes or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for inhibiting tumour growth, enhances vascular permeability and immune response, for inducing regeneration of auditory hair cells and for

CC treating hearing loss in mammals, and for treating bone and/or cartilage
 CC disorders such as sports injuries and arthritis. This sequence encodes a
 CC novel human secreted and transmembrane polypeptide

XX SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 8; Length 43;

Best Local Similarity 76.9%; Pred. No. 2.5e+03;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GCCACATGAGTGGCAAGCGCTGCTG 26

||||| ||||| ||||| ||||| |||||

Db 43 GCCACAGTGTGGCAAGATGTGCTG 18

RESULT 7

ID ACA65624/c

XX ACA65624 standard; DNA; 43 BP.

AC ACA65624;

XX 19-JUN-2003 (first entry)

XX Human secreted/transmembrane protein PRO4999 probe.

KW Human; ss; probe; secreted protein; transmembrane protein; PRO;

KW genetic disorder; gene therapy.

XX OS Homo sapiens.

XX US2003032057-A1.

XX 13-FEB-2003.

XX 15-NOV-2001; 2001US-00002796.

XX 26-AUG-1997; 97US-0056974P.

XX 17-SEP-1997; 97US-0059115P.

XX 18-SEP-1997; 97US-0059263P.

XX 19-SEP-1997; 97US-0059588P.

XX 17-OCT-1997; 97US-0062285P.

XX 24-OCT-1997; 97US-0062815P.

XX 24-OCT-1997; 97US-0063082P.

XX 27-OCT-1997; 97US-0063329P.

XX 29-OCT-1997; 97US-0063733P.

XX 21-NOV-1997; 97US-0066364P.

XX 15-NOV-1997; 97US-0066840P.

XX 16-DEC-1997; 97US-0069694P.

XX 09-FEB-1998; 98US-0074086P.

XX 09-FEB-1998; 98US-0074092P.

XX 25-MAR-1998; 98US-0079294P.

XX 08-APR-1998; 98US-0081049P.

XX 14-JUL-1998; 98WO-US014552.

XX 10-AUG-1998; 98US-0095998P.

XX 18-AUG-1998; 98US-0097000P.

XX 09-SEP-1998; 98US-0099601P.

XX 10-SEP-1998; 98US-0099803P.

XX 10-SEP-1998; 98US-0099811P.

XX 10-SEP-1998; 98US-0099812P.

XX 10-SEP-1998; 98WO-US018824.

XX 14-SEP-1998; 98WO-US019093.

XX 16-SEP-1998; 98WO-US019330.

XX 17-SEP-1998; 98US-0100858P.

XX 17-SEP-1998; 98WO-US019437.

XX 24-SEP-1998; 98US-0101922P.

XX 28-OCT-1998; 98US-0106032P.

XX 20-NOV-1998; 98US-0109304P.

XX 20-NOV-1998; 98WO-US024855.

XX 25-NOV-1998; 98WO-US025130.

XX 01-DEC-1998; 98WO-US025108.

XX 08-MAR-1999; 98WO-US005028.

XX 23-MAR-1999; 98US-0125778P.

XX 02-JUN-1999; 98WO-US012252.

PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US0211547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030399.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein DA, Deanovers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;

XX WPI; 2003-341960/32.

XX Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.

XX Example 17; Page 60; 255pp; English.

XX The invention relates to an isolated, secreted/transmembrane polypeptide,
 CC termed PRO polypeptide, having at least 80% sequence identity to a
 CC sequence selected from any one of the 37 sequences appearing as ABU79779
 CC -ABU79815 or to a sequence encoded by a nucleic acid molecule deposited
 CC under any one of the ATCC numbers given in the specification. Also
 CC included are an isolated nucleic acid molecule having at least 80%
 CC sequence identity to a sequence selected from any one of the 37 cDNA
 CC sequences defined in the specification (or encoding the mature PRO
 CC protein or a PRO protein extracellular domain), a PRO expression vector,
 CC a host cell comprising the vector, PRO fusion proteins, anti-PRO
 CC antibodies and a method for linking a bioactive molecule to a cell
 CC expressing the above PRO polypeptides, the bioactive molecule is a toxin,
 CC radiolabel or an antibody and causes the death of the cell. PRO or the
 CC antibody is useful for modulating at least one biological activity of
 CC cell expressing the above polypeptides. PRO is useful for identifying
 CC agonists or antagonists of PRO, for preparing a variant of PRO, as
 CC molecular weight markers for protein electrophoresis purpose and PRO
 CC nucleic acid is useful for recombinantly expressing those markers. PRO is
 CC also useful as therapeutic agent. PRO is useful in assays to identify

CC other proteins or molecules involved in binding interaction. PRO nucleic
CC acid is useful as hybridisation probes, in chromosome and gene mapping,
CC in generation of antisense RNA and DNA, in the preparation of PRO
CC polypeptide, in gene therapy, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, to construct hybridisation
CC probes for mapping the gene which encodes the PRO and for the genetic
CC analysis of individuals with genetic disorders, for chromosome
CC identification, as a chromosome marker, and for generating probes for
CC polymerase chain reaction (PCR), Northern analysis, Southern analysis and
CC Western analysis. The antibody is useful in diagnostic assays for PRO,
CC e.g. detecting its expression in specific cells, tissues or serum, for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. PRO or Ab is useful for the preparation of medicament for
CC treating conditions which is responsive to the PRO polypeptide or anti-
CC PRO antibody. PRO and PRO nucleic acid are useful for tissue typing. The
CC present sequence is a probe used to isolate cDNA encoding a PRO
CC polypeptide
XX
SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 9; Length 43;
Best Local Similarity 76.9%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GCCACATGAGTGCACAGGCGTCTGGT 26
Db 43 GCCACATGTTGTGCAAGATGTGGT 18

RESULT 8
ADA47233/c
ID ADA47233 standard; DNA; 43 BP.
XX AC ADA47233;
XX DT 20-NOV-2003 (first entry)
XX DE Human secreted/transmembrane polypeptide PRO4999 probe.
XX KW human; ss; probe; secreted protein; transmembrane protein; PRO;
KW VEGF inhibitor; vascular endothelial growth factor;
KW endothelial cell proliferation; T-lymphocyte proliferation;
KW endothelial cell apoptosis; c-fos stimulation;
KW pancreatic beta cell differentiation; chondrocyte proliferation;
KW Glucose uptake; free fatty acid; FFA uptake; tissue typing.
XX OS Homo sapiens.
XX PN US2003044844-A1.
XX PD 06-MAR-2003.
XX PF 01-FEB-2002; 2002US-00066211.
XX PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-00591115P.
PR 18-SEP-1997; 97US-0059283P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.

PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 14-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 17-SEP-1998; 98US-0101922P.
PR 24-SEP-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.

(GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Gurney AL, Kljavin LJ, Mather JP, Napier MA, Pan J;
XX Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW;
XX Wood WI, Zhang Z;
XX WPI; 2003-615775/58.
XX Novel isolated PRO polypeptides e.g. PRO365 and PRO187, useful for
XX inducing redifferentiation and/or proliferation of chondrocytes, and for
XX modulating glucose or free fatty acid uptake by skeletal muscle cells.
XX Example 17; Page 60; 254pp; English.

XX The invention relates to an isolated secreted/transmembrane PRO
CC polypeptide. The polypeptide and its nucleic acid is useful as an
CC inhibitor of vascular endothelial growth factor stimulated proliferation
CC of endothelial cells, as a stimulator of T-lymphocyte proliferation, as
CC an inducer of endothelial cell apoptosis, c-fos and differentiation of
CC pancreatic beta cell precursors into mature cell, for induction of
CC redifferentiation and/or proliferation of chondrocytes and for modulating
CC glucose or free fatty acid (FFA) uptake by skeletal muscle cells. The
CC polypeptide and its nucleic acid is useful for generating transgenic or
CC knock-out animals, for tissue typing and for chromosome identification.
CC The polypeptide is useful in a number of functional biological assays, as
CC molecular weight marker for protein electrophoresis, and as therapeutic
CC agents. The nucleic acid is useful as a hybridisation probe, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC and for the preparation PRO polypeptides. The nucleic acid is also useful
CC as hybridisation probe for a cDNA library to isolate the full length PRO
CC cDNA, to isolate other cDNA and in gene therapy. The nucleic acid is also
CC useful in the construction of hybridisation probes for mapping the gene
CC encoding PRO, and for the genetic analysis of individuals with the
CC genetic disorders. The present sequence represents a human
CC secreted/transmembrane PRO polypeptide probe.

SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 9; Length 43;
Best Local Similarity 76.9%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGAGTGGCAAGCGCTGGT 26

Db 43 GCCACAGTGTGGCAAGATGTGGT 18

RESULT 9

ACD30240/c

ID ACD30240 standard; DNA; 43 BP.

XX ACD30240;

DT 29-AUG-2003 (first entry)

XX Human secreted/transmembrane protein PRO4999 probe.

XX Human; ss; PCR; secreted and transmembrane protein; gene therapy;
KW enterocolitis; gastrointestinal ulceration; skin disease; asthma; primer;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; inflammatory disease; organ failure;
KW rheumatoid arthritis; multiple sclerosis; atherosclerosis; infertility;
KW cardiac injury; birth defect; premature aging; AIDS; cancer;
XX diabetic complication; wound repair.

OS Homo sapiens.

XX US2003044902-A1.

PD 06-MAR-2003.

PF 01-FEB-2002; 2002US-00066193.

XX 26-AUG-1997; 97US-0056974P.

PR 17-SEP-1997; 97US-0059115P.

PR 18-SEP-1997; 97US-0059263P.

PR 19-SEP-1997; 97US-0059588P.

PR 17-OCT-1997; 97US-0062283P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063082P.

PR 27-OCT-1997; 97US-0063329P.

PR 29-OCT-1997; 97US-0063733P.

PR 21-NOV-1997; 97US-0066364P.

PR 25-NOV-1997; 97US-0066840P.

PR 16-DEC-1997; 97US-0069694P.

PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 10-AUG-1998; 98US-0095988P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012552.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Padoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;

DR WPI; 2003-492261/46.

XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing or

PT treating inflammatory diseases, organ failure, atherosclerosis, cardiac
PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
XX disease.

PS Example 17; Page 60; 154pp; English.

XX The invention relates to an isolated native sequence PRO polypeptide
CC (secreted and transmembrane protein) having 80% sequence similarity to
CC one of 37 proteins sequences (or PRO lacking its signal peptide, a PRO
CC extracellular domain (with or without a signal peptide) encoded by a
CC nucleic acids, 80% identical to one of 37 cDNA sequences, shown in the
CC specification. Also included are vectors comprising the PRO nucleic
CC acids, host cells comprising the vectors (used to produce the PRO
CC proteins), a chimeric molecule comprising the PRO polypeptide fused to a
CC heterologous amino acid sequence, an anti-PRO antibody, linking a
CC bioactive molecule to a cell expressing the PRO polypeptides and
CC modulating at least one biological activity of a cell expressing the
CC polypeptides. The PRO polypeptides and nucleic acids are useful in
CC diagnosing or treating enterocolitis, gastrointestinal ulceration, skin
CC diseases associated with abnormal keratinocyte differentiation, e.g.
CC psoriasis or epithelial cancers such as squamous cell carcinoma.
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
CC inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple
CC sclerosis, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, AIDS, cancer, diabetic complications, or
CC mutations in general. The polypeptides are also useful for wound repair
CC and associated therapies concerned with re-growth of tissue. The
CC nucleotide sequences may be used as hybridisation probes in chromosome
CC and gene mapping, or in generating antisense RNA and DNA. PRO nucleic
CC acids are also useful in preparing PRO polypeptides, in assays to
CC identify other proteins or molecules involved in binding reaction, to
CC generate transgenic animals or knockout animals, which in turn are useful
CC in the development and screening of therapeutically useful reagents, for
CC chromosome identification, and tissue typing. The PRO polypeptides and
CC nucleic acid molecules are also useful in gene therapy, and as molecular
CC weight markers for protein electrophoresis purposes. The anti-PRO
CC antibodies may be used in diagnostic assays for PRO, or for the affinity
CC purification of PRO from recombinant cell culture or natural sources. The
CC present sequence is a PCR primer used to isolate a cDNA encoding a PRO
CC protein of the invention

XX SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 9; Length 43;
Best Local Similarity 76.9%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGATGTCACAGCGCTCTGGT 26
||||| ||||| ||||| |||||
DB 43 GCCACAGTTGTGGCAAGATCTGTGGT 18

RESULT 10

ADG63742/c
ID ADG63742 standard; DNA; 43 BP.

XX AC ADG63742;

XX DT 11-MAR-2004 (first entry)

DE Human secreted/transmembrane polypeptide PRO4999 probe.

XX human; ss; probe; secreted protein; transmembrane protein; PRO;

KW VEGF inhibitor; vascular endothelial growth factor;

KW endothelial cell proliferation; T-lymphocyte proliferation;

KW endothelial cell apoptosis; c-fos stimulation;

KW pancreatic beta cell differentiation; chondrocyte proliferation;

KW glucose uptake; free fatty acid; FFA uptake; tissue typing.

XX OS Homo sapiens.

XX PN US2003170721-A1.

XX

PD 11-SEP-2003.
XX
PF 01-FEB-2002; 2002US-00066198.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066164P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095988P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0098601P.
PR 10-SEP-1998; 98US-0098803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 98US-0125778P.
PR 02-JUN-1999; 98WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 30-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.

PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 XX Ferrara N, Fong S, Gao W, Gerber H, Gerratzen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX WPI; 2003-787545/74.
 XX New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide (PRO), for use in recombinantly producing a PRO polypeptide,
 PT as a hybridization probe, and in gene therapy.
 XX Example 17; SEQ ID NO 61; 161pp; English.
 CC The invention relates to an isolated secreted/transmembrane PRO
 CC polypeptide. The polypeptide and its nucleic acid is useful as an
 CC inhibitor of vascular endothelial growth factor stimulated proliferation
 CC of endothelial cells, as a stimulator of T-lymphocyte proliferation, as
 CC an inducer of endothelial cell apoptosis, c-fos and differentiation of
 CC pancreatic beta cell precursors into mature cell, for induction of
 CC redifferentiation and/or proliferation of chondrocytes and for modulating
 CC glucose or free fatty acid (FFA) uptake by skeletal muscle cells. The
 CC polypeptide and its nucleic acid is useful for generating transgenic or
 CC knock-out animals, for tissue typing and for chromosome identification.
 CC The polypeptide is useful in a number of functional biological assays, as
 CC molecular weight marker for protein electrophoresis, and as therapeutic
 CC agents. The nucleic acid is useful as a hybridisation probe, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC and for the preparation PRO polypeptides. The nucleic acid is also useful
 CC as hybridisation probe for a cDNA library to isolate the full length PRO
 CC cDNA, to isolate other cDNA and in gene therapy. The nucleic acid is also
 CC useful in the construction of hybridisation probes for mapping the gene
 CC encoding PRO, and for the genetic analysis of individuals with the
 CC genetic disorders. The present sequence represents a human
 CC secreted/transmembrane PRO polypeptide probe.
 XX SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;
 Query Match 49.7%; Score 16.4; DB 10; Length 43;
 Best Local Similarity 76.9%; Fred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GCCACATGAGTGGCAAGGCGTCTGGT 26
 DB 43 GCCACAGTTGTGGCAAGATGTGTGT 18
 RESULT 11
 ACD42354/c
 ID ACD42354 standard; DNA; 43 BP.
 AC ACD42354;
 XX
 XX
 DT 05-SEP-2003 (first entry)
 DE Novel human secreted and transmembrane protein related probe #8.
 XX Human; secreted and transmembrane protein; PRO; antidiabetic;
 KW ophthalmological; cytostatic; immunostimulant; gene therapy;
 KW vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
 KW protein secretion disorder; pancreas disorder; diabetes;
 KW vascular permeability; retinal neuron cell survival; retinal disorder;
 KW immune response; inflammation; mononuclear cell infiltration;
 KW eosinophil infiltration; apoptosis; neoplastic growth; probe; ss

XX OS Homo sapiens.
 XX US2003040014-A1.
 XX 27-FEB-2003.
 XX 01-FEB-2002; 2002US-0006269.
 XX 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 27-OCT-1997; 97US-0063082P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0066994P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0095998P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 14-SEP-1998; 98WO-US018824.
 PR 16-SEP-1998; 98WO-US019093.
 PR 17-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 25-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025190.
 PR 08-MAR-1999; 98WO-US025108.
 PR 23-MAR-1999; 99WO-US005028.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 07-DEC-1999; 99WO-US028565.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.

PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX WPI; 2003-503396/47.
DR New secreted and transmembrane PRO polypeptides, useful for treating
XX diabetes, retinal disorders and stimulating an immune response.
XX Example 17; Page 60; 254pp; English.
XX The invention describes an isolated polypeptide (I) having at least 80 %
CC amino acid sequence identity to 30 secreted and transmembrane
CC polypeptides. PRO polypeptides are also useful for stimulating
CC hypertrophy of adult heart, for inhibiting vascular endothelial growth
CC factor stimulated proliferation of endothelial cells, stimulating
CC proliferation of stimulated T-lymphocytes and for inducing proliferation
CC of PDB12 pancreatic ductal cells and are thus useful in the treatment of
CC disorders which involve protein secretion by the pancreas, including
CC diabetes. PRO polypeptides are useful for inducing vascular permeability
CC and in enhancing survival of retinal neurons cells and are thus useful
CC for the treatment of retinal disorders. PRO polypeptides are also useful
CC for stimulating an immune response and inducing inflammation by inducing
CC mononuclear cell and eosinophil infiltration at the site of infection of
CC an animal. The PRO polypeptides are further useful for inducing apoptosis
CC in endothelial cells for inhibiting neoplastic growth. This sequence
CC represents a probe used to detect DNA encoding a novel human secreted and
CC transmembrane PRO polypeptide
XX Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;
XX Query Match 49.7%; Score 16.4; DB 10; Length 43;
XX Best Local Similarity 76.9%; Pred. No. 2.Se+03;
XX Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GCCACATGAGTGGCAAGCGCTGTGGT 26
Db 43 GCCACAGTTGTGGCAGATGTGTGGT 18
RESULT 12
ADE41156/c
ID ADE41156 standard; DNA; 43 BP.
XX AC ADE41156;
XX AC ADE41156;
XX 29-JAN-2004 (first entry)
XX Human secreted/transmembrane polypeptide PRO4999 probe.
XX human; ss; probe; secreted protein; transmembrane protein; PRO;
KW VEGF inhibitor; vascular endothelial growth factor;
KW endothelial cell proliferation; T-lymphocyte proliferation;
KW endothelial cell apoptosis; c-fos stimulation;
KW pancreatic beta cell differentiation; chondrocyte proliferation;
KW glucose uptake; free fatty acid; FFA uptake; tissue typing.
XX

OS Homo sapiens.
XX US2003104558-A1.
XX 05-JUN-2003.
XX 23-AUG-2002; 2002US-00226739.
XX 15-JUN-1999; 99US-0139695P.
XX 26-JUL-1999; 99US-0145070P.
XX 26-JUL-1999; 99US-0145698P.
XX 17-AUG-1999; 99US-0149336P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 02-DEC-1999; 99WO-US028565.
XX 07-DEC-1999; 99US-0169495P.
XX 05-JAN-2000; 2000WO-US000219.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 02-MAR-2000; 2000WO-US007377.
XX 10-MAR-2000; 2000WO-US008439.
XX 15-MAR-2000; 2000WO-US013358.
XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.
XX 11-JUN-2000; 2000WO-US015264.
XX 11-AUG-2000; 2000WO-US022031.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 01-DEC-2000; 2000WO-US032678.
XX 28-FEB-2001; 2001WO-US006520.
XX 30-MAY-2001; 2001WO-US017443.
XX 01-JUN-2001; 2001WO-US017800.
XX 20-JUN-2001; 2001WO-US019692.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-JUL-2001; 2001WO-US021735.
XX 15-NOV-2001; 2001US-00002796.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX WPI; 2004-008995/01.
XX New isolated, secreted and transmembrane PRO polypeptides and nucleic
XX acids, useful for diagnosing, preventing and/or treating diabetes
XX mellitus and tumors, such as renal, colon, breast, prostate and/or
XX ovarian tumors.
XX Example 17; SEQ ID NO 61; 259pp; English.
XX The invention relates to an isolated secreted/transmembrane PRO
XX polypeptide. The polypeptide and its nucleic acid is useful as an
XX inhibitor of vascular endothelial growth factor stimulated proliferation
XX of endothelial cells, as a stimulator of T-lymphocyte proliferation, as
XX an inducer of endothelial cell apoptosis, c-fos and differentiation of
XX pancreatic beta cell precursors into mature cell, for induction of
XX redifferentiation and/or proliferation of chondrocytes and for modulating
XX glucose or free fatty acid (FFA) uptake by skeletal muscle cells. The
XX polypeptide and its nucleic acid is useful for generating transgenic or
XX knock-out animals, for tissue typing and for chromosome identification.
XX The polypeptide is useful in a number of functional biological assays, as

CC molecular weight marker for protein electrophoresis, and as therapeutic
 CC agents. The nucleic acid is useful as a hybridisation probe, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC and for the preparation of cDNA libraries. The nucleic acid is also useful
 CC as hybridisation probe for a cDNA library to isolate the full length PRO
 CC cDNA, to isolate other cDNA and in gene therapy. The nucleic acid is also
 CC useful in the construction of hybridisation probes for mapping the gene
 CC encoding PRO, and for the genetic analysis of individuals with the
 CC genetic disorders. The present sequence represents a human
 CC secreted/transmembrane PRO polypeptide probe.

SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 12; Length 43;

Best Local Similarity 76.9%; Pred. No. 2.5e+03;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGATGGCAAGCGCTGGT 26

Db 43 GCCACATGATGGCAAGATGTGGT 18

RESULT 13

ID ADG63591/C
 ADG63591 standard; DNA; 43 BP.

XX AC ADG63591;

XX DT 11-MAR-2004 (first entry)

XX DE Human secreted/transmembrane polypeptide PRO4999 probe.

XX KW human; ss; probe; secreted protein; transmembrane protein; PRO;
 KW VEGF inhibitor; vascular endothelial growth factor;
 KW endothelial cell proliferation; T-lymphocyte proliferation;
 KW endothelial cell apoptosis; c-fos stimulation;
 KW pancreatic beta cell differentiation; chondrocyte proliferation;
 KW glucose uptake; free fatty acid; FFA uptake; tissue typing.

XX OS Homo sapiens.

XX PN US2003180796-A1.

XX PD 25-SEP-2003.

XX PF 01-FEB-2002; 2002US-00066203.

XX PR 26-AUG-1997; 97US-0056974P.

PR 17-SEP-1997; 97US-0059111P.

PR 18-SEP-1997; 97US-0059263P.

PR 19-SEP-1997; 97US-0059588P.

PR 17-OCT-1997; 97US-0062285P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063082P.

PR 27-OCT-1997; 97US-0063329P.

PR 29-OCT-1997; 97US-0063733P.

PR 21-NOV-1997; 97US-0066364P.

PR 25-NOV-1997; 97US-0066840P.

PR 16-DEC-1997; 97US-0069694P.

PR 09-FEB-1998; 98US-0074086P.

PR 09-FEB-1998; 98US-0074092P.

PR 25-MAR-1998; 98US-0079294P.

PR 08-APR-1998; 98US-0081049P.

PR 14-JUL-1998; 98WO-US014552.

PR 10-AUG-1998; 98US-0095998P.

PR 18-AUG-1998; 98US-0097000P.

PR 09-SEP-1998; 98US-0099601P.

PR 10-SEP-1998; 98US-0099803P.

PR 10-SEP-1998; 98US-0099811P.

PR 10-SEP-1998; 98US-0099812P.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 98WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030399.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032878.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.

(GETH) GENENTECH INC.

Askenazi AJ, Baker KP, Botstein DA, Deanovers L, Eaton DL,
 Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 Wood WI, Zhang Z;

WPI; 2004-031858/03.

Seventy four nucleic acids encoding PRO polypeptides, useful for treating
 pericyte-associated tumors,.

Example 17; SEQ ID NO 61; 261pp; English.

The invention relates to an isolated secreted/transmembrane PRO
 polypeptide. The polypeptide and its nucleic acid is useful as an
 inhibitor of vascular endothelial growth factor stimulated proliferation
 of endothelial cells, as a stimulator of T-lymphocyte proliferation, as
 an inducer of endothelial cell apoptosis, c-fos and differentiation of
 pancreatic beta cell precursors into mature cell, for induction of
 redifferentiation and/or proliferation of chondrocytes and for modulating
 glucose or free fatty acid (FFA) uptake by skeletal muscle cells. The

polypeptide and its nucleic acid is useful for generating transgenic or knock-out animals, for tissue typing and for chromosome identification. The polypeptide is useful in a number of functional biological assays, as molecular weight marker for protein electrophoresis, and as therapeutic agents. The nucleic acid is useful as a hybridisation probe, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and for the preparation of cDNA libraries. The nucleic acid is also useful as hybridisation probe for a cDNA library to isolate the full length cDNA, to isolate other cDNA and in gene therapy. The nucleic acid is also useful in the construction of hybridisation probes for mapping the gene encoding PRO, and for the genetic analysis of individuals with the genetic disorders. The present sequence represents a human secreted/transmembrane PRO polypeptide probe.

XX Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 12; Length 43;
Best Local Similarity 76.9%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGATGCGCAAGCGTCTGGT 26
DB 43 GCCACATGTTGTGCGCAAGATGTGGT 18

RESULT 14
ACT165292/c
ID ACT165292 standard; DNA; 25 BP.

XX AC ACT165292;

XX DT 13-OCT-2003 (first entry)

XX DE Human microarray DNA oligonucleotide SEQ ID NO 65283.

XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX DR WPI; 2003-567953/53.

XX PT New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

XX PS Claim 1; SEQ ID NO 65283; 9pp; English.

XX CC The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms,

CC or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 2 A; 9 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 47.3%; Score 15.6; DB 9; Length 25;
Best Local Similarity 81.8%; Pred. No. 5.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCCACATGATGCGCAAGCGTCT 22
DB 22 GCCACATGATGCGCGCGCAC 1

RESULT 15

ADI61875

ID ADI61875 standard; DNA; 40 BP.

XX AC ADI61875;

XX DT 22-APR-2004 (first entry)

XX DE Adenovirus 35 pIX gene promoter deletion PCR primer pIXcosF-2.

XX KW Adenovirus; viral vector; ss; PCR; primer; cytostatic; virucide; pIX;
XX KW E1B 55k; cancer; viral infection; gene therapy; vector stability;
XX KW vector packaging capacity.

XX OS Human adenovirus type 35.

XX PN WO2004001032-A2.

XX PD 31-DEC-2003.

XX PF 24-APR-2003; 2003WO-EP050126.

XX PR 25-APR-2002; 2002WO-NL000281.

XX PR 15-OCT-2002; 2002WO-NL000656.

XX PR 25-NOV-2002; 2002EP-00102631.

XX PA (CRUC-) CRUCELL HOLLAND BV.

XX PI Vogels R, Havenga MJE, Zuidgeest DAT;

XX DR WPI; 2004-082501/08.

XX PT New recombinant adenovirus comprising a functional pIX coding sequence, useful for preparing a medicament for the treatment and prevention of diseases or disorders (e.g. cancer or viral infection) in humans or animal subjects.

XX PS Example 7; SEQ ID NO 27; 181pp; English.

XX CC The invention relates to a recombinant adenovirus comprising a functional pIX coding sequence under the control of an expression sequence comprising part of an E1B 55k sequence capable of increasing expression of the pIX coding sequence in a given packaging cell, relative to the expression of the pIX coding sequence behind its endogenous proximal pIX upstream sequence without the part of the E1B 55k sequence, with the proviso that the part of an E1B 55k sequence does not code for a functional E1B 55k gene product. Also included are an isolated nucleic acid that upon introduction into a suitable packaging cell constitutes the genome of the above recombinant adenovirus, a method for increasing the stability and/or the packaging capacity of a recombinant adenovirus

DR WPI; 2003-689778/65.
 XX New double-stranded short interfering nucleic acid comprises sugar-
 PT modified pyrimidine bases useful for treating infection with hepatitis C
 PT virus.
 XX
 PS Example 3; SEQ ID NO 1594; 183pp; English.
 XX
 CC This invention relates to novel double-stranded short interfering nucleic
 CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
 CC one strand is an antisense strand (ASS) that is complementary to (part
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
 CC modification. The invention may allow development of compounds with
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
 CC interference. The siNA's of the invention may be used to inhibit
 CC replication of HCV, in cells, tissue explants or organisms, for treating
 CC HCV infection and its consequences (liver failure; hepatocellular cancer
 CC and cirrhosis), and also for drug screening, diagnosis, target
 CC identification and validation, genetic engineering, pharmacogenomics,
 CC studying gene function and gene mapping (for example of single-nucleotide
 CC polymorphisms). The chemical modification improves stability, activity,
 CC cellular uptake and/or binding affinity. The siNA can be directed to
 CC conserved regions of HCV genes, so are active against many different
 CC strains. NOTE: This sequence may contain one or more of several
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
 CC modifications are specified in table 3 of the specification (pages 150-
 XX 158).
 XX
 SQ Sequence 21 BP; 4 A; 8 C; 4 G; 2 T; 3 U; 0 Other;
 Query Match 46.7%; Score 15.4; DB 10; Length 21;
 Best Local Similarity 94.1%; Pred. No. 6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 12 GGCAAGGCGTCTGGTGA 28
 DB 17 GCCAAGGCGTCTGGTGA 1
 RESULT 18
 ACI57909
 ID ACI57909 standard; DNA; 25 BP.
 XX
 AC ACI57909;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 57900.
 DE
 XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 XX Homo sapiens.
 OS
 XX US2003104410-A1.
 PN
 XX 05-JUN-2003.
 XX
 XX 15-MAR-2002; 2002US-00098263.
 XX
 XX 16-MAR-2001; 2001US-0276759P.
 PR
 XX (AFFY-) AFFYMETRIX INC.
 XX
 XX Mittmann MP;
 XX
 XX WPI; 2003-567953/53.
 DR
 XX

PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 57900; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, antisense match, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 46.7%; Score 15.4; DB 9; Length 25;
 Best Local Similarity 76.0%; Pred. No. 6.2e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 3 CACATGAGTGGCAAGCGTCTGGTG 27
 DB 1 CACATGAGGCGTCAAGTCGTCGCGAG 25
 RESULT 19
 AAD00911
 ID AAD00911 standard; DNA; 30 BP.
 XX
 AC AAD00911;
 XX
 DT 04-OCT-2000 (first entry)
 XX
 DE PCR Primer KXD to construct humanised antibody H24B4k-1 VL region.
 XX
 KW Humanised antibody; H24B4k-1; human 4-1BB receptor protein; mouse;
 KW light chain variable region; VL; heavy chain variable region; VH; Mab;
 KW monoclonal antibody 4B4-1-1; complementarity determining region; CDR; FR;
 KW framework region; treat; transplant rejection; rheumatoid arthritis;
 KW autoimmune disease; immunosuppressant; antirheumatic; antiarthritic;
 KW PCR primer; ss.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 XX WO200029445-A1.
 FN
 XX 25-MAY-2000.
 XX
 XX 17-NOV-1999; 99WO-KR000689.
 PF
 XX 17-NOV-1998; 98KR-00049177.
 PR
 XX 11-MAY-1999; 99KR-00016750.
 XX
 XX (GLDS) LG CHEM LTD.
 XX
 XX Hong HJ, Park SS, Kang YJ, Kang CY, Yoon SK;

XX WPI; 2000-387750/33.
 XX Humanized antibody specific for human 4-1BB, the composition comprising
 PT the antibody useful for treating autoimmune diseases e.g. rheumatoid
 PT arthritis or as an immuno suppressant to prevent graft rejection.
 XX Example 2; Page 63; 83pp; English.
 XX The present sequence is the PCR primer KXD, used to construct the gene
 CC encoding the humanised antibody H24B4k-1 kappa light chain variable
 CC region (VL). The humanised antibody is specific to human 4-1BB receptor
 CC protein and comprises of the complementarity determining region (CDR) of
 CC mouse monoclonal antibody (MAB) 4B4-1-1, grafted on to a human antibody.
 CC In order to increase the antigen binding affinity of this humanised
 CC antibody, about 10 critical amino acid substitutions are made in the
 CC framework region (FR) of humanised VL, to resemble the mouse antibody. It
 CC functions to block human 4-1BB protein receptor. The humanised antibody
 CC can be used to treat autoimmune diseases, especially rheumatoid arthritis
 CC and for immune suppression in transplant rejection. It acts as an
 CC effective immunosuppressant, by inhibiting T cell activation, without any
 CC adverse side effects
 XX Sequence 30 BP; 6 A; 5 C; 9 G; 10 T; 0 U; 0 Other;
 SQ Query Match 46.7%; Score 15.4; DB 3; Length 30;
 Best Local Similarity 76.0%; Pred. No. 6.4e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 8 GAGTGGCAGGCGTCTGGTGATACC 32
 |||||
 DB 2 GACTGCCAGGTTTGTGTGATACC 26
 RESULT 20
 AAX789229/c
 ID AAT48229 standard; DNA; 33 BP.
 XX
 AC AAT48229;
 XX
 DT 20-OCT-1997 (first entry)
 XX
 DE Chloramphenicol acetyl transferase gene primer.
 XX
 DE att recombination site; core region; mutation; enhance; recombination;
 KW vector; subcloning; regulation; exchange; primer; PCR; toxic gene; ss.
 XX
 OS Synthetic.
 XX
 PN WO9640724-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US010082.
 XX
 PR 07-JUN-1995; 95US-00486139.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA;
 XX
 DR WPI; 1997-065168/06.
 XX
 PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
 PT using recombinant proteins and engineered recombination sites in vitro or
 PT in vivo.
 XX
 PS Example 6; Page 49; 106pp; English.
 XX
 CC AAT48228-29 are primers for amplification of the chloramphenicol acetyl
 CC transferase (CAT) gene. This reporter gene was cloned into a
 CC recombinational cloning gene donor plasmid (containing the uracil DNA
 CC glycosylase gene) using the method and vectors of the invention. The

CC vectors contain recombination sites having a core sequence having at
 CC least one engineered mutation that enhances recombination in vitro in the
 CC formation of a Cointegrate or Product DNA. The nucleic acids, vectors and
 CC methods of the invention are used to obtain chimeric nucleic acid using
 CC recombination proteins and engineered recombination sites in vitro or in
 CC vivo. The improved specificity, speed and yields of the invention
 CC facilitates DNA or RNA subcloning, regulation or exchange useful for any
 CC related purpose, e.g. in vitro recombination of DNA segments, and in
 CC vitro or in vivo insertion or modification of transcribed, replicated,
 CC isolated or genomic DNA or RNA
 XX Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
 SQ Query Match 46.7%; Score 15.4; DB 2; Length 33;
 Best Local Similarity 76.0%; Pred. No. 6.4e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 6 ATGAGTGGCAGGCGTCTGGTGATA 30
 |||||
 DB 32 ATGAGTGGCAGGCGGCGGTATA 8
 RESULT 21
 AAX78962/c
 ID AAX78962 standard; DNA; 33 BP.
 XX
 AC AAX78962;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Oligonucleotide #28 for recombination and cloning method.
 XX
 KW Cloning; donor; recombination site; vector; chimeric; ss.
 XX
 OS Synthetic.
 XX
 PN WO9921977-A1.
 XX
 PD 06-MAY-1999.
 XX
 PF 26-OCT-1998; 98WO-US022589.
 XX
 PR 24-OCT-1997; 97US-0065930P.
 PR 23-OCT-1998; 98US-00177387.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Fox DK;
 XX
 DR WPI; 1999-303011/25.
 XX
 PT New nucleic acid cloning methods.
 XX
 PS Disclosure; Page 166; 185pp; English.
 XX
 CC The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
 CC more desired nucleic acid segments flanked by at least 2 recombination
 CC sites which do not recombine with each other; (2) one or more vector
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do
 CC not recombine with each other; and (3) one or more site-specific
 CC recombination proteins; (b) incubating the combination to transfer one or
 CC more of the desired segments into one or more of the VDMs, thereby
 CC producing one or more desired product molecules (PMs). The methods can be
 CC used for the efficient and specific recombination of NAM segments. They
 CC can be used to generate chimeric DNA or RNA molecules that have the
 CC desired characteristics and/or nucleic acid segments. The methods can
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
 CC are used in the method of the invention
 XX Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
 SQ

Query Match 46.7%; Score 15.4; DB 2; Length 33;
Best Local Similarity 76.0%; Pred. No. 6.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
32 ATGAGTGGCAGGCGGGCGCGTAATA 8

Db

RESULT 22
AAC87893/C
ID ID AAC87893 standard; DNA; 33 BP.
XX
XX AAC87893;
XX
XX
XX 02-MAR-2001 (first entry)
XX
XX
XX
XX Chloramphenicol acetyl transferase PCR primer SEQ ID NO:28.

Query Match 46.7%; Score 15.4; DB 4; Length 33;
Best Local Similarity 76.0%; Pred. No. 6.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGTCTGGTGATA 30
Db 32 ATGAGTGGCAGCGCGGGCGTAATA 8

RESULT 23
AAF55762/c
ID AAF55762 standard; DNA; 33 BP.

Query Match	46.7%	Score 15.4;	DB 4;	Length 33;
Best Local Similarity	76.0%;	Pred. No. 6.4e+03;		
Matches 19: Conservative	0: Mismatches	6: Indels	0: Gaps	0: 0:

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
|||||
db 32 ATGAGTGGCAGGGCGGGCGGTAATA 8

RESULT 24
AAD14456/C
ID AAD14456 standard: DNA: 33 BP.

XX
AC AAD14456;
XX
DT 01-NOV-2001 (first entry)

XX
AC AAD14456;
XX
DT 01-NOV-2001 (first entry)

DE Chloramphenicol acetyl transferase gene amplifying CAT right PCR primer.
 XX
 KW Recombination site; copy number; replicon; recombinatorial cloning;
 KW Chloramphenicol acetyl transferase; CAT; PCR primer; DNA-RNA hybrid; ss.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT misc_RNA 1..11
 FT /*tag= a
 FT /label= RNA
 XX
 PN US6270969-B1.
 XX
 PD 07-AUG-2001.
 XX
 XX 20-JAN-1999; 99US-00233492.
 XX
 PR 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 XX
 PA (INVI-) INVITROGEN CORP.
 XX
 XX Hartley JL, Brasch MA;
 PI
 XX WPI; 2001-488248/53.
 DR
 XX
 XX Methods for apposing nucleic acids comprising an expression signal and a
 PT gene/partial gene, using recombinatorial cloning by incubating the
 PT nucleic acids in the presence of a recombination protein under conditions
 PT for recombination.
 XX
 PS Example 6; Col 29; 76pp; English.
 XX
 CC The invention relates to a method for apposing an expression signal and a
 CC gene or partial gene, using recombinatorial cloning. The method incubates
 CC nucleic acids comprising the expression signal and the gene/partial gene
 CC in the presence of a recombination protein under conditions sufficient to
 CC cause recombination and therefore appose the expression signal and the
 CC gene or partial gene. The methods are useful for apposing an expression
 CC signal and a gene or partial gene using recombinatorial cloning. The
 CC methods are also useful for changing vectors, constructing genes for
 CC fusion proteins, changing copy number, changing replicons, cloning into
 CC phages, and cloning e.g., PCR products (with an attB site at one end and
 CC a loxP site at the other end), genomic DNAs, and cDNAs. The methods are
 CC highly specific, rapid, and less labour intensive than prior art methods.
 CC The present sequence is a PCR primer used for amplifying Chloramphenicol
 CC acetyl transferase (CAT) gene used in the exemplification of the
 CC invention
 XX
 SQ Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
 Query Match 46.7%; Score 15.4; DB 4; Length 33;
 Best Local Similarity 76.0%; Pred. No. 6.4e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
 |||||
 Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8
 RESULT 25
 ACD28423/c
 ID ACD28423 standard; DNA; 33 BP.
 XX
 AC ACD28423;
 XX
 DT 02-OCT-2003 (first entry)
 XX
 DE CAT 5' uracil extension primer CAT right.
 XX
 KW CAT; 5' uracil extension; vector donor DNA; flanking recombination site;
 KW ss; chloramphenicol acetyl transferase; PCR; primer.

XX Synthetic.
 XX US2003064515-A1.
 PN
 XX 03-APR-2003.
 PD
 XX
 PF 30-JAN-2002; 2002US-00058291.
 XX
 PR 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 PR 20-JAN-1999; 99US-00233493.
 PR 02-NOV-1999; 99US-00432085.
 XX
 XX (HART/) HARTLEY J L.
 PA (BRAS/) BRASCH M A.
 XX
 XX Hartley JL, Brasch MA;
 PI
 XX WPI; 2003-540791/51.
 DR
 XX
 XX New Vector Donor DNA molecule for recombinational cloning using
 PT engineered recombination sites, comprises first and second DNA segments
 PT that do not recombine with each other and that contain a Selectable
 PT marker.
 XX
 PS Example 6; Page 17; 71pp; English.
 XX
 CC The invention relates to a vector donor DNA molecule comprising a first
 CC DNA segment and a second DNA segment containing at least one selectable
 CC marker. The first and second segments are separated either by, in a
 CC circular vector donor, a first and a second recombination site, or in a
 CC linear vector donor, at least a first recombination site, where each pair
 CC of flanking recombination sites are engineered and do not recombine with
 CC each other. The nucleic acid molecule, vectors and methods are useful for
 CC moving or exchanging segments of DNA molecules using engineered
 CC recombination sites and recombination proteins to provide chimeric DNA
 CC molecules that have the desired characteristic(s) and/or DNA segment(s).
 CC The present sequence represents the Chloramphenicol acetyl transferase,
 CC CAT 5' uracil extension primer CAT right
 XX
 SQ Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
 Query Match 46.7%; Score 15.4; DB 9; Length 33;
 Best Local Similarity 76.0%; Pred. No. 6.4e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
 |||||
 Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8
 RESULT 26
 ACD28602/c
 ID ACD28602 standard; DNA; 33 BP.
 XX
 AC ACD28602;
 XX
 DT 09-OCT-2003 (first entry)
 XX
 DE CAT 5' uracil extension primer CAT right.
 XX
 KW CAT; 5' uracil extension; cointegrate DNA; flanking recombination site;
 KW ss; chloramphenicol acetyl transferase; PCR; primer.
 XX
 OS Synthetic.
 XX
 XX US2003068799-A1.
 PN
 XX 10-APR-2003.
 PD
 XX
 PF 06-JUN-2002; 2002US-00162879.
 XX

PR 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 PR 20-JAN-1999; 99US-00233493.
 PR 02-NOV-1999; 99US-00432085.
 XX
 PA (INVI-) INVITROGEN CORP.
 XX
 PI Hartley JL, Brasch MA;
 XX
 DR WPI; 2003-540884/51.
 XX
 PT Making Cointegrate DNA molecule, by combining recombination sites
 PT flanking the desired DNA segment in insert donor DNA, with the
 PT recombination sites of vector donor DNA, using site specific
 PT recombination protein.
 XX
 PS Example 6; Page 17; 71pp; English.
 XX
 CC The invention relates to a method of making a cointegrate DNA molecule.
 CC The method is useful for making a cointegrate DNA molecule. The method is
 CC useful for a variety of DNA exchanges, such as subcloning of DNA, in
 CC vitro or in vivo. The method enables efficient and specific recombination
 CC of DNA segments using recombination proteins. The method is highly
 CC specific, rapid and less labour intensive. The improved specificity,
 CC yield and speed of the method facilitates DNA or RNA subcloning,
 CC regulation and exchange useful for other related purposes. Since single
 CC molecules of the recombinations product can be introduced into a
 CC biological host, propagation of the desired product DNA in the absence of
 CC other DNA molecules is more readily realised. Reaction conditions can be
 CC freely adjusted in vitro to optimise enzyme activities. The present
 CC extension represents the chloramphenicol acetyl transferase, CAT 5', uracil
 CC extension primer CAT right
 XX
 SQ Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
 Query Match 46.7%; Score 15.4; DB 9; Length 33;
 Best Local Similarity 76.0%; Pred. No. 6.4e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
 |||||
 DB 32 ATGAGTGGCAGCGGGCGGCGTAATA 8
 |||||
 RESULT 27
 ADA38189/c
 ID ADA38189 standard; DNA; 33 BP.
 XX
 AC ADA38189;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE PCR primer CAT right containing a 12-base 5' extension of uracil bases.
 XX
 KW engineered recombination site; cloning; recombinase; subcloning; attB;
 KW attP; attL; attR; selectable marker; cointegrate; ss; primer; PCR;
 KW DNA/RNA hybrid; CAT right; chloramphenicol acetyl transferase; pACYC184.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 FN US2003054552-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 30-JAN-2002; 2002US-00058292.
 XX
 PR 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 PR 20-JAN-1999; 99US-00233493.
 PR 02-NOV-1999; 99US-00432085.
 XX
 PA (HART/) HARTLEY J L.

PA (BRAS/) BRASCH M A.
 XX
 PI Hartley JL, Brasch MA;
 XX
 DR WPI; 2003-585168/55.
 XX
 PT New Vector Donor DNA molecule, useful for recombinational cloning
 PT purposes, comprises a first and a second DNA segment that contains a
 PT selectable marker and is separated by a pair of flanking, engineered
 PT recombination sites.
 XX
 PS Example 6; Page 18; 72pp; English.
 XX
 CC This invention relates to novel DNA and vectors having engineered
 CC recombination sites for use in a cloning method that enables efficient
 CC and specific recombination of DNA segments using recombination proteins
 CC including recombinases. As such, it provides a method for obtaining
 CC chimeric nucleic acids with the desired characteristics, facilitating DNA
 CC or RNA subcloning, regulation and/ or exchange. The recombination site is
 CC derived from attB attP, attL or attR, where the att site is att1, att2 or
 CC att3. Engineered mutations of the att sites (either one or multiple
 CC mutations) can enhance specificity or efficiency of the recombination
 CC reaction and the properties of the product DNA molecules. Accordingly,
 CC the present invention describes a nucleic acid molecule comprising at
 CC least one DNA segment having at least two engineered recombination sites
 CC flanking a selectable marker and/ or a desired DNA segment. Furthermore,
 CC at least one of the engineered sites must enhance recombination in vitro
 CC to form a cointegrate or product DNA molecule. This oligonucleotide
 CC sequence is the PCR primer CAT right used to amplify the chloramphenicol
 CC acetyl transferase (CAT) gene from plasmid pACYC184, and containing a 12-
 CC base 5' extension of uracil bases in an exemplification of the invention.
 XX
 SQ Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
 Query Match 46.7%; Score 15.4; DB 9; Length 33;
 Best Local Similarity 76.0%; Pred. No. 6.4e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
 |||||
 DB 32 ATGAGTGGCAGCGGGCGGCGTAATA 8
 |||||
 RESULT 28
 AAD60585/c
 ID AAD60585 standard; DNA; 33 BP.
 XX
 AC AAD60585;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Chloramphenicol acetyl transferase gene amplifying primer, CAT right.
 XX
 KW Recombinational cloning; DNA exchange; core region; CAT; PCR; primer;
 KW chloramphenicol acetyl transferase; ss.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT misc_RNA 1..11
 FT /*tag= a
 FT /label= RNA
 XX
 PN US2003100110-A1.
 XX
 PD 29-MAY-2003.
 XX
 PF 02-NOV-1999; 99US-00432085.
 XX
 PR 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 PR 20-JAN-1999; 99US-00233493.
 XX
 PA

PA (HART/) HARTLEY J L.
 PA (BRAS/) BRASCH M A.
 PI Hartley JL, Brasch MA;
 XX WPI; 2003-730143/69.
 DR
 XX New Vector Donor DNA molecule for recombinational cloning using
 PT engineered recombination sites, comprises first and second DNA segments
 PT that do not recombine with each other and that contain a Selectable
 PT marker.
 XX
 XX Example 6; Page 17; 71pp; English.
 XX
 XX The invention relates to a vector donor DNA molecule which comprises
 CC first and second DNA segments that do not recombine with each other and
 CC that contain a selectable marker. The invention also relates to a method
 CC for recombinational cloning using engineered recombination sites. The
 CC invention is useful for moving or exchanging segments of DNA molecules
 CC using engineered recombination sites and recombination proteins to
 CC provide chimeric DNA molecules that have the desired characteristic(s)
 CC and/or DNA segment(s). The present sequence is a PCR primer used for
 CC amplifying chloramphenicol acetyl transferase (CAT) gene. This sequence
 CC is used to illustrate the method of the invention
 XX
 XX Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
 SQ
 Query Match 46.7%; Score 15.4; DB 10; Length 33;
 Best Local Similarity 76.0%; Pred. No. 6.4e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY
 6 ATGAGTGGCAAGGCGTCTGTGTGATA 30
 |||||
 32 ATGAGTGGCAGGCGGGCGGTAATA 8
 Db
 RESULT 29
 ADL93443/c
 ID ADL93443 standard; DNA; 33 BP.
 XX
 AC ADL93443;
 XX
 XX 01-JUL-2004 (first entry)
 XX
 XX Chloramphenicol acetyl transferase (CAT) primer seqid 28.
 XX
 XX recombination protein; recombination site; Insert Donor DNA;
 KW Vector Donor DNA; repression cassette; DNA cloning;
 KW recombination site core region; chloramphenicol acetyl transferase; CAT;
 KW PCR; primer; ss.
 XX
 XX Unidentified.
 OS
 XX US6720140-B1.
 FN
 XX 13-APR-2004.
 PD
 XX 04-FEB-2000; 2000US-00498074.
 PF
 XX 07-JUN-1995; 95US-00486139.
 PR
 XX 07-JUN-1996; 96US-00663002.
 PR
 XX 12-JAN-1998; 98US-00005476.
 XX
 XX (INVI-) INVITROGEN CORP.
 PA
 XX Hartley JL, Brasch MA;
 PI
 XX WPI; 2004-313648/29.
 DR
 XX New composition comprising recombination proteins and isolated nucleic
 PT acid molecule comprising recombination site, useful for moving or
 PT exchanging segments of DNA molecules to provide chimeric DNA molecules.
 XX

PS Example 6; SEQ ID NO 28; 80pp; English.
 XX
 XX The invention describes a composition comprising recombination proteins
 CC and an isolated nucleic acid molecule comprising a recombination site.
 CC The composition comprises one or more isolated recombination proteins and
 CC at least one Insert Donor DNA molecule comprises: at least a first
 CC recombination site, containing at least one mutation, where the mutation
 CC removes one or more stop codons from the recombination site and avoids
 CC hairpin formation; a first recombination site and a second recombination
 CC site where the first and second recombination sites do not recombine with
 CC each other, and at least one Vector Donor DNA molecule comprising a first
 CC recombination site and a second recombination site, where the first and
 CC second recombination sites do not recombine with each other. The Vector
 CC Donor DNA molecule comprises a repression cassette encoding a repressor
 CC and a Selectable marker that is repressed by the repressor where the
 CC Selectable marker and the repression cassette are on different DNA
 CC segments separated from each other by at least one recombination site; at
 CC least a first recombination site containing at least one nucleic acid
 CC sequence selected from a nucleic acid sequence comprising 25 bp (SEQ ID NO. 1-
 CC 16). Also described are: a kit for in vitro cloning of DNA segments
 CC comprising one or more isolated recombination proteins and at least one
 CC Insert Donor DNA molecule; a method for in vitro cloning; a method for
 CC making a reaction mixture; and a reaction mixture made by the method
 CC above. The compositions, methods and kits of the invention are useful for
 CC moving or exchanging segments of DNA molecules using engineered
 CC recombination sites and recombination proteins to provide chimeric DNA
 CC molecules that have the desired characteristics and/or DNA segments. This
 CC sequence represents a primer used to isolate DNA encoding chloramphenicol
 CC acetyl transferase (CAT) used in the creation of a vector for
 CC recombinational cloning.
 XX
 XX Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
 SQ
 Query Match 46.7%; Score 15.4; DB 12; Length 33;
 Best Local Similarity 76.0%; Pred. No. 6.4e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY
 6 ATGAGTGGCAAGGCGTCTGTGTGATA 30
 |||||
 32 ATGAGTGGCAGGCGGGCGGTAATA 8
 Db
 RESULT 30
 AAZ56255
 ID AAZ56255 standard; DNA; 34 BP.
 XX
 AC AAZ56255;
 XX
 XX 15-MAR-2000 (first entry)
 DT
 XX pIVCAT1 construction oligonucleotide sequence SEQ ID NO:24.
 DE
 XX Recombinant negative strand viral RNA template; virus particle;
 KW RNA directed RNA polymerase complex; expression; chimeric virus; vaccine;
 KW packaging; ss.
 XX
 XX Influenza virus.
 OS
 XX Synthetic.
 XX
 XX US6001634-A.
 FN
 XX 14-DEC-1999.
 PD
 XX 29-JUN-1998; 98US-00106377.
 PF
 XX 28-AUG-1989; 89US-00399728.
 PR
 XX 21-NOV-1989; 89US-00440053.
 PR
 XX 22-MAY-1990; 90US-00527237.
 PR
 XX 04-AUG-1992; 92US-00925061.
 PR
 XX 01-FEB-1994; 94US-00190698.
 PR
 XX 01-JUN-1994; 94US-00252508.
 XX

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PA (PALE/) PALESE P.
PA (GARC/) GARCIA-SASTRE A.
XX
PI Palese P, Garcia-Sastre A;
XX
DR WPI; 2000-071660/06.
XX
XX Chimeric virus containing influenza virus RNA segments, useful for
PT expressing heterologous gene products in appropriate host cell systems.
XX
PS Example; Col 65; 67pp; English.
XX
CC The present invention describes a chimeric virus comprising influenza
CC virus containing a heterologous RNA segment from another strain of
CC influenza virus or 8 genomic segments from different strains of influenza
CC virus, with each segment comprising the reverse complement of a mRNA
CC coding sequence operatively linked to a binding site specific for an RNA-
CC directed RNA polymerase of a negative strand RNA virus. The recombinant
CC negative strand virus RNA templates may be used to express heterologous
CC gene products in appropriate host cell systems and/or to construct
CC recombinant viruses that express, package and/or present the heterologous
CC gene product. The expression products and chimeric viruses may be used in
CC vaccine formulations. AAY57746 to AAY57748, and AAZ56234 to AAZ56290,
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 34 BP; 8 A; 5 C; 15 G; 6 T; 0 U; 0 Other;
Query Match 46.7%; Score 15.4; DB 3; Length 34;
Best Local Similarity 76.0%; Pred. No. 6.5e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db ||||| ||||| |||||
7 ATGAGTGGCAGGCGGGCGGTAAATA 31
RESULT 31
AAZ56253
ID AAZ56253 standard; DNA; 34 BP.
XX
AC AAZ56253;
XX
DT 15-MAR-2000 (first entry)
XX
DE CAT gene expression/packaging oligonucleotide SEQ ID NO:22.
XX
KW Recombinant negative strand viral RNA template; virus particle;
KW RNA directed RNA polymerase complex; expression; chimeric virus; vaccine;
KW packaging; ss.
XX
OS Influenza virus.
OS Synthetic.
XX
PN US6001634-A.
XX
PD 14-DEC-1999.
XX
PF 29-JUN-1998; 98US-00106377.
XX
PR 28-AUG-1989; 89US-00399728.
PR 21-NOV-1989; 89US-00440053.
PR 22-MAY-1990; 90US-00527237.
PR 04-AUG-1992; 92US-00925061.
PR 01-FEB-1994; 94US-00190698.
PR 01-JUN-1994; 94US-00252508.
XX
XX (PALE/) PALESE P.
PA (GARC/) GARCIA-SASTRE A.
XX
PI Palese P, Garcia-Sastre A;
XX
DR WPI; 2000-071660/06.
XX
XX Chimeric virus containing influenza virus RNA segments, useful for
PT expressing heterologous gene products in appropriate host cell systems.
XX
PS Example; Col 65; 67pp; English.
XX
CC The present invention describes a chimeric virus comprising influenza
CC virus containing a heterologous RNA segment from another strain of
CC influenza virus or 8 genomic segments from different strains of influenza
CC virus, with each segment comprising the reverse complement of a mRNA
CC coding sequence operatively linked to a binding site specific for an RNA-
CC directed RNA polymerase of a negative strand RNA virus. The recombinant
CC negative strand virus RNA templates may be used to express heterologous
CC gene products in appropriate host cell systems and/or to construct
CC recombinant viruses that express, package and/or present the heterologous
CC gene product. The expression products and chimeric viruses may be used in
CC vaccine formulations. AAY57746 to AAY57748, and AAZ56234 to AAZ56290,
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 34 BP; 8 A; 5 C; 15 G; 6 T; 0 U; 0 Other;
Query Match 46.7%; Score 15.4; DB 3; Length 34;
Best Local Similarity 76.0%; Pred. No. 6.5e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db ||||| ||||| |||||
7 ATGAGTGGCAGGCGGGCGGTAAATA 31
RESULT 32
AAZ56254/c
ID AAZ56254 standard; DNA; 38 BP.
XX
AC AAZ56254;
XX
DT 15-MAR-2000 (first entry)
XX
DE CAT gene expression/packaging oligonucleotide SEQ ID NO:23.
XX
KW Recombinant negative strand viral RNA template; virus particle;
KW RNA directed RNA polymerase complex; expression; chimeric virus; vaccine;
KW packaging; ss.
XX
OS Influenza virus.
OS Synthetic.
XX
PN US6001634-A.
XX
PD 14-DEC-1999.
XX
PF 29-JUN-1998; 98US-00106377.
XX
PR 28-AUG-1989; 89US-00399728.
PR 21-NOV-1989; 89US-00440053.
PR 22-MAY-1990; 90US-00527237.
PR 04-AUG-1992; 92US-00925061.
PR 01-FEB-1994; 94US-00190698.
PR 01-JUN-1994; 94US-00252508.
XX
XX (PALE/) PALESE P.
PA (GARC/) GARCIA-SASTRE A.
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XX
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XX
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CC virus containing a heterologous RNA segment from another strain of

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CC directed RNA polymerase of a negative strand RNA virus. The recombinant
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CC gene product. The expression products and chimeric viruses may be used in
CC vaccine formulations. AAY57746 to AAY57748, and AAZ56234 to AAZ56290,
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 38 BP; 7 A; 16 C; 6 G; 9 T; 0 U; 0 Other;
Query Match 46.7%; Score 15.4; DB 3; Length 38;
Best Local Similarity 76.0%; Pred. No. 6.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 6 ATGAGTGGCAGGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGCGGCGTAATA 8
RESULT 33
AAZ56256/C
ID AAZ56256 standard; DNA; 38 BP.
XX
AC AAZ56256;
XX
DT 15-MAR-2000 (first entry)
XX
DE pIVCAT1 construction oligonucleotide sequence SEQ ID NO:25.
XX
KW Recombinant negative strand viral RNA template; virus particle;
KW RNA directed RNA polymerase complex; expression; chimeric virus; vaccine;
KW packaging; ss.
XX
OS Influenza virus.
OS Synthetic.
XX
PN US6001634-A.
XX
PD 14-DEC-1999.
XX
PF 29-JUN-1998; 98US-00106377.
XX
PR 28-AUG-1989; 89US-00399728.
PR 21-NOV-1989; 89US-00440053.
PR 22-MAY-1990; 90US-00527237.
PR 04-AUG-1992; 92US-00925061.
PR 01-FEB-1994; 94US-00190698.
PR 01-JUN-1994; 94US-00252508.
XX
PA (PALE/) PALESE P.
PA (GARC/) GARCIA-SASTRE A.
XX
PI Palese P, Garcia-Sastre A;
XX
DR WPI; 2000-071660/06.
XX
PT Chimeric virus containing influenza virus RNA segments, useful for
PT expressing heterologous gene products in appropriate host cell systems.
XX
PS Example; Col 65; 67pp; English.
XX
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CC virus containing a heterologous RNA segment from another strain of
CC influenza virus or 8 genomic segments from different strains of influenza
CC virus, with each segment comprising the reverse complement of a mRNA
CC coding sequence operatively linked to a binding site specific for an RNA-
CC directed RNA polymerase of a negative strand RNA virus. The recombinant
CC negative strand virus RNA templates may be used to express heterologous
CC gene products in appropriate host cell systems and/or to construct
CC recombinant viruses that express, package and/or present the heterologous

CC gene product. The expression products and chimeric viruses may be used in
CC vaccine formulations. AAY57746 to AAY57748, and AAZ56234 to AAZ56290,
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 38 BP; 7 A; 16 C; 6 G; 9 T; 0 U; 0 Other;
Query Match 46.7%; Score 15.4; DB 3; Length 38;
Best Local Similarity 76.0%; Pred. No. 6.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 6 ATGAGTGGCAGGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGCGGCGTAATA 8
RESULT 34
ADJ14718/C
ID ADJ14718 standard; DNA; 41 BP.
XX
AC ADJ14718;
XX
DT 20-MAY-2004 (first entry)
XX
DE Debrisoquine 4-hydroxylase (CYP2D6)-related target DNA - SEQ ID 282.
XX
KW SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; target.
XX
OS Unidentified.
XX
PN US2003235848-A1.
XX
PD 25-DEC-2003.
XX
PF 11-APR-2003; 2003US-00411954.
XX
PR 11-APR-2002; 2002US-0371819P.
XX
PA (NEVI/) NEVILLE M.
PA (INDI/) INDIG M D A.
XX
PI Neville M, Indig MDA;
XX
DR WPI; 2004-070577/07.
XX
PT Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT with the primer set and detecting at least one of the footprint regions
XX with the assay probe.
XX
PS Example 3; SEQ ID NO 282; 55pp; English.
XX
CC The invention relates to a novel method for characterising a cytochrome
CC p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC comprises providing a sample with at least Y target sequences, a primer
CC set comprising a forward and a reverse primer sequence for each of the Y
CC target sequences and at least one assay probe configured to detect a
CC footprint region, amplifying the Y target sequences with the primer set
CC and detecting at least one of the footprint regions with the assay probe.
CC The method of the invention may be useful for characterising a cytochrome
CC p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC (cytochrome p450 2D6; CYP2D6)-related target oligonucleotide of the
XX invention.
XX
SQ Sequence 41 BP; 5 A; 20 C; 10 G; 6 T; 0 U; 0 Other;
Query Match 46.1%; Score 15.2; DB 12; Length 41;
Best Local Similarity 85.0%; Pred. No. 8.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 9 AGTGGCAGGCGCTCTGGTGA 28
Db 37 AGTGGCAGGCGGCGCTGGTGA 18

QY 2 CCACATGAGTGGCAAGGGCTCTGGTGATACC 32

Db 3 CCATATGATGAGCAAGGAGACTGCCCATCCC 33

RESULT 40
ADC64088/c
ID ADC64088 standard; DNA; 38 BP.
XX
AC ADC64088;
XX
DT 18-DEC-2003 (first entry)
XX
DE Polyhydroxyalkanoate-related PCR primer #36.
XX
KW polyhydroxyalkanoate-containing structure; PHA-containing structure;
KW PHA synthase; polyhydroxyalkanoate synthase; 3-hydroxyacyl coenzyme A;
KW pigment dispersant; electrophotography toner; laminated structure;
KW OHP film; microcapsule pigment ink; electrophoresis particle;
KW electrophoresis display; colour filter; enzyme; ss; primer; PCR.
XX
OS Unidentified.
XX
XX
PN EP1275728-A1.
XX
PD 15-JAN-2003.
XX
PF 10-JUL-2002; 2002EP-00015374.
XX
PR 10-JUL-2001; 2001JP-00210052.
PR 13-JUN-2002; 2002JP-00172978.
XX
PA (CANO) CANON KK.
XX
PI Nomoto T, Yano T, Kozaki S, Honma T;
XX
XX WPI; 2003-459566/44.
XX
PT Manufacturing polyhydroxyalkanoate-containing structure useful as toner
PT for electrophotography, by immobilizing polyhydroxyalkanoate synthase on
PT base material and synthesizing polyhydroxyalkanoate on base material.
XX
PS Example 16; SEQ ID NO 87; 277pp; English.
XX
CC The invention comprises a method for producing a polyhydroxyalkanoate
CC (PHA)-containing structure. The method involves immobilising a PHA
CC synthase enzyme on a base material surface and then synthesising PHA
CC using 3-hydroxyacyl coenzyme A as a substrate. The method of the
CC invention is useful for manufacturing a PHA-containing structure. The PHA
CC containing structure has a wide range of applications as a variety of
CC functional structures, such as: a pigment dispersant of excellent
CC dispersion stability; a toner for electrophotography of excellent
CC electrostatic property; and the laminated structure as an OHP film. The
CC structure is also useful for microcapsule pigment ink of excellent
CC dispersion stability, an electrophoresis particle for electrophoresis
CC display, and colouring composition for a colour filter. The present DNA
CC sequence represents a PCR primer that was used in the exemplification of
CC the invention.
XX
XX Sequence 38 BP; 8 A; 10 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 45.5%; Score 15; DB 10; Length 38;
Best Local Similarity 67.7%; Pred. No. 9.8e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 CCACATGAGTGGCAAGCGCTCTGGTGATACC 32
DB 38 CAACGTGACCAGCAGCCGCTTTATTGATACC 8

Search completed: November 23, 2004, 17:28:50
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RM 1A54
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